Improving Root Cause Analysis of Bacteriological Water Quality Failures

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Abstract

The goals of drinking water quality monitoring are to assure the safety of water for consumers and to monitor the performance of treatment processes. Water samples are routinely collected from water treatment works (WTWs), service reservoirs and customers' taps. A range of analyses are conducted for physical, chemical and microbiological parameters; including water temperature, free and total chlorine, and bacterial enumeration. Drinking water quality in England and Wales is very high, with 99.96 % compliance with the Regulations in 2011 (Drinking Water Inspectorate, 2012). Of the failures that are measured, approximately half are for bacteriological parameters: coliforms, *Escherichia coli*, *Clostridium perfringens* and Enterococci (UK Water Industry Research, 2006).

The aim of this research was to improve the outcomes of root cause analyses in the event of bacteriological failures and inform future compliance initiatives. It has focussed on explaining non-compliances that were observed under 'normal' operating conditions, that is, those that were not related to reported pipe bursts, severe weather events or major disruptions to WTW processes. This makes the findings of this work applicable to the greater part of water company operating periods.

This research has analysed the failure data for 218 bacteriological non-compliances between 2008 and 2011 from the partner UK water company. One third of these failures were from WTWs or service reservoirs. Coliforms were the most commonly detected indicator organism and often fewer than 10 colony forming units 100 ml^{-1} were counted. The majority of failures had no cause identified; this meant that no action could be taken to prevent a future failure. It was observed that none of the routinely measured parameters alone (free chlorine, turbidity, water temperature, etc.) is a suitable predictor for bacteriological quality and that even with water quality parameters within normal ranges at the time of sampling, non-compliances were still detected. Thus, the development of more effective investigatory tools is needed.

Cross-correlation and self-organising maps (SOMs) were used to determine whether on-line water quality data could be used to inform root cause analyses of bacteriological failures at WTWs and thereby protect the quality of water in reservoirs and at customers' taps downstream. This research demonstrated the first application of these

analyses for this purpose. Cross-correlation is a measure of the similarity of two variables as a function of the time lag between them. SOMs enable the identification of correlations among more than two parameters (without the time element) and help to account for the fact that several parameters may be involved at once in bacteriological compliance. These tools were used to improve the root cause analysis of WTW failures at two sites operated by the partner UK water company. The tools required the raw data to be manipulated prior to analysis, which was considered their principal weakness. Nevertheless, the use of cross-correlation and SOMs highlighted high risk water quality conditions and issues with the operation of the WTWs in the periods preceding the bacteriological failures. The outcomes of the analyses show that these tools can resolve root cause analyses where no cause could be identified through the routine investigations.

The costs of bacteriological failures to the partner UK water company were calculated for the first time. The average costs were an order of magnitude larger than the company had been using in their financial forecasts. The use of accurate costs ensures realistic projections and prevents monetary losses from regulatory operations. The method that was employed has promise for use by other water companies and in other countries that have the same or similar investigatory requirements in the event of bacteriological failures.

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Kate Ellis, December 2013.

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List of Abbreviations Used Throughout Thesis

.csv	File extension, of type Comma Separated Values
.txt	File extension, of type Text
AOC	Assimilable organic carbon
BAA	Bile aesculin agar
BDOC	Biodegradable dissolved organic carbon
BOC	Biodegradable organic carbon
CFU	Colony forming unit
CSU	Carbon Source Utilisation
DNA	Deoxyribonucleic acid
DO	Dissolved oxygen
DPD	Diethyl-p-phenylene diamine
DWI	Drinking Water Inspectorate
EPS	Extracellular polymeric substances
FAME	Fatty Acid Methyl Ester
FCM	Flow cytometry
FTU	Formazin turbidity units
GAC	Granular activated carbon
HDPE	High-density polyethylene
HPC	Heterotrophic plate count
HPC22	Heterotrophic plate counts at 22 °C
HPC37	Heterotrophic plate counts at 37 °C
KAAA	Kanamycin aesculin azide agar
mEA	Membrane Entrococcus agar
MPN	Most probable number
NaN	Not a number
NF	Nanofiltration
NMLG tests	Nitrate, motility, fermentation of lactose and liquefaction of gelatin tests
NOM	Natural organic matter
NTU	Nephelometric turbidity units
PB	Polybutylene
PCR	Polymerase chain reaction
PE	Polyethylene
PVC	Polyvinyl chloride
QMRA	Quantitative Microbial Risk Assessment
SOM	Self-Organising Maps
STW	Severn Trent Water Ltd.
UKWIR	UK Water Industry Research

VBNC	Viable, but non-culturable
WHO	World Health Organization
WIMS	Works Management Master Log
WTW	Water treatment works
XCORR	Cross-correlation function in MATLAB

List of Abbreviations Used in Chapter 6

	Sampling location	Parameter
RawCO	Raw water	Coliforms
RawEC	Raw water	*E. coli*
RawNC	Raw water	Non-coliforms
RawCLOS	Raw water	*C. perfringens*
RawEN	Raw water	Enterococci
RawTurb	Raw water	Turbidity
RawpHSpot	Raw water	Spot-sampled pH
RawpHMon	Raw water	Monitor pH
RawTemp	Raw water	Monitor temperature
ASettCO	Settlement Tank A	Coliforms
ASettEC	Settlement Tank A	*E. coli*
ASettNC	Settlement Tank A	Non-coliforms
ASettTurb	Settlement Tank A	Turbidity
ASettpH	Settlement Tank A	Spot-sampled pH
BSettCO	Settlement Tank B	Coliforms
BSettEC	Settlement Tank B	*E. coli*
BSettNC	Settlement Tank B	Non-coliforms
BSettTurb	Settlement Tank B	Turbidity
BSettpH	Settlement Tank B	Spot-sampled pH
CSettCO	Settlement Tank C	Coliforms
CSettEC	Settlement Tank C	*E. coli*
CSettNC	Settlement Tank C	Non-coliforms
CSettTurb	Settlement Tank C	Turbidity
CSettpH	Settlement Tank C	Spot-sampled pH
DSettCO	Settlement Tank D	Coliforms
DSettEC	Settlement Tank D	*E. coli*
DSettNC	Settlement Tank D	Non-coliforms
DSettTurb	Settlement Tank D	Turbidity
DSettpH	Settlement Tank D	Spot-sampled pH
ABCFiltCO	Filter Block ABC	Coliforms
ABCFiltEC	Filter Block ABC	*E. coli*
ABCFiltNC	Filter Block ABC	Non-coliforms
ABCFiltTurb	Filter Block ABC	Turbidity
ABCFiltph	Filter Block ABC	Spot-sampled pH
DFiltCO	Filter Block D	Coliforms
DFiltEC	Filter Block D	*E. coli*

	Sampling location	Parameter
DFiltNC	Filter Block D	Non-coliforms
DFiltTurb	Filter Block D	Turbidity
DFiltpH	Filter Block D	Spot-sampled pH
GACCO	GAC Filter	Coliforms
GACEC	GAC Filter	*E. coli*
GACNC	GAC Filter	Non-coliforms
GACpH	GAC Filter	Spot-sampled pH
CONCO	Contact Tank	Coliforms
CONHPC22	Contact Tank	Heterotrophic plate counts at 22 °C
CONHPC37	Contact Tank	Heterotrophic plate counts at 37 °C
CONFreeCL	Contact Tank	Spot-sampled free chlorine
CONTotalCL	Contact Tank	Spot-sampled total chlorine
CONTurb	Contact Tank	Turbidity
CONpH	Contact Tank	Spot-sampled pH
BALCO	Balance Tank	Coliforms
BALFreeCL	Balance Tank	Spot-sampled free chlorine
BALTotalCL	Balance Tank	Spot-sampled total chlorine
BALTurb	Balance Tank	Turbidity
BALpH	Balance Tank	Spot-sampled pH
FINCLMon	Final water	Monitor free chlorine
FINFlow	Final water	Flow
FINTurbMon	Final water	Monitor turbidity
FINCO	Final water	Coliforms
FINEN	Final water	Enterococci
FINHPC22	Final water	Heterotrophic plate counts at 22 °C
FINHPC37	Final water	Heterotrophic plate counts at 37 °C
FINCO1L	Final water	1 L coliforms
FINNC1L	Final water	1 L non-coliforms
FINFreeCL	Final water	Spot-sampled free chlorine
FINTotalCL	Final water	Spot-sampled total chlorine
FINTurb	Final water	Spot-sampled turbidity
FINpH	Final water	Spot-sampled pH
Rainfall	Regional	Rainfall
AirTemp	Regional	Air temperature

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1. Introduction

1.1. Background

Bacteria are ubiquitous in environmental media: air, soil, and water, and are present in the digestive tracts of higher organisms. Rainfall, land-slips, atmospheric deposition and ingress can transfer bacteria to surface waters and groundwaters used as sources for drinking water production (Lester and Birkett, 1999). The extent of the treatment required to make water safe for consumption depends on the quality of the source water; key treatment processes for the removal of bacteria include clarification (with coagulation and flocculation) and filtration. Disinfection is the final process in water treatment and is intended to inactivate pathogens before they enter the distribution system (Parsons and Jefferson, 2006). The distribution system conveys drinking water from the water treatment works (WTW) to the consumer via pipes, service reservoirs and disinfection booster stations.

The World Health Organization (WHO) report 'Guidelines for Drinking-water Quality' states that the primary concern of water companies across the world continues to be that of managing microbial hazards to deliver safe drinking water (World Health Organization, 2004). It is also asserted that a systematic approach to water supply is required to ensure microbial safety. The WHO recommends multiple-barrier risk management practices beginning with source water protection, through appropriate and well-operated treatment steps, to management of the distribution system to maintain and safeguard water quality. The Drinking Water Directive requires that water intended for human consumption is 'wholesome and clean'. This principally means it is "free from any microorganisms and parasites and from any substances which, in numbers or concentrations, constitute a potential danger to human health" (Council of the European Communities, 1998).

Waterborne disease is a global phenomenon. Cholera and typhoid are still epidemic across the developing world, largely due to contaminated drinking water sources and inadequate treatment. In the Western world, waterborne pathogens no longer represent the community risk that is found in the developing world. Nevertheless, pathogenic *Escherichia coli*, *Campylobacter jejuni* and *Yersinia enterocolitica* cause diarrhoeal disease, which in the young, elderly and immuno-compromised can result in death (Crittenden *et al.*, 2005). It is thus important to monitor water quality to protect

consumers. Pathogens are rarely isolated from drinking water due to their low numbers under normal circumstances. For this reason, microbiological quality monitoring focuses on indicator organisms (Lester and Birkett, 1999). Routine sampling and analyses are conducted at WTWs, service reservoirs and through randomised point-of-use (customer tap) sampling. The indicator organisms that must be measured under European Standards are *E. coli* and Enterococci; and in many cases 'additional monitoring requirements' are provided for *Clostridium perfringens* and coliform bacteria. The genera that are classified as coliforms include: *Buttiauxella*, *Citrobacter*, *Enterobacter*, *Escherichia*, *Hafnia*, *Klebsiella*, *Leclercia*, *Pantoea*, *Raoultella*, *Serratia* and *Yersinia* (Standing Committee of Analysts, 2009). Positive results in these analyses are indicative of faecal or environmental contamination of treated water and thus all four parameters have prescribed values of 0 cells per 100 ml. Trend analysis is carried out through heterotrophic plate counts (HPCs) at 22 and 37 °C, and any 'abnormal change' requires investigation by the water company. These standards have been determined based on public health considerations and an overall risk analysis (Council of the European Communities, 1998). Routine bacteriological testing is based on culture techniques.

Bacteriological quality failures are rare in England and Wales; annual reports of quality compliance are made to the Drinking Water Inspectorate (DWI). The DWI report for 2009 (Drinking Water Inspectorate, 2010) observed that of the quality failures in England and Wales the majority were due to failures in water treatment processes or for bacteriological parameters. The DWI report is critical of water companies' reactive approach to these failures. UK Water Industry Research's 'Validating the Cause of Coliforms in Drinking Water' report (2009) observed the responses of water companies in England, Wales, Scotland and Northern Ireland to detections of coliforms, *E. coli*, Enterococci and *C. perfringens* in routine analyses. They commented that although all companies responded immediately to investigate the origins of bacteriological test failures, the investigations were not always conclusive and many investigations were closed with the cause unknown. As a result, it meant that actions to prevent future non-compliances could not be taken. If water companies do not know where their bacteriological contamination is coming from, they cannot pro-actively protect consumers and thus their response can only ever be reactive.

This project was commissioned as part of the STREAM Programme to provide insight into the causes of, and factors impacting, bacteriological non-compliance and to evolve guidance for the water industry to prevent failures.

1.2. STREAM Programme

The STREAM Programme is the Industrial Doctoral Centre for the Water Sector and it is funded by the Engineering and Physical Sciences Research Council and companies who sponsor the research projects. The Programme is delivered by five UK universities with centres of excellence in water science and engineering: Cranfield University, Exeter University, Imperial College London, Newcastle University and the University of Sheffield.

This research project was sponsored by Severn Trent Water Ltd. (STW) in collaboration with the University of Sheffield, Imperial College London and the author. The STREAM project title was 'Towards Zero Bacteriological Failures in Distribution Systems'.

1.3. Severn Trent Water

STW delivers 1.9 billion litres of drinking water every day to 7.4 million customers. They operate and maintain 141 WTWs, 485 service reservoirs and 46,000 km of water mains (Severn Trent Water, 2013).

Severn Trent Water has a business target of zero water quality failures in distribution systems in its 25-year plan (Severn Trent Water, 2010). The company exhibits near excellent compliance with regulations. Of the water quality failures that are observed, a greater proportion is for microbiological parameters. For this reason, STW have made significant investment in this research.

1.4. Thesis structure

Chapter 2 provides an overview of techniques for the detection and enumeration of indicator bacteria and the ability of these to inform root cause analyses. The potential sources for indicator organisms and modes for their survival in the distribution system are explored with the aid of an illustrative distribution system. The chapter concludes with the research questions upon which the remaining thesis is based.

Chapter 3 investigates spot-sampling data for STW's bacteriological non-compliances at WTW finals, service reservoirs and customers' taps between 2008 and 2011. Chapter 4 determines the cost of these failures to STW. It includes an overview of sanctions for failures administered by the UK government's Office for Water.

Chapters 5 and 6 study two WTWs which have experienced multiple bacteriological failures. They analyse spot-sampled and archived on-line monitoring data using cross-correlation and self-organising maps to provide insight into the factors that affected compliance at these sites. Chapter 5 utilises data from the final monitoring point only, whilst Chapter 6 also analyses through-plant data.

Chapter 7 assesses the merit of the project to STW in terms of research findings and value for money.

Chapter 8 draws together the key findings of this research; Chapter 9 evaluates the answers to the research questions; and Chapter 10 lays out recommendations for STW, the water industry and research organisations.

1.5. Remit

For the purpose of this research, water quality compliance in the distribution system included samples from WTW finals, service reservoirs and customers' taps. The samples of interest were routine samples, and data from investigations and surveys were excluded.

The microbiological monitoring focussed on coliforms, *E. coli*, *C. perfringens* and Enterococci. Data for HPCs were included with reference to the indicator parameters, but those for oocysts (for example, *Cryptosporidium* sp.), amoebae and algae were not.

The failures studied in this project have been detected under 'normal' operating conditions and were not related to reported pipe bursts, severe weather events or major disruption to WTW processes. 'Normal operating conditions' means that water quality parameters, such as free chlorine and turbidity, were within acceptable limits; and in the distribution system, 'normal' includes undetected leaks. The outcomes of this work are, therefore, applicable to the greater part of water company operating periods.

Chapters 5 and 6 have focussed on the quality of treated water leaving the WTW. The focus on WTWs was for three reasons: 1) the quality of water as it enters the distribution system is a significant factor in the quality of water at downstream service reservoirs and customers' taps; and 2) WTWs have the highest density of on-line monitors and thus provide greater scope for analysis than service reservoirs or district metering areas near customers' properties. Furthermore, the analytical tools have been applied to bacteriological water quality data for the first time and it was important to limit the number of potential causative agents; at WTWs, these could be poor raw water quality, reduced treatment efficacy and inadequate disinfection.

1.6. List of publications

The following publications have been produced over the course of this project:

1. K Ellis, B Ryan, M R Templeton and C A Biggs. (2012). 'Improving Bacteriological Water Quality Compliance of Drinking Water'. IN: D Kay and C Fricker (eds.). *The Significance of Faecal Indicators in Water: A Global Perspective*. Cambridge: Royal Society of Chemistry.
2. K Ellis, B Ryan, M R Templeton and C A Biggs. (2013). 'Bacteriological Water Quality Compliance and Root Cause Analysis: An Industry Case Study'. IN: *Water Science and Technology: Water Supply*. 13 (4), pp 1034-1045.
3. K Ellis, S R Mounce, B Ryan, M R Templeton and C A Biggs. (In Press). 'Use of On-line Water Quality Monitoring Data to Predict Bacteriological Failures'. IN: Procedia Engineering – 12th International Conference on Computing and Control for the Water Industry.

Papers 1 and 2 were based, in part, on the work in Chapter 3 and Paper 3 was derived from the work in Chapter 5.

2. Literature Review

2.1. Introduction

Access to clean, safe drinking water is something that is taken for granted in much of the Western world; yet it is responsible for vast improvements in human health and well-being. Globally, in 2010, approximately 89 % of the population had access to an improved drinking water source (UNICEF and World Health Organization, 2012). Even so, it is estimated that one quarter of all hospital beds worldwide are occupied by patients suffering from a waterborne infection (Straub and Chandler, 2003). The practices that have enabled, and continue to enable, improvements in public health are source water protection, water treatment and distribution, operation and maintenance of water treatment works (WTWs), water quality monitoring and training and education of practitioners (Szewzyk *et al.*, 2000; Parsons and Jefferson, 2006).

The goals of water quality monitoring are to assure the safety of drinking water for consumers and to monitor the performance of treatment processes. Water samples are routinely collected from WTWs, service reservoirs and customers' taps. A range of analyses are conducted for physical, chemical and microbiological parameters; including water temperature, free and total chlorine, and bacterial enumeration. Drinking water quality in England and Wales is very high, with 99.96 % compliance with the Regulations in 2011 (Drinking Water Inspectorate, 2012). Of the failures that are detected, approximately half are for bacteriological parameters (UK Water Industry Research, 2006). It is important to note, that in the Western world, drinking water is not deemed to be a significant source of bacteria in the diet, representing 0.048 – 4.5 % of an individual's total bacterial intake in the USA (Stine *et al.*, 2005). Stine *et al.* (2005) showed that the greatest numbers of heterotrophic plate count (HPC) bacteria and total coliforms were found on raw fruits and vegetables.

The most basic microbiological monitoring tool is the HPC. It is used for monitoring from a wide range of substrates, including drinking water (Ramalho *et al.*, 2001; Srinivasan *et al.*, 2008; Francisque *et al.*, 2009), environmental water (Hoefel *et al.*, 2003), and foodstuffs (Stine *et al.*, 2005). Heterotrophic microorganisms require organic carbon for growth and include bacteria, fungi and protozoa. There are a variety of HPC tests, but they all use agar gels containing organic carbon (Bartram *et al.*, 2003). HPCs are used as a broad indicator of the microbiological quality of a sample and for

detecting significant changes from the normal trend for that sampling location (Francisque *et al.*, 2009; Standing Committee of Analysts, 2012). Regulatory bacteriological monitoring focuses on indicator organisms, because pathogens are rarely isolated from drinking water due to their low numbers under normal circumstances (Lester and Birkett, 1999). The World Health Organization states that a good bacteriological indicator of faecal contamination has the following qualities: the organism is universally present in the faeces of humans and warm-blooded animals in large numbers; it is easily detected using simple methods; it does not grow in natural waters, the general environment or in water distribution systems; it persists in water; and the extent to which it is removed by water treatment processes is similar to that of waterborne pathogens (World Health Organization, 1996). The principal bacteriological indicators in drinking water are coliforms, *Escherichia coli*, *Clostridium perfringens* and Enterococci (Standing Committee of Analysts, 2002).

Coliform bacteria are a broad group of microorganisms that can be found in soil, decaying vegetation, water and faeces. Their presence does not always indicate a threat to health, but may indicate inadequate treatment or disinfection at the WTW or a breach in the distribution system. *E. coli* are considered to be exclusively faecal in origin, and some *E. coli* strains are pathogenic. Enterococci can occur naturally in faeces and do not multiply in the environment, but their numbers are small compared to *E. coli* bacteria. *C. perfringens* can persist in the environment for longer than coliforms, *E. coli* and Enterococci through the formation of spores. They are found in faeces in much smaller numbers than the other indicators. Their correlation with the presence and quantity of pathogens has not been proven (Standing Committee of Analysts, 2002). Positive results in analyses for these bacteria signify environmental or faecal contamination of treated water and all four parameters have prescribed values of zero colony forming units (CFU) 100 ml^{-1} (Council of the European Communities, 1998). Similar regulatory requirements exist throughout the developed world. Table 1 shows high compliance for coliforms and *E. coli* in countries of the UK and the Republic of Ireland, Germany, New York City and the province of Ontario, Canada. The rare occurrence of reported drinking water-related disease outbreaks in the Western world makes it more difficult to develop tools and techniques for the further improvement of compliance.

Table 1: Recent coliform and *E. coli* compliance data from developed world regions that use chlorination as their principal mode of disinfection.

	Coliforms			*E. coli*			
	No. Detections	Total No. Samples	% Compliance	No. Detections	Total No. Samples	% Compliance	Year
England and Wales (Drinking Water Inspectorate, 2012)	554	527607	99.895	42	527300	99.992	2011
Northern Ireland (Drinking Water Inspectorate for Northern Ireland, 2012)	49	58553	99.916	6	58553	99.990	2011
Republic of Ireland (Office of Environmental Enforcement, 2011)	854	15304	94.420	46	15304	99.699	2010
Scotland (Drinking Water Quality Regulator for Scotland, 2012)	128	32500	99.606	2	32498	99.994	2011
Germany (Bundesministerium für Gesundheit, 2011)	549	80297	99.316	59	80214	99.926	2009
New York City (Bloomberg and Strickland, 2012)	45	9944	99.547	0	9944	100.000	2011
Ontario (Stager, 2012)	455	230045	99.802	26	230033	99.989	2010-11

Monitoring for indicator bacteria is currently reliant on culture-based methods, which are cheap and easy, but take at least 24 h to generate a result. It is estimated that between 0.1 and 1.0 % of microorganisms can be enumerated using such methods (Osborn and Smith, 2005; Berry *et al.*, 2006). Research has shown that protozoan and viral pathogens have been detected in waters from which indicator bacteria were absent (Straub and Chandler, 2003). Furthermore, there have been questions raised about the suitability of culture-based methods for monitoring stressed bacteria in drinking water, but thus far, the development of suitable alternatives is in its infancy (Múrtula *et al.*, 2012). Many newer monitoring tools, for example those based on polymerase chain reaction (PCR), have been able to provide insight into the sources and survival of indicator bacteria in drinking water (Pitkänen *et al.*, 2008).

The aims of this review are: to identify the tools and techniques for detecting indicator bacteria in drinking water; and to understand how these bacteria enter, survive in, and spread through water distribution systems.

2.2. Method

This review demonstrates current knowledge and investigative techniques for addressing bacteriological concerns in water distribution systems. Papers and reports were gathered from ScienceDirect, U. S. National Library of Medicine (PubMed), and Severn Trent Water's Library, amongst others. The following principal search terms were used: 'drinking water', 'bacteriological quality', 'biofilm'; 'distribution system', 'chlorination', 'disinfection', and 'monitoring'. The review includes articles published before June 2013.

Figure 1 shows a supply line from a WTW to a service reservoir and marks the off-takes to consumers along the way. It also identifies the pipeline materials and the land-uses between the WTW and the service reservoir. This review will assume that there has been a coliform detection (water quality failure) at the service reservoir. The different bacteriological monitoring techniques, potential sources of indicator bacteria and modes for their survival in the distribution system will be explored with reference to Figure 1.

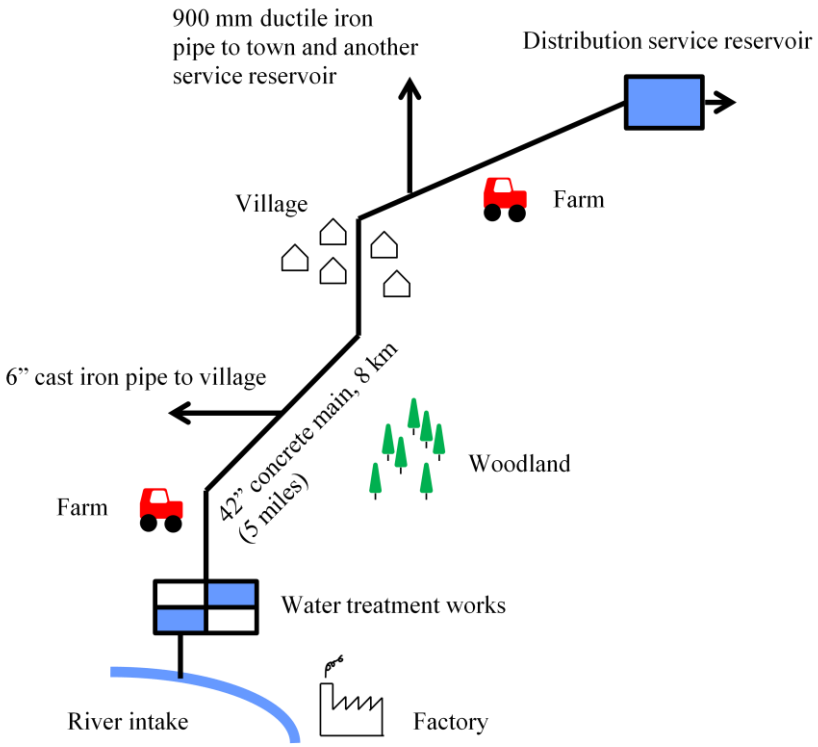

Figure 1: Schematic of a simple supply line and surrounding land-use.

2.3. Bacteriological monitoring

There are a number of potential sources for the failure at the reservoir in Figure 1: the raw water could have suddenly become highly contaminated; treatment at the WTW could have failed and coliforms in the raw water could have passed into supply; the pipeline could be damaged, in which case the coliforms could have come via ingress from either of the farms, the woodland, or the village; the innate bacteriological community could have been disturbed; the sample tap could have been contaminated; or, there could have been poor hygiene practices during sampling or analysis. Determining the potential sources of indicator bacteria in drinking water samples is crucial to being able to prevent future quality failures.

There are two broad groups of tools that could be applied to the identification of microorganisms and their source: phenotypic and genotypic (Scott *et al.,* 2002). Phenotyping methods are based on classification of microorganisms on the basis of traits expressed or physical characteristics; the majority of routine culture-based methods are phenotypic. Genotyping tools separate out bacteria by genera and species on the basis of their deoxyribonucleic acid (DNA); these techniques include PCR and gene-probe luminescence. To date, with the exception of routine bacteriological water quality tools, these techniques have been applied most successfully to point source pollution of natural waters (US Environmental Protection Agency, 2005).

2.3.1. Phenotyping

The routine bacteriological monitoring techniques are all phenotypic. They rely on the use of specific media and confirmation tests to enumerate only the bacteria of interest. These methods are simple to conduct and the results are easy to interpret.

The most basic microbiological monitoring tool is the HPC test. Heterotrophic microorganisms use organic compounds as their energy sources. HPCs can include bacteria, fungi and protozoa (Berry *et al.,* 2006). These organisms grow on media enriched with carbonaceous compounds and they are incubated at 22 and 37 °C. The original use for this monitoring technique was for public health reasons: if more microorganisms grew at 37 °C than at 22 °C, the water was considered to be impacted by faecal pollution (Water Research Centre, 1976). High numbers of HPC microorganisms may not necessarily present a risk to public health (Allen *et al.* 2004; Sartory, 2004). However, counts in excess of 500 CFU ml^{-1} can interfere with coliform and *E. coli* enumeration, especially where membrane filtration methods are used (Allen *et al.*, 2004). For some microorganisms, for example those from oligotrophic environments, such as are found in drinking water distribution systems, these media can be both too rich and lacking in micro-nutrients, thereby inhibiting growth (Reasoner and Geldreich, 1985). Some researchers have found that using HPC tests instead of direct counting (microscopic) methods under-estimates the microbiological load by a factor of 500 (McCoy and Olson, 1986). However, Ramalho *et al.* (2001) found that direct counting and culture-based techniques gave similar results when testing bottled drinking waters. Hoefel *et al.* (2003) observed that correlations between direct counting methods and HPCs were inconsistent; this means that numbers of viable microorganisms cannot be reliably extrapolated from HPCs.

Analyses for coliforms and *E. coli* are the most important routine tests conducted on drinking water samples. Coliform bacteria are oxidase-negative, produce acid from lactose or express β-galactosidase at 37 °C. The genera that are classified as coliforms include: *Buttiauxella*, *Citrobacter*, *Enterobacter*, *Escherichia*, *Hafnia*, *Klebsiella*, *Leclercia*, *Pantoea*, *Raoultella*, *Serratia* and *Yersinia*. *E. coli* are also oxidase-negative, produce acid from lactose or express β-galactosidase but at 44 °C, and they produce indole from tryptophan (Standing Committee of Analysts, 2009). *E. coli* have a strong potential to survive long-term starvation conditions, as typically found in drinking water distribution systems (Szewzyk *et al.*, 2000). There are two groups of methods for enumerating these microorganisms: membrane filtration techniques and most probable number (MPN) techniques. The former are suitable for low to medium turbidity samples, whilst the latter can also be used with more turbid samples (Standing Committee of Analysts, 2009).

The membrane filtration methods are: two membrane filtration technique using lauryl sulphate broth or agar incubated at 37 and 44 °C; and single membrane filtration technique using membrane lactose glucoronide agar incubated at 37 °C. For both methods, an aliquot of water sample, usually 100 ml, is filtered through a cellulose membrane of 0.45 μm pore size. In the two membrane method, both membranes are incubated for 4 h at 30 °C and then one is transferred to a 37 °C incubator and the other to a 44 °C incubator for 14 h. The colonies of both coliforms and *E. coli* are yellow in colour; those that grow at 37 °C are presumptive coliforms, whilst those that grow at 44 °C are presumptive *E. coli*. In the single membrane method, the cellulose membrane is placed on lactose glucoronide agar and incubated for 4 h at 30 °C and then 14 h at 37 °C. As in the previous method, coliform colonies are yellow in colour. *E. coli* bacteria produce β-glucoronidase, which gives their colonies a green colour (Standing Committee of Analysts, 2009).

The MPN methods are: multiple tube MPN technique using minerals modified glutamate medium incubated at 37 °C; and defined substrate MPN technique incubated at 37 °C. The minerals modified glutamate medium is a liquid medium containing lactose and bromocresol purple; bromocresol purple changes to yellow when the solution is acidic and this confirms the presence of coliforms or *E. coli*. In the defined substrate method, coliforms produce β-galactosidase and a yellow colour through the enzymatic breakdown of ortho-nitrophenyl-β-D-galactopyranoside, and *E. coli* produce

β-glucoronidase and both a yellow colour and blue-white fluorescence under ultraviolet light through the enzymatic breakdown of 4-methylunbelliferyl-β-D-glucoronide. The defined substrate MPN technique is regarded as highly specific for coliforms and *E. coli* and confirmation tests are not usually required (Standing Committee of Analysts, 2009).

Coliforms and thermo-tolerant coliform bacteria can be confirmed by testing for lactose fermentation and the production of acid in lactose peptone water at both 37 and 44 °C which indicate the presence of the β-galactosidase enzyme, and for the absence of the oxidase enzyme. *E. coli* can be confirmed similarly, but with the inclusion of a test for indole production in the tryptone water at 44 °C. Other tests enable the direct detection of β-galactosidase at 37 and 44 °C and indole production at 44 °C by growing colonies on nutrient agar supplemented with tryptone and with a disc containing ortho-nitrophyl-β-D-galactopyranoside on the agar surface (Standing Committee of Analysts, 2009).

Whilst most *E. coli* are non-pathogenic, their detection could indicate the presence of *E. coli* O157:H7. *E. coli* O157:H7 can alter its physiological state to enable survival in hostile environments, such as drinking water distribution systems. This makes it difficult to recover from environmental samples (Standing Committee of Analysts, 2009). However, the infective dose of *E. coli* O157:H7 is low and estimated to be less than 100 organisms through ingestion (Szewzyk *et al.*, 2000). It is implicated in the development of haemorrhagic colitis and haemolytic uraemic syndrome; some strains of the bacterium also produce a toxin which is similar to that produced by *Shigella dysenteriae* Type 1. These infections have occasionally been traced back to contaminated water, but are more commonly food-borne, or transferred person-to-person (Szewzyk *et al.*, 2000; Standing Committee of Analysts, 2009). Szewzyk *et al.* (2000) state that most *E. coli* O157:H7 do not ferment lactose, as is typical of *E. coli*, which may mean that they are not detectable using routine methods. Schets *et al.* (2005) suggest that another reason for the rare recovery of indicator bacteria is because of the analysis of 100 ml volumes; in their study of *E. coli* O157:H7 occurrence in private water supplies, the organism was more often isolated from 1 L sample volumes compared to 100 ml samples.

In the UK, Enterococci are considered to be secondary indicators of faecal pollution. Their principal use is to determine the importance of coliform detections in the absence of *E. coli*. Enterococci are Gram-positive cocci which often occur in pairs or short

chains; they are catalase-negative and possess Lancefield's Group D antigen (Standing Committee of Analysts, 2012). (Lancefield's classification is used for species of Streptococci. The Lancefield's Group D bacteria were later re-classified as a separate genus: Enterococci; Schleifer and Kilpper-Bälz, 1984). They grow in the presence of bile salts, in concentrations of sodium azide that are inhibitory to coliform bacteria and most other Gram-negative bacteria, and at a temperature of 44 °C. They also express the enzyme β-glucosidase. Some species of Enterococci have other characteristics that are useful for identification: the ability to survive at 60 °C for 30 min, to tolerate pH 9.6, or to grow in nutrient broth containing 6.5 % sodium chloride (Standing Committee of Analysts, 2012).

There are two principal methods for detecting Enterococci: growth on Enterococcus agar, with or without membrane filtration; or the defined substrate MPN technique. As with the detection of coliforms and *E. coli*, the use of membrane filtration is only suited to water with low-medium turbidity. After incubation at 37 or 44 °C, presumptive Enterococci reduce triphenyltetrazolium chloride to insoluble red formazan to produce red, maroon or pink colonies in membrane Enterococcus agar (mEA). Confirmatory tests are required and these rely on the demonstration of aesculin hydrolysis on bile aesculin agar (BAA) or kanamycin aesculin azide agar (KAAA). Presumptive colonies are either sub-cultured from mEA to BAA or KAAA and incubated at 44 °C for 18 h or, if membrane filtration was employed, by transferring the membrane filter from mEA to plates of BAA or KAAA and incubating at 44 °C for 4 h. There are additional methods for the confirmation of Enterococci following their growth on BAA or KAAA. These include tests for catalase, bile tolerance, heat resistance, growth at pH 9.6 and salt tolerance (Standing Committee of Analysts, 2012).

Clostridium perfringens is also tested for during water quality monitoring. It is considered a subsidiary parameter in comparison with coliforms, *E. coli* and Enterococci. These bacteria form spores which are resistant to environmental stresses and are able to persist in the environment for long periods. *C. perfringens* is associated with faecal contamination and if it is detected in the absence of other indicator bacteria it suggests a remote or intermittent source of water pollution. These bacteria are Gram-negative, anaerobic, spore-forming, and rod-shaped. They are able to reduce sulphite to sulphide at 44 °C in less than 24 h. *C. perfringens* also reduce nitrate, are non-motile, ferment lactose and liquefy gelatine. These bacteria produce the enzyme acid

phosphatase and this is a specific diagnostic characteristic for *C. perfringens* amongst the Clostridia (Standing Committee of Analysts, 2010b).

In monitoring for *C. perfringens* in water of low-medium turbidity, membrane filters are placed on an agar medium containing sulphite, ferric iron and D-cycloserine. The D-cycloserine inhibits other bacteria and reduces the size of the colonies that develop. Plates are incubated under anaerobic conditions at 44 °C. *C. perfringens* typically form black colonies as a result of the reduction of sulphite to sulphide, which then reacts with the ferric iron. These bacteria can be confirmed using either the nitrate, motility, fermentation of lactose and liquefaction of gelatine tests (NMLG tests) or the acid phosphatase test (Standing Committee of Analysts, 2010b).

The tests for coliforms, *E. coli*, Enterococci and *C. perfringens* are simple, low-cost and effective. However, as introduced with *E. coli* O157:H7, some bacteria, and not just pathogens, are able to enter a physiological state which means they do not grow during culture-based testing. This is termed a viable, but non-culturable (VBNC) condition. It is the ability of bacteria to enter this state that has led to culture-based tools being regarded as unrepresentative in the enumeration of stressed bacteria isolated from drinking water (Szewzyk *et al.*, 2000; Hoefel *et al.*, 2003; UK Water Industry Research, 2006; 2009).

The routine culture-based methods are useful for detecting indicator bacteria, but they are not capable of identifying the source of the environmental or faecal contamination. There are additional phenotypic methods that are intended to provide this information. Of these, the three most common are antibiotic resistance, carbon source utilisation (CSU) or fatty acid methyl ester (FAME) analysis.

Bacteria from hosts exposed to antibiotics and not killed by them develop resistance to those antibiotics. Resistance genes can be spread among bacterial communities in the environment (Biyela *et al.*, 2004). Antibiotic resistance produces a selection pressure which can be used to discriminate between faecal bacteria from different host animals (US Environmental Protection Agency, 2005). In Figure 1, faecal bacteria could enter the distribution system through faults in the pipes or connections, enabling ingress close to either of the farms or the village. It is possible that any antibiotics in use at the farms could be identified and resistance tested for in the coliforms cultured in the failing

sample. Identifying antibiotics in use in the human population would be more complex. By narrowing down the potential source of the coliforms, it would be possible to reduce the search area for the ingress point and improve the likelihood of preventing future contamination (Armstrong *et al.*, 1981). In larger and more complex distribution systems, the need to know in advance which antibiotics to test for renders this tool impractical for developing a standard protocol for source identification.

CSU has been applied in environmental water and soil studies with the aim of assessing microbial diversity. It involves introducing microbial suspensions to a range of carbon-based substrates to assess their ability to oxidise the carbon sources, usually in a microtitre plate. Work by Calbrix *et al*. (2005) indicated that more than 1,500 CFU were required per microtitre well (well volume = 150 µl) for reproducible results; Konopka *et al.* (1998) concluded similarly. Furthermore, Garland and Mills (1991), Haack *et al.* (1995) and Calbrix *et al.* (2005) observed that truly representative community fingerprints would require analysis of a large number of samples to compensate for temporal and spatial variability. This tool could be applied to characterise the river supplying the WTW in Figure 1, as well as the farms and woodland along the length of the pipeline. In larger, more complex distribution systems, this would become impractical. The requirement for a high-density of coliforms in a drinking water sample makes this tool inappropriate for monitoring treated water.

FAME analysis has been utilised in a broad range of disciplines: determining food residues in archaeological samples (Koirala and Rosentrater, 2009), distinguishing between strains of flowering plants (Adiguzel *et al.*, 2006), diagnosing fungal infections in hospitals (Peltroche-Llacsahuanga *et al.*, 2000); identifying degrading bacteria on works of art and buildings (Heyrman *et al.*, 1999) and contaminants in food (Whittaker *et al.*, 2003*)*; characterisation of soil bacterial communities (Kozdrój and van Elsas, 2001; Song *et al.*, 2008) and identification of faecal sources and the tracking of these in bathing and shellfish water (US Environmental Protection Agency, 2005). Norton and LeChevallier (2000) applied FAME analysis to the characterisation of drinking water bacterial populations based on water treatment process, application of free chlorine disinfection, and the impact of pipe material. Their findings are explored later in this Chapter. Detection limits can be specified for animal, plant or microbial FAMEs. Whittaker *et al*. (2003) and Lu and Harrington (2010) report that result generation takes approximately 60 hours, or longer if multiple samples are to be analysed. This is longer

than the current culture-based methods take to indicate a failure. Furthermore, it may be difficult to obtain sufficient biomass from drinking water for FAME extraction. Koirala and Rosentrater (2009) highlighted the ability of FAME to detect other contaminants including waxes, resins, tar and pitch. Historically, metal pipes have been protected from corrosion by a variety of linings, including bitumen and coal-tar. These specific linings have now been discontinued in England and Wales due to potential risks to public health from release of polycyclic aromatic hydrocarbons (Salvato *et al.*, 2003). These pipe linings could have been used in the two iron pipes supplying water to the town, village and second service reservoir in Figure 1.

Antibiotic resistance, CSU and most forms of FAME analysis require culture-based growth of microorganisms to ensure ample biomass for identification. It is recognised that any cultivation-based methods of analysis for drinking water quality are limited in their ability to accurately reflect microbial communities (UK Water Industry Research, 2006; 2009).

Culture-based methods have been applied for tracking indicator bacteria through environmental and drinking water systems (Jofre *et al.*, 1995; UK Water Industry Research, 2008). The principal finding from these methods is that indicator bacteria are ubiquitous in natural waters, wastewaters and faecal slurries. They can be used for the identification of potential sites of environmental or faecal pollution, but it is not possible to use them to identify the source of bacteriological contamination.

2.3.2. Genotyping

Genotypic tools for molecular analysis and fingerprinting of DNA are used to identify specific microorganisms. A variety of methods exist that vary in sensitivity and ease of use. There are two broad groups of methods: PCR-based and luminescence/fluorescence methods. Most of the available tools are reliant on culture-grown reference material and enrichment of samples (US Environmental Protection Agency, 2005). Most DNA testing tools cannot provide evidence of the viability or infectivity of an organism they simply confirm its presence (Straub and Chandler, 2003).

The variety of uses for PCR-based methods and the wealth of research into developing these tools indicate that there is potential for their future use in drinking water monitoring. Eichler *et al.* (2006) achieved good characterisation and found that the

distribution system had a stable community throughout their investigation. US Environmental Protection Agency (2005), however, has observed variable success for these tools in other studies and a small number of well-defined markers for the range of faecal sources that would apply across a catchment. These issues need to be resolved to make PCR-based methods standard practice in the water industry. In addition, the reliance on culturing of environmental consortia for the quantification and calibration of these tools still leaves them open to the same bias as traditional water quality assessments, and does not make them faster.

The success of using gene-probe luminescence for identifying faecal bacteria is also variable. Gourmelon *et al.* (2007) found that correct classification of contaminated samples was lower with luminescence than with a PCR-based method. Bastholm *et al.* (2008) and Bukh and Roslev (2010) concluded that gene-probe luminescence was sensitive. The latter achieved a signal from *E. coli* in drinking water at a cell concentration of 100 – 1,000 CFU 100 ml^{-1} without prior concentration or resuscitation. Sensor technologies are constantly developing and there is potential for better system calibration and larger numbers of training samples to overcome the classification issue.

Flow cytometry (FCM) uses specific fluorescent cell stains and can be used as a tool for counting microbial cells in liquid substrates. It has been used to study the life cycle of bacterial cells and to monitor marine phytoplankton, but technical advances are expanding its remit and popularity (Czechowska *et al.*, 2008; Wang *et al.*, 2010). Berney *et al.* (2008) and Hammes *et al.* (2008) recommend the use of FCM for monitoring drinking water quality. Hammes *et al*. (2008) conclude that its sensitivity and speed (the only time expended is in staining cells in the water sample) will benefit WTW operators as they will be able to act more quickly on changes in bacteriological water quality. They observed that FCM detected 1 – 2 log more cells than traditional HPC methods. Berney *et al*. (2008) suggest that FCM could be used as an alternative to HPC measurements. This review found no FCM methods that could specifically identify indicator bacteria or waterborne pathogens.

A wide variety of tools and techniques have been applied to the identification of sources of faecal contamination. In general, these tools have been effective for highly contaminated receptors (US Environmental Protection Agency, 2005; Stapleton *et al.*, 2007), with few showing value for the identification of sources of contamination in

drinking water. The majority of tools require culturing prior to identification, both in the generation of reference libraries and the analysis of environmental samples. This means that they still possess selection bias, do not enable quicker results than traditional media-based methods and may be a more expensive means of achieving the same result. PCR and luminescence/fluorescence methods that do not require sample-enriching prior to analysis have the greatest potential for future application.

Wu *et al.* (2009) observed that there were seven stages in a water quality failure event: (1) potential cause occurred; (2) drinking water was contaminated; (3) abnormalities were sensed; (4) warning signals were generated; (5) warnings were noticed; (6) action was taken; and (7) system function was recovered. At present, culture-based methods are the simplest and cheapest tools available and are well-used within water utilities globally. Using these culture-based tools, stages 4 and 5 occur at least 24 h after the contamination event. Therefore, there is a need to develop reliable, rapid assessment methods that would generate warning signals sooner (Hoefel *et al.*, 2003).

2.4. Sources of indicator bacteria

During a failure investigation, for example in response to the failure at the service reservoir in Figure 1, several steps are taken: re-sampling from the failing sample point, swabbing of the sample tap, and investigations up- and down-stream of the failing sample point. Re-sampling and swabbing check for the persistence of the failure and the potential for false-positives caused by a dirty tap or contaminated local pipe-work (Standing Committee of Analysts, 2002).

2.4.1. Raw water

In Figure 1, the raw water could have been impacted by the factory, as well as run-off from farms along the catchment or sewage outfalls, both treated and from combined sewer overflow spills (Kistemann *et al.*, 2001). Surface water WTWs have a treatment train that includes screening for large particulates, coagulation, flocculation and clarification (by settlement or dissolved air flotation) for small particulates, filtration and disinfection (Parsons and Jefferson, 2006). These treatment processes are intended to render raw water chemically and microbiologically safe for human consumption. Whilst disinfection is the final stage in treatment for the control of bacteria, it does not render water sterile (Sawyer *et al.*, 2003). Its effectiveness is greatly impacted by the ability of upstream treatment processes to remove bacteria. The treatment processes

required for groundwater are focussed more on the removal of metals and organic contaminants. Groundwater is expected to have a lower bacteriological loading and its disinfection is often marginal (Parsons and Jefferson, 2006) – that is, designed to protect water in distribution rather than kill bacteria post-treatment (World Health Organization, 2004).

Several studies have begun to show a link between climate and bacteriological contamination of water supplies. Schets *et al.* (2005) and Pitkänen *et al.* (2008) identified that heavy rainfall was a risk factor in raw water contamination. Both Curriero *et al*. (2001) and Thomas *et al.* (2006) observed that disease outbreaks were more likely to occur within two months of heavy rainfall affecting their source waters. Two months was the time lag between a rainfall event and detection of an outbreak from a groundwater source; the time lag was shorter when a surface water source was impacted (Curriero *et al.*, 2001). Curriero *et al.* (2001) were more rigorous than Thomas *et al*. (2006), because they removed outbreaks of disease that had been linked back to contaminated taps and cross-connected water supplies. Half of the remaining failures coincided with an extreme weather event. Potential breaches in the distribution system were not considered by Curriero *et al*. (2001) or Thomas *et al.* (2006); these could also have been impacted by rainfall.

2.4.2. Ingress

Infrastructure design should prevent drinking water contamination by environmental water adjacent to distribution pipes (van Lieverloo *et al.*, 2007). However, the distribution system can become compromised through age, damage, operational practices or poor maintenance. If cracks or holes develop in the pipe-work they can allow the ingress of contaminated water into the pipe (Fricker, 2003; Besner *et al.*, 2011). In pressurised distribution systems, insensitive operation of valves (rapid opening or closing) or sudden increases in water flow rate, for example during a burst, can cause depressurisation in the distribution system. This can weaken damaged portions of the network and allow the pulse of negative pressure to draw in environmental water surrounding the pipe. Once the pulse has passed, the damaged pipe will leak (Besner *et al.*, 2011; Collins *et al.*, 2012). It has been estimated that 6.5 – 24.6 % of water transmitted in the distribution system is lost via leakage (Ghazali *et al.*, 2012).

Work by Helbling and VanBriesen (2008) sought to determine whether free chlorine monitors could be used to determine whether water supplies had been compromised through ingress events. They noted a reduction in monitored free chlorine when they introduced *E. coli* suspension to their laboratory-scale distribution system in a simulated ingress event. Wojcicka *et al.* (2008) observed that the addition of particulate matter from various environmental sources also resulted in consumption of chlorine residual. In reality, if soil and wastewater particulate matter enter the distribution system through ingress, bacteria will enter as well (Besner *et al.*, 2011).

If there had been an incident of ingress along the length of the distribution system in Figure 1, the microorganisms could have come from either of the farms, from the village, the woodland or the land in between these sites. Bacteriological monitoring tools are not yet able to identify the source of indicator organisms (Fuchs and Riehle, 1991; Gao *et al.*, 2005). If the system is pressurised, the location of the ingress point could be identified using audible leak detection (American Water Works Association, 1999; Bimpas *et al.*, 2010) or through prior strategic placement of water pressure sensors in the distribution system (Farley *et al.*, 2011).

2.4.3. Biofilm

Bacteria can enter the distribution system in low numbers from the environment and source water (Geldreich *et al.*, 1977) and are able to persist through the formation of biofilms. All surfaces within a system are covered by biofilms, from the WTW, through the pipelines and plumbing to the tap (Szewzyk *et al*., 2000; Deines *et al.*, 2010; Lautenschlager *et al.* 2010). Biofilms are complex communities made up of varying consortia of microorganisms, mostly bacteria, but also fungi, algae, protozoa and amoebae held together in a matrix of extracellular polymeric substances (EPS) (James *et al.*, 1999; Berry *et al.*, 2006; Gamby *et al*., 2008; Gouider *et al.*, 2009). Biofilm formation begins with adsorption of carbohydrates and organic acids from the bulk water, then proteins and polymers adhere, and lastly microorganisms. Initially microorganisms colonise as individual cells separated by empty spaces and then they spread to cover the surface (Gamby *et al.*, 2008). Biofilm formation has implications not just for bacteriological compliance but also bio-corrosion, discolouration and taste and odour quality criteria (Al-Jasser, 2007; Meckes *et al.*, 2007; Rubulis and Juhna, 2007; Vreeburg and Boxall, 2007; Hu *et al*., 2008; Gouider *et al.*, 2009; Deines *et al.*,

2010). Cell detachment is part of the normal life cycle of the biofilm enabling its stabilisation and spread (Dukan *et al.*, 1996; Hu *et al.*, 2008; Deines *et al.*, 2010).

There are four detachment processes that lead to cells leaving the biofilm: (1) abrasion which occurs when there are collisions with other surfaces; (2) grazing detachment follows consumption of part of the biofilm by higher organisms; (3) erosion is the continual loss of cells or small groups of cells from the biofilm; and (4) sloughing is the loss of discrete portions of biofilm. The cells are subsequently entrained in the bulk water (Moore *et al.*, 2000). The strength of biofilms is impacted by chemical and physical factors and its level of maturity (Berry *et al.*, 2006).

Whilst Shui-Li *et al.* (2007) and Blanch *et al.* (2007) concluded that pathogens did not significantly interact with biofilms, many researchers are of the opinion that they represent an important 'reservoir' in distribution systems (Cooper *et al.*, 2007; Juhna *et al.*, 2007; Lehtola *et al.*, 2007; Obst and Schwartz, 2007; Gião *et al.*, 2008; Helmi *et al.*, 2008; Gião *et al.*, 2010). Rogers *et al.* (1994) suggest that there is a pipe material-dependency in the interactions of pathogens with the biofilm; for example, pathogens were not detected in biofilms grown on copper, but were present in those developed on plastics. Torvinen *et al.* (2007) observed that survival of pathogens in biofilms was impacted by the presence of competing microorganisms, to the pathogens' detriment. Blanch *et al.* (2007) and Obst and Schwartz (2007) isolated pathogenic and faecal bacteria from biofilms despite their absence in treated water; they suggested that biofilms act like a memory of past contamination and treatment breakthrough. Lehtola *et al.* (2007) observed the same phenomenon at laboratory-scale.

No long-term temperature, water chemistry and disinfection studies have been completed to assess the importance of seasons when determining biofilm management measures. Gamby *et al.* (2008) observed that biofilm colonisation took 12 days at 20 °C and only a few days at 37 °C at the laboratory-scale; these water temperatures would be rare to non-existent in the UK context. The World Health Organization (2004) recommends that distributed water is maintained at below 15 °C to control microbiological growth in the distribution system. Even with this recommendation, the observation that pathogenic *E. coli* are able to grow at temperatures ranging from 8 to 48 °C (Szewzyk *et al.*, 2000) means that achieving a temperature that can serve to restrict general bacterial growth may not be sufficient to prevent the growth of

pathogens. Seasonal differences have been observed in the occurrences of faecal coliforms and *E. coli*. Blanch *et al.* (2007) showed that most coliforms exhibited counts greater in spring than summer, summer than autumn and autumn than winter; but *E. coli* counts had the following profile: summer > spring > winter > autumn. It is notable that neither *E. coli* nor coliforms occur according to a strict temperature pattern. This demonstrates that factors other than temperature are involved in the seasonal growth of coliforms and *E. coli*, for example, nutrient availability or competition. A similar conclusion was reached after observations of seasonal HPCs by Kerneïs *et al*. (1995).

The conclusion that biofilm caused the failure at the reservoir in Figure 1 would most likely be reached by draining the reservoir and conducting an internal inspection. Swabbing and analysing the internal surfaces of the reservoir may demonstrate that the biofilm is harbouring indicator organisms. Swabs for microbiological analyses are less often applied to the pipes themselves, but may be used to assess pipe-work local to the sample tap (Standing Committee of Analysts, 2010a).

2.4.4. Contamination at the sampling facility

Bacteria can be transferred to the tap surfaces through human or animal contact, splash-back from contaminated water, or carriage in air currents (Eboigbodin *et al.*, 2008). Taps in customers' homes are often warmer than those at WTWs or service reservoirs, which promotes the growth and survival of bacteria (Lautenschlager *et al.*, 2010). However, even dedicated sampling facilities can become contaminated, especially if they are inadequately maintained or protected (Standing Committee of Analysts, 2010a).

Studies in hospitals have traced the source of infections back to taps from which water was drawn for consumption or cleaning purposes (Ferroni *et al.*, 1998; Muscarella, 2004; Horcajada *et al.*, 2006). These studies indicate that the tap can serve as a reservoir for environmental or pathogenic bacteria.

Clear protocols are laid out both for the collection of samples and their subsequent analysis (Standing Committee of Analysts, 2002; 2010a). The aim of these protocols is to ensure that samples are representative of the water being investigated, are transported and stored appropriately and are not contaminated during sampling or analysis. Samplers are required to use correctly sterilised sample bottles. They must also employ

appropriate tap flushing (where taps are not constantly running) and disinfection processes. Generally this involves flushing the tap to dislodge any debris, sediment or biofilm and applying a suitable disinfection protocol prior to sampling. The disinfection can be by application of a chlorine-based solution with 1 % available chlorine or, if the taps are solid metal with no plastic fittings, they can be flame disinfected (Standing Committee of Analysts, 2010a).

Contamination of the reservoir sample tap in Figure 1 could be tested for by swabbing the tap and analysing for indicator bacteria.

2.4.5. Poor hygiene practice by samplers or analysts

The Standing Committee of Analysts places a high level of responsibility on those who train, audit and monitor samplers and analysts for ensuring that proper hygiene is maintained (Standing Committee of Analysts, 2010a). As detailed above, samplers must take care to use sterile bottles and correct tap disinfection protocols. Furthermore, it is recommended that laboratories monitor the working environment to rule out contamination of agar plates during preparation. Routine assessment of the sterility of newly prepared media is encouraged to ensure that this is not a source of contamination either (Standing Committee of Analysts, 2002). Internal and external quality control procedures should be conducted to be certain of the reproducibility of results between analysts and between laboratories (Standing Committee of Analysts, 2002).

Emphasis is made on several occasions in both guidance documents (Standing Committee of Analysts, 2002; 2010a) of the need to instruct samplers and analysts in good hygiene practices. The importance of hand-washing and personal hygiene is reiterated. The requirement to ensure work-surfaces are thoroughly cleansed on a regular basis is also detailed (Standing Committee of Analysts, 2002).

This review found no research into the likelihood of water quality monitoring failures being related to sampler or analyst contamination. This is a sensitive issue, the investigation of which would likely cause offence; therefore it means that such risks can only be hinted at. Laboratories that do conduct environmental hygiene testing should have the records to demonstrate their risk of sample contamination. Popovska *et al.* (2011) identified that there was a need to continuously train laboratory staff in appropriate hygiene practices, as they found bacteriological surface contamination

during routine and spot-check inspections. Seaman and Eves (2010) and Worsfold and Griffith (2003) found that the benefits of training food handling staff were short-lived due to it typically being a staff induction activity, without post-training support and refresher courses. Worsfold and Griffith (2003) also noted that hand-washing and personal hygiene protocols were poorly documented, often not highlighted in the workplace with appropriate signage, and reinforcement strategies were lacking. Egan *et al.* (2007) observed that there was a need for training methods that were proven to change behaviour rather than merely imparting knowledge to participants. They also commented that training was more effective when managers took part in the courses. A review by Pittet (2001) identified several barriers to the utilisation of appropriate hand hygiene amongst hospital employees. These included: skin irritation, inaccessible hand cleansers and sinks, risk of offending patients, having gloves on, forgetfulness, ignorance of hygiene guidelines, lack of time, high workload and under-staffing, and lack of proof that hand hygiene practices make a difference to hospital infection rates. Many of these barriers could play a part in reduced application of strict hygiene practices when collecting or analysing samples; especially when collecting from customers' taps. The conclusion of both Pittet (2001) and Seaman and Eves (2010) was that single session training for hygiene practices, which was the most common training mode used, was frequently ineffective in the long-term. They observed a lack of post-training support and evaluation of effectiveness.

If a rigorous and well-accepted system of staff hygiene monitoring was in place, it would be possible to identify whether the sampler, analysts or laboratory cleanliness impacted the failure at the service reservoir in Figure 1.

2.5. Survival of indicator bacteria in the distribution system

2.5.1. Disinfectants

Disinfection is, typically, the final unit process at the WTW. Its purpose is to prevent the spread of waterborne disease (Sawyer *et al*., 2003). The process has been shown to result in small numbers of injured bacteria entering the distribution system (LeChevallier *et al.*, 1985). However, McFeters *et al.* (1986) found that 96.8 % of coliforms in treated water were injured but not dead. Under the correct environmental conditions of nutrition and temperature injured microorganisms can recover (LeChevallier *et al.*, 1985). Disinfection efficacy is dependent upon the performance of the upstream treatment processes. Of particular importance are the removal of

significant numbers of bacteria and interfering compounds, such as turbidity, organic carbon and ammonia, which exert demand on oxidising agents. The most common chemical disinfectants are chlorine, compounds of chlorine such as chloramines and chlorine dioxide, and ozone. Physical disinfection includes such treatments as membrane filtration, heat treatment or ultraviolet light (Parsons and Jefferson, 2006). Chlorine and chloramines enable residual disinfection to be maintained through the distribution system, which discourages bacterial re-growth and reduces the impact of breaches in integrity (Victoreen, 1977; Damikouka *et al.*, 2007). The Water Supply (Water Quality) Regulations 2000, in England and Wales, require a residual in treated drinking water; final disinfection with chlorine or chloramines must be provided by water companies (Her Majesty's Stationery Office, 2000).

2.5.1.1. Chlorine

Chlorine is the most common chemical disinfectant employed in water treatment because of its ease of application and high inactivation potential. A further benefit is that when dosed to above the water demand, a chlorine residual is maintained in the water to protect it in the distribution system (White, 1999). Chlorine is supplied as either liquefied chlorine gas, or liquid or solid sodium hypochlorite. The available chlorine in all three instances dissolves in water to form hypochlorous acid (HOCl) and hypochlorite ions (OCl^-) – both of which are involved in the disinfection process (Parsons and Jefferson, 2006). The first and second dissociations (of chlorine gas) are shown in equations 1 and 2:

(1) $Cl_2 + H_2O \rightarrow HCl + HOCl$
(2) $HOCl \rightarrow H^+ + OCl^-$

Chlorine kills cells by penetrating the cell wall and damaging the cytoplasm. It diffuses more easily into cells as HOCl than as OCl^-; therefore HOCl is a more efficient disinfectant. The second dissociation of chlorine becomes apparent in high pH waters. Since the pH of water at WTWs is rarely in the control of operators, dosing to 0.5 – 1.0 mg l^{-1} after treatment is expected to leave a residual in the water at the customer's tap (Parsons and Jefferson, 2006).

The disinfectant residual can be consumed by pipe materials, biofilms, free-living bacteria, scales and chemicals in the water (Levi, 2004; Al-Jasser, 2007). Chlorine is a

potent oxidising agent and is consumed by reactions with other compounds such that little disinfection is achieved until doses in excess of the chlorine demand of the water are applied (Sawyer *et al.*, 2003). Its reactivity with organic molecules in treated water forms disinfection by-products (DBPs), with trihalomethanes and haloacetic acids typically found at the highest concentrations. DBPs are a concern because of their potential carcinogenicity and other health risks. For this reason, water companies must ensure that disinfection is applied in adequate doses, and boosted at appropriate locations, to control microorganisms, and also minimise DBP formation (Crittenden *et al.*, 2005; Parsons and Jefferson, 2006).

A number of studies have suggested that 0.3 mg l^{-1} free chlorine controls re-growth in distribution and offers some protection against ingress of bacteria (Mahto and Goel, 2008; Francisque *et al.*, 2009; Wang *et al.*, 2009). However, Norton and LeChevallier (2000) observed that biofilms still developed in drinking water with a free chlorine concentration of 2.0 mg l^{-1} and several other studies concluded that chlorine residuals have little impact on biofilm bacteria in distribution (Deborde and von Gunten, 2008; Helbling and VanBriesen, 2008; Chow *et al.*, 2009). Chien *et al.* (2009) and Chow *et al.* (2009) concluded that chlorination increased the biofilm re-growth potential of distributed water because of the oxidising of organic carbons to more biodegradable and assimilable compounds.

Biofilm growth enhances microbial resistance to disinfection (LeChevallier *et al.*, 1988b; Berry *et al.*, 2006; Deborde and von Gunten, 2008). Szewzyk *et al*. (2000), Berry *et al.* (2006) and Bichai *et al.* (2008) comment that the mechanisms for resistance are not fully understood but they suggest several potential modes: evolved disinfection resistance from past treatment failures, protection due to the EPS matrix, survival in a VBNC state, and harbouring by amoebae and protozoa. Morrow *et al.* (2008) observed that bacteria associated with the biofilm were more difficult to disinfect than those in the bulk water; likewise, Deborde and von Gunten (2008) comment that free chlorine exhibits low activity upon the biofilm, but is beneficial for controlling microorganisms released from it. Sartory and Holmes (1996) observed heightened chlorine sensitivity in coliforms removed from biofilms when compared to those isolated from bulk water. They concluded that disinfection resistance is a function of the EPS matrix and not the organisms themselves. Srinivasan *et al*. (2008) showed that increasing chlorine concentration decreased the ratio of culturable bulk water to biofilm bacteria; they also

suggest that at the extremities of the system, where residual chlorine may be at or near 0.0 mg l^{-1}, bacteria suspended in the bulk water dominate. This may additionally be the case for storage tanks and reservoirs with long residence times and lower chlorine residuals.

The rate of chlorine decay increases with water temperature (Sawyer *et al.* 2003; Parsons and Jefferson, 2006). Francisque *et al.* (2009) concluded that when water temperatures were higher, residual free chlorine concentrations should be increased. They observed a greater proportion of cases with free chlorine lower than 0.3 mg l^{-1} when temperatures were above 18 °C and that when disinfectant concentrations were below 0.3 mg l^{-1} the probability of exceeding their HPC standard of 50 CFU ml^{-1} increased significantly. They also noted that when free chlorine fell below 0.15 mg l^{-1}, the risk of exceeding 50 CFU ml^{-1} was greater than 50 % regardless of temperature.

Booster dosing of chlorine is useful for avoiding excessive doses near to the WTW whilst ensuring a stable and continuous residual for customers at the furthest reaches of the network (Simms *et al.*, 1998; Parks, 2008). Suitable, secure points for booster chlorination may be obtained through modelling of the distribution system. Consideration must be given to the changing or mixing of different source streams and the impact that these may have on the resultant residuals (Chambers *et al*, 2004). Parks (2008) demonstrated through modelling exercises that booster chlorination systems must be tailored to specific distribution systems to ensure water is aesthetically and microbiologically satisfactory.

2.5.1.2. Chloramines

Chloramination is achieved by adding ammonium sulphate, either mixed with the chlorine, or a short time after chlorine has been dosed. Chloramines are less potent disinfectants but have higher stability making them beneficial for long distribution systems or those with slow turnover (Parsons and Jefferson, 2006). By introducing the ammonium sulphate after the chlorine dose, the process can utilise the greater potency of the chlorine, reducing the risk of inadequate disinfection. The reactions between hypochlorous acid and ammonia form three chloramine compounds: first, monochloramine (NH_2Cl); second, dichloramine ($NHCl_2$); and third, trichloramine (NCl_3), shown in equations 1 to 3. As with chlorination, the rate of reaction is affected by pH and the HOCl concentration (Parsons and Jefferson, 2006).

(1) $NH_4^+ + HOCl \rightarrow NH_2Cl + H_2O + H^+$

(2) $NH_2Cl + HOCl \rightarrow NHCl_2 + H_2O$

(3) $NHCl_2 + HOCl \rightarrow NCl_3 + H_2O$

Treatment with chloramines requires careful control as it can lead to odour complaints; the presence of free ammonia in the pipeline can result in the growth of nitrifying bacteria and subsequent failure of nitrate and nitrite standards (Cunliffe, 1991; Yang *et al.*, 2007; Zhang and Edwards, 2009). Chow *et al.* (2009) found that biofilm re-growth potential was lower when using chloramines and LeChevallier *et al.* (1988) observed that chloramines were more effective in penetrating biofilms than chlorine. LeChevallier *et al.* (1988) also noted that combined chlorine disinfection resulted in reduced sloughing and water discolouration. This finding is supported by Zhang and Edwards (2009) who found that chloramines reduced HPCs in distributed water. Their work concluded that in systems without nitrifying bacteria, chloramines are more persistent and reduce pipe corrosion, but where nitrification risk has been identified, chlorine is better for controlling microbial re-growth.

Approximately two thirds of medium to large chloraminated distribution systems in the USA experience nitrification (Dykstra *et al.*, 2007). Water companies that use chloramines as their residual disinfectant are often required by state authorities to cease ammonia addition and flush the distribution system with free chlorine for at least one month in twelve (Rosenfeldt *et al.*, 2009). Rosenfeldt *et al.* (2009) showed that in their studied system, cell counts declined from 1,500 to 500 cells ml^{-1} in the first week and had fallen further to 300 cells ml^{-1} in week three of treatment. Immediately following the end of the flushing month, cell counts rose to 750 cells ml^{-1}. This suggests that the microorganisms in the system were adapted for chloramination, and that the chlorine flush represented a shock treatment. Humrighouse *et al.* (2006) noted that the microbial community was impacted by the choice of disinfectant; *Sphingomonas* genus was abundant in chlorinated systems, whilst *Hyphomicrobium*-like bacteria dominated in chloraminated ones.

The presence of organic nitrogen in treated water can lead to the formation of organic chloramines. These were found to have little to no inactivation potential on *E. coli* by Donnermair and Blatchley (2003). Since organic and inorganic chloramines cannot be

distinguished by conventional analytical methods (Amiri *et al.*, 2010) there is the potential for inadequate disinfection if treated water contains organic nitrogen.

A key confounding presence in disinfection is that of turbidity (Scarpino *et al.*, 1977; LeChevallier *et al.*, 1981; Sawyer *et al.*, 2003, Parsons and Jefferson, 2006). Turbidity can protect microorganisms from disinfectants and generate chlorine demand. Farooq *et al.* (2008) identified that coliforms adsorbed onto organic particulates were more resistant to disinfection than those adsorbed to inorganic turbidity. Wojcicka *et al.* (2008) observed that turbidity can reduce the capacity of disinfectants to inactivate microorganisms even without adsorption to the surface of particulates. The treatment processes within a WTW are designed to remove turbidity, which aids effective disinfection. However, one treatment process that often immediately precedes disinfection, granular activated carbon (GAC) filtration, has attracted research because of concerns that it a) encourages the growth of bacteria and b) enables them to survive disinfection through adsorption onto GAC particulates. Camper *et al.* (1985) observed at the laboratory-scale that pathogens and a mixture of HPC and pathogenic bacteria readily colonised sterile GAC. They also showed that if pathogens and HPCs were introduced to GAC which had been colonised by natural river water bacteria attachment was reduced and the die-off rate was more rapid. They concluded that there was a high risk of pathogen colonisation when GAC was new or freshly regenerated. They continued their work by studying GAC particulates in GAC-filtered water at a WTW (Camper *et al.*, 1986). From 201 samples collected over one year they found that 41.4 % of water samples had HPCs attached to GAC particles and 17.0 % of water samples had coliforms attached. These results concurred with studies by LeChevallier *et al.* (1984; 1988a), Stewart *et al.* (1990) and Hammes *et al.* (2008). LeChevallier *et al.* (1984) observed that bacteria attached to GAC particles remained viable even after disinfection with chlorine at 2.0 mg l^{-1} for 1 h. Camper *et al.* (1986) postulate that by attachment to GAC particles pathogens and indicator bacteria may survive disinfection and subsequently colonise the distribution system. Nevertheless, work by Pernitsky *et al.* (1997) concluded that after disinfection, bacteria attached to GAC particles represented a low public health risk.

2.5.2. Nutrients

Heterotrophic bacteria require a ratio of carbon to nitrogen to phosphorus of approximately 100:10:1 for growth and reproduction (Lester and Birkett, 1999), but

there is no clear consensus on what constitutes 'biological stability' of water (Zappia *et al*., 2008). Water that leaves the WTW is oligotrophic, and may contain disinfectants. It is a hostile environment for microorganisms, but their adaptation and persistence is well documented (James *et al.*, 1999; Berry *et al.*, 2006; Juhna *et al.*, 2007). Studies investigating the impact of nutrient-removal have tended to assume that the specific nutrient they are investigating is the limiting nutrient in the system. Many of the nutrient-based studies have been carried out on non-disinfected water. Hammes and Egli (2005) suggest that the presence of residual chlorine would have an impact on nutrient utilisation by microorganisms in the distribution system. Whilst it is generally accepted that the presence of nutrients, especially carbon, nitrogen and phosphorus, increases the ability of coliforms and other heterotrophic bacteria to grow in the pipes, pH and dissolved oxygen (DO) concentration have also been implicated (Meckes *et al*., 2007; Teng *et al*., 2008). The impacts of water chemistry on microorganisms are enhanced by long residence times in the distribution system (Norton and Weber, 2006; Srinivasan and Harrington, 2007; Vreeburg and Boxall, 2007). It is important to ensure appropriate turnover of water through system design and flow management. It has been suggested however that some bacteria are not controlled through nutrient-based methods alone (Shui-Li *et al*., 2007), and therefore it is imperative that strategies employed are system-specific (Srinivasan and Harrington, 2007).

2.5.2.1. Carbon

Natural organic matter (NOM) is a term used to describe the complex of carbon-based molecules present in all natural water sources. The majority of NOM is removed by well-managed treatment processes (Parsons and Jefferson, 2006). Biodegradable organic carbon (BOC) is usually a small fraction of NOM and it represents the portion of carbon that is available for use as a nutrient by microorganisms. Two main analytical methods exist for the analysis of the fractions utilised by bacteria: biodegradable dissolved organic carbon (BDOC) and assimilable organic carbon (AOC). The former relies on the indigenous microbial consortia and the latter utilises an assay of known bacteria. The BDOC content is frequently greater than that for AOC due to the potential range of microorganisms contributing to the carbon consumption (American Water Works Association, 2003).

The numbers of certain microorganisms have been shown to correlate closely with NOM concentrations, for example, species of *Mycobacteria* (Humrighouse *et al*., 2006)

and heterotrophic bacteria (Srinivasan and Harrington, 2007). AOC concentrations below 10 μg l^{-1} are effective in controlling biofilm growth in non-disinfected distribution systems (Hammes and Egli, 2005). Meylan *et al*. (2007) state that as little as 30 μg l^{-1} is sufficient to render water microbiologically unstable, but that 100 μg l^{-1} is the threshold for *E. coli* re-growth in the distribution system. Carter *et al.* (2000) observed no correlation between AOC and bacterial numbers. They postulated that this was because of the low concentration (0.01 – 0.27 mg l^{-1}) of AOC in their water. Environmental water and particulates entering the pipes through ingress will impart BOC to the system and encourage re-growth (Blanch *et al*., 2007; Wojcicka *et al*., 2008). Biofilm dislodged from the pipe surface can also contribute to the nutrient content of the bulk water (Chien *et al.*, 2009). Between 1.0 and 12.0 % of the organic matter particulates in the distribution system may be because of bacterial biomass (Vreeburg and Boxall, 2007).

Ozonation of NOM-rich waters can generate biodegradable fractions that had not been present in the raw water (Hu *et al*., 1999; Chien *et al*., 2009). To reduce bacterial re-growth potential and DBP-formation, Hu *et al*. (1999) and Chien *et al.* (2009) recommend following ozonation with GAC filtration which was shown to remove greater than 80 % of AOC. Other methods for the removal of BOC from drinking water include the use of reverse osmosis or nanofiltration (NF). Both processes are able to remove larger molecules, turbidity and microorganisms. Meylan *et al*. (2007) reported poor removal of AOC with NF; furthermore, when trialled with mixtures of AOC compounds as would be found in natural waters, NF performance declined. They suggested that its use produces an imbalance in the AOC:microorganism ratio. In so doing, selective re-growth in the distribution system is favoured through reduced competition. They therefore recommend a biological filtration step in conjunction with NF.

Kerneïs *et al*. (1995) and Dukan *et al.* (1996) noted that using BDOC as a control mechanism for bacterial growth is only beneficial when associated with temperature. For higher temperatures, the minimum BDOC for control is much lower than in winter or early spring when high levels of BDOC cannot be degraded (Kerneïs *et al*., 1995). Dukan *et al.* (1996) concluded that a BDOC concentration below 0.25 mg l^{-1}, combined with a water temperature of less than 16 °C enabled a natural limitation of bacterial biomass in the distribution system without the use of chlorine-based disinfection.

Volk and LeChevallier (1999) observed that reducing BOC concentrations resulted in improved chlorine stability in distribution, but that chloramines were unaffected. They also showed that biofilm density and bulk water HPCs were reduced after several months of improved BOC removal from the raw water. In contrast, Norton and LeChevallier (2000) showed that reducing BOC concentrations in treated water reduced the growth rate of biofilms only in the short-term, and Kerneïs *et al*. (1995) found that the numbers of heterotrophic bacteria were unaltered even with demonstrable reductions in BOC.

The inconsistent response of microorganisms to carbon-removal strategies suggests that limiting this nutrient alone is insufficient as a control mechanism.

2.5.2.2. Nitrogen

This review has not found any studies considering nitrogen as a nutrient to be removed from the raw water. The presence of high levels of nitrate in drinking water can cause methaemoglobinaemia in bottle-fed babies. It is very rare and no cases have been recorded in the UK since 1972. However, the condition is serious and thus nitrate is regulated under the Water Supply (Water Quality) Regulations 2000 in England and Wales (Her Majesty's Stationery Office, 2000) and the Europe-wide Drinking Water Directive (Council of the European Communities, 1998). The principal source of nitrate in drinking water is raw water impacted by agricultural fertilisers. A secondary source is as a result of disinfection with chloramines (Parsons and Jefferson, 2006); the presence of nitrifying bacteria in the distribution system can lead to the depletion of residual chloramines and the formation of nitrate and nitrite (Sawyer *et al.*, 2003; Crittenden *et al.*, 2005). Nitrifying bacteria are present in the distribution system regardless of the water temperature and can only be controlled by very high or very low concentrations of chloramines. In the former case, the high chlorine concentration inactivates the nitrifying bacteria; whilst in the latter case, the low ammonia concentration limits their growth (Berry *et al.*, 2006).

2.5.2.3. Phosphorus

Phosphorus is rarely the limiting nutrient in natural waters (Lehtola, 2002). Lehtola (2002) observed that phosphorus was effectively removed by coagulation and flocculation at the WTW. Concerns have been raised over the application of phosphate-based corrosion inhibitors for metal pipes and additives used in plastic pipe manufacture

(Szewzyk *et al*., 2000). The principal reason for adding phosphorus (as orthophosphate) to water supplies is to reduce plumbosolvency. This protects consumers from lead, which has been found to cause mental retardation in children and damage to the brain and kidneys of adults; it is also considered a probable carcinogen (Drinking Water Inspectorate, 2003; Sawyer *et al.*, 2003).

Findings differ on the impact of phosphorus on microbial growth in the distribution system. Gouider *et al*. (2009) concluded there was no effect; whilst Juhna *et al*. (2007), Rubulis and Juhna (2007) and Fang *et al*. (2009), demonstrated significant impacts through addition of phosphorus. Fang *et al*. (2009) found that adding phosphorus inhibited the production of EPS. Biofilms with less EPS were looser and less stable, making them more prone to sloughing. Juhna *et al*. (2007) and Rubulis and Juhna (2007) observed that *E. coli* culturability, but not number, was increased in phosphorus-enriched water. Rubulis and Juhna (2007) observed that even by reducing phosphorus to below detectable limits biofilm formation was not impeded. Their study did not consider the possibility that phosphorus was not the limiting nutrient in their system. Lehtola (2002) observed that Finland and Japan have phosphorus limited water supplies; Rubulis and Juhna were analysing Latvian tap water. Juhna *et al.* (2007) determined that increased phosphorus concentrations enabled *E. coli* to persist in the distribution system for 10 days before washout, as compared to four days without nutrient enrichment.

2.5.3. Plumbing/pipe materials

Distribution systems are frequently long, reticulated and formed from pipes of varying age, diameter, material and quality (Francisque *et al.*, 2009). The majority of drinking water pipes are made of iron, steel, plastics, asbestos cement, concrete, lead and copper. Of these, asbestos cement and lead are no longer used for new pipes (Crittenden *et al.*, 2005). Taste and discolouration issues have been associated with iron and copper pipes (Parsons and Jefferson, 2006; Vreeburg and Boxall, 2007). Copper piping is used primarily in domestic plumbing (Sawyer *et al.*, 2003). Galvanised steel was common in household pipe-work, but is no longer used in the UK (Crittenden *et al.*, 2005).

Biofilms develop on any surface in contact with water and can be evident within a few weeks of installation of new pipes (Gouider *et al.*, 2009). Rogers *et al.* (1994) and Obst and Schwartz (2007) demonstrated that differences in biofilm development and

coverage on different pipe materials were short-term (24 h and 15 days, respectively), and that an investigative period of months rather than weeks resulted in comparable coverage. This is supported by Percival *et al.* (1998) and Traczewska and Sitarska (2009). Much of the research into biofilm development has relied on the use of coupons placed perpendicular to the flow of water, which renders the hydraulic conditions within the system un-representative (Hall-Stoodley *et al.*, 1999). Deines *et al.* (2010) have developed a coupon that fits flush with the pipe wall thereby resolving this issue in biofilm studies.

Corrosion of iron pipe walls can lead to the release of iron in a form that is bio-available to bacteria encouraging biofilm development (Norton and LeChevallier, 2000; Berry *et al.*, 2006). Wang *et al.* (2009) observed that iron release rate decreased with pH, alkalinity and increasing DO, but increased with increasing chlorine concentration. Iron pipe surfaces consume chlorine residuals representing further inducement toward bacterial re-growth in the distribution system (Berry *et al.*, 2006). Pitting corrosion of iron pipe-work has been noted at the lower layers of biofilms (Chien *et al.*, 2009). Teng *et al.* (2008) found that this corrosion period was short-lived and that after 7 days, the biofilm served to inhibit further corrosion of iron pipes. Percival *et al.* (1998) observed similar processes on stainless steel.

The dissolution of copper has been shown to reduce biofilm development (Berry *et al*., 2009; Molteni *et al.*, 2010; Warnes *et al.*, 2010). Rogers *et al.* (1994) and Molteni *et al.* (2010) observed different levels of effectiveness due to the presence of copper-resistance in some bacteria. In contrast, Obst and Schwartz (2007) and Morrow *et al*. (2008) found no benefit to using copper pipes. Obst and Schwartz (2007) observed that their biofilms supported hygienically-relevant bacteria and Morrow *et al*. (2008) found equal biofilm coverage on copper and polyvinyl chloride (PVC).

Many plastics exhibit low reactivity with disinfectants; for example, PVC and high density polyethylene (HDPE) (Yang *et al*., 2007). Traczewska and Sitarska (2009) assessed the rate of biofilm development on various plastics: PVC, polyethylene (PE), polybutylene (PB) and polypropylene (PP). They observed lower surface roughness in PVC and PE with more cohesive and less spatially diverse biofilms. In contrast, PB and PP had rougher surfaces and exhibited pitting damage; interestingly, they also had biofilm cells that could not be removed by ultrasonic treatment, even though it was

believed that the increased surface roughness resulted in poorer cell adhesion. The smoother surfaces of PE and PVC only delayed the initial stage of biofilm growth, subsequent stages tended to be more rapid because of the release of carbon compounds from the plastic fixers, stabilisers and hardeners used in their manufacture and installation. A tendency for more rapid biofilm establishment on rough surfaces was also observed by Shui-Li *et al.* (2007).

Systematic assessment and management of the disinfection apparatus, storage reservoirs and pipe-work are crucial to the maintenance of bacteriological quality (Geldreich *et al.*, 1977; Damikouka *et al.*, 2007; Dong *et al.*, 2009). The principal techniques for removing microorganisms and other deposits from pipes are flushing, air scouring and swabbing (Vitanage *et al.*, 2004; Al-Jasser, 2007), or the more aggressive pipeline internal gauging ('pigging') (Lehtola *et al.*, 2004; Miettinen *et al.*, 2001). Routine and emergency response flushing may not necessarily represent an optimal management strategy (LeChevallier *et al.*, 1987); Chow *et al.* (2009) advocate a biofilm-based pipe inspection programme to optimise maintenance. Hu *et al.* (2008) found that biofilm growth reached a maximum at 40 days and recommended that removal techniques be applied approximately monthly. Flushing involves discharging water through pipelines at sufficient velocity to dislodge accumulated material and biofilms. It is a simple technique, but it does not remove all of the biofilm and consumes large volumes of treated water. Air scouring entails injecting water and compressed air into pipes. If the rates are well controlled, parcels of water are driven along the pipe at high velocity by the air. This technique is more effective at removing deposits from pipes than flushing alone. Swabbing uses water pressure to push a large foam sponge through the pipe. The effectiveness is determined by the velocity of the water and is more efficient than either flushing or air scouring (Vitanage *et al.*, 2004). Pigging uses a rigid steel form in place of the swab and is the best technique for removing harder deposits (Videla *et al.*, 2002). Maintenance practices have been linked to approximately 17 % of discolouration and taste and odour complaints (Furnass *et al.*, 2013).

Pipes that have been cleaned can be lined with more biofilm-resistant materials. The most common linings include PE slip-liners or epoxy or PVC resin coatings (Ainsworth and Holt, 2004). The World Health Organization (2004) recommends that distribution systems with a high risk of failure for bacteriological parameters undergo full pipe replacement to protect consumers.

The distribution system detailed in Figure 1 contains ductile iron, cast iron and concrete pipes. Biofilms will grow on all three materials. Maintenance work or valve operations in the distribution system could have disturbed stable biofilms in the lead up to the coliform detection at the reservoir.

2.6. Modelling of bacteria in the distribution system

Low numbers of indicator bacteria are recovered from distribution systems and thus it has proven difficult to model their occurrence (Piriou *et al.*, 1997). Modelling work by Clark and Coyle (1990) and van Lieverloo *et al.* (2007) concluded that this problem will persist while the sampling programmes for these bacteria are based on periodic monitoring. And, like Schets *et al.* (2005), they concluded that small sample volumes also reduced the likelihood of detecting indicator bacteria. Clark and Coyle (1990) stated that it was important for improved models of travel time in water distribution systems to be developed. Gronewold *et al.* (2009) aimed to model and predict faecal indicator bacteria in raw waters. They stressed that their *E. coli* models were only as good as the bacterial decay rates used and the manner in which data variability was addressed. Besner *et al.* (2011) applied the Quantitative Microbial Risk Assessment (QMRA) model to the issue of microbial intrusion to the distribution system. They concluded that, at present, most models are based on estimates because empirical data for all possible factors involved in a contamination event are not yet available.

Dong *et al.* (2009) used principal components variables and a binary response to model and predict the probability of an HPC event, which was defined as $\geq$100 CFU ml^{-1}. Using this method, they were able to identify regions of high microbiological risk in their water distribution system. On-line monitoring tools for physical and chemical parameters (for example, temperature, residual chlorine and turbidity) have become more widespread in recent years. They are often combined to develop an understanding of potential bacteriological risk. McCoy and Olson (1986) observed that turbidity and particle counts in drinking water distribution systems were directly proportional, but that neither parameter correlated with bacteriological quality (measured as HPCs). Clark *et al.* (1995) employed the then new EPANET model to identify the impact of pipe diameter and flow rate on chlorine demand. Their work concluded that loss of chlorine residual was impacted by: pipe wall demand, water age, flow rate, pipe radius and bulk water demand.

The use of on-line chlorine sensors has been suggested as a surrogate for monitoring bacteriological quality in distribution (Farooq *et al*., 2008; Helbling, 2008; Helbling and VanBriesen, 2008). The influencing factors identified by Clark *et al.* (1995) would need to be accounted for if on-line chlorine monitors were used for this purpose. Helbling and VanBriesen (2008) observed that there was a high level of specificity between different bacteria and chlorine demand in pure cultures. Helbling (2008) comments that for low density *E. coli* suspensions, less than 10^5 colonies ml^{-1}, no chlorine demand was observed, but that at higher densities directly proportional chlorine demand and cell survival was demonstrated. Farooq *et al.* (2008) found only a weak inverse correlation between chlorine concentration and coliform counts. Mahto and Goel (2008) observed that no strict correlation existed between free and total chlorine residuals and faecal or total coliforms and HPCs in either double distilled water or tap water. They concluded that this was because of the independence of microbial growth from chlorine residuals at concentrations below 0.3 mg l^{-1} free chlorine and 0.75 mg l^{-1} total chlorine. Any use of chlorine sensors as a surrogate for bacteriological quality should be cautious.

2.7. Summary

Access to clean, safe drinking water is responsible for vast improvements in human health. Developments in source water protection, water treatment and distribution, operation and maintenance of WTWs, water quality monitoring and training and education of practitioners continue this upward trend.

The aims of water quality monitoring are to assure the safety of drinking water for consumers and to monitor the performance of treatment processes. Bacteriological quality monitoring at present relies on relatively cheap and easy culture-based techniques; these methods take at least 24 h to generate a result. HPCs are measured to provide trend information on bacteriological quality and the following indicator organisms are tested for: coliforms, *E. coli*, *C. perfringens* and Enterococci. The presence of indicator bacteria in treated water suggests environmental or faecal contamination.

Newer techniques, based on PCR and luminescence/fluorescence, have the potential for future use in bacteriological monitoring.

Raw water can be impacted by land-uses in the river catchment or areas surrounding groundwater sources. Surface water and groundwater WTWs have different treatment priorities because of differences in perceived raw water risks. Heavy rainfall is a risk factor for bacteriological contamination of both surface water and groundwater sources.

Ingress can occur in damaged portions of the distribution system, for example where pipes have holes or cracks in them. Weaknesses in the pipe-line can be exacerbated during system depressurisation following insensitive valve operations or a burst.

Disinfection is designed to prevent the spread of waterborne disease. It does not produce sterile water. One study showed that up to 96.8 % of coliforms in treated water were injured but not killed by disinfection. Injured microorganisms can recover when environmental conditions improve. The most common chemical disinfectants are chlorine, compounds of chlorine such as chloramines and chlorine dioxide, and ozone. Chlorine and chloramines enable residual disinfection to be maintained through the distribution system to discourage bacterial re-growth and reduce the impact of breaches in integrity. In England and Wales final disinfection with chlorine or chloramines is a regulatory requirement. Chlorine and chloramines must be dosed with due consideration of organic matter in the water to avoid exceeding DBP limits. This is of especial concern when a distribution system requires booster-disinfection. Chlorine decay rate increases with water temperature and it is necessary to increase residual free chlorine concentrations as water temperatures rise. Free chlorine concentrations in excess of $0.3\ mg\ l^{-1}$ have been shown, by some researchers, to control bacterial re-growth in distribution and protect supplies if an ingress event occurs. Other studies found that chlorine residuals had little impact on re-growth. Turbidity can protect microorganisms from disinfectants and generate chlorine demand. Coliforms adsorbed onto organic particulates were more resistant to disinfection than those adsorbed on inorganic turbidity. GAC particulates in filtered water have been shown to hinder effective disinfection and allow viable bacteria to enter the distribution system.

The majority of drinking water pipes are made of iron, steel, plastics, asbestos cement, concrete, lead and copper. Biofilms develop on any surface in contact with water and can be evident within a few weeks of installation of new pipes. Bacteria enter the distribution system in low numbers from the environment and source water and are able to persist through the formation of biofilms. All surfaces within a system are covered by

biofilms, which are made up of bacteria, fungi, algae, protozoa and amoebae held together in an EPS matrix. Cell detachment is a normal part of the biofilm life-cycle. Most researchers have shown that biofilms represent an important reservoir for pathogens within the distribution system. Bacteria persisting in biofilms are more difficult to disinfect than those in bulk water. It is thought that the EPS matrix confers disinfectant resistance upon biofilm bacteria.

In order for heterotrophic bacteria to grow and reproduce, the ratio of carbon to nitrogen to phosphorus is approximately 100:10:1. NOM is present in all natural water sources. The majority of NOM is removed during water treatment, but ozonation can generate biodegradable carbon compounds that were absent in the raw water. At warmer water temperatures, the minimum NOM concentration for control of bacterial re-growth is much lower than in winter or early spring when high levels of NOM cannot be degraded. Reducing NOM in final water enhances the stability of chlorine in distribution, but not that of chloramines. Biofilm dislodged from the pipe surface can contribute to the nutrient content of the bulk water. Between 1.0 and 12.0 % of organic matter particulates in the distribution system may be because of bacterial biomass. Nitrogen has not been identified as a limiting nutrient. Care must be taken to ensure nitrate and nitrite concentrations are within safe limits: these can enter raw water through agricultural fertiliser run-off or be produced when chloramine disinfection is used. Phosphorus is rarely the limiting nutrient in natural waters. Phosphorus may be added to supplies where the distribution system contains lead pipes; the impact of this practice on microbial growth depends on the source water.

Bacteria can be transferred to tap surfaces through human or animal contact, splash-back from contaminated water, or carriage in air currents.

Samplers and laboratory staff undergo training in hygienic working practices. Studies show that there must be continuous reinforcement of this training to ensure its success.

The low numbers of indicator bacteria recovered from distribution systems has made it difficult to model their occurrence. It has been suggested that this is due to the dominance of periodic, rather than continuous, bacteriological monitoring. Using changes in free chlorine concentration as a surrogate for bacteriological quality in distribution systems has produced conflicting results.

2.8. Conclusions

Distribution systems are complex. Indicator bacteria in the distribution system are affected by the presence or absence of disinfectants, the type of disinfectant, the availability of nutrients, and the plumbing and pipe materials in use in the network. Water samples collected to monitor the bacteriological quality of distributed supplies can be impacted by many factors: raw water quality, treatment failure, ingress to the system, biofilm in the pipes, contamination of the sample taps and poor hygiene practice by samplers or analysts. Any of these factors, or combinations thereof, could have impacted the water quality at the reservoir in Figure 1.

At present, bacteriological models for distribution systems lack robustness in light of the number of factors that must be accounted for. In addition, the tools that are currently relied upon for microbiological monitoring are culture-based, and therefore slow and susceptible to selection bias. The development of genotypic identification tools and on-line monitoring is in progress, but it will be some time before culture-based methods are replaced by less time-consuming techniques.

The complexity of distribution systems and of the factors that affect bacteriological quality within them means that methods to prevent failures must be tailored to individual systems. There is a need for better standardisation in experimental design and improved translation of laboratory-findings to real-world situations.

2.9. Research Questions

In light of this review, and with regard to the overall research topic – 'Improving Root Cause Analysis of Bacteriological Water Quality Failures,' the following questions will be addressed in this thesis:

1. What are the main causes of bacteriological non-compliances in UK water supplies?
2. Where in the water supply system do most bacteriological failures occur?
3. Which indicator organism is most frequently detected?
4. Is UK bacteriological compliance impacted by weather phenomena?
5. Can improved analysis of on-line monitoring and spot-sample data be used to inform the root cause analysis of bacteriological failures?

Furthermore, to meet the Doctorate of Engineering thesis requirements, a further research question will be answered:

6. What financial impact do bacteriological failures have on a UK water company?

Between 2008 and 2011, Severn Trent Water (STW) experienced 218 bacteriological failures across the three sample points: WTW finals, service reservoirs and customers' taps. Questions 1, 2 and 3 will be answered through analysis of the data collected as part of the root cause analysis for these non-compliances (Chapter 3). Question 4 incorporates climate data into the analyses to determine their impacts on the tendency for bacteriological water quality samples to fail (Chapters 3 and 6).

The cost of bacteriological failures will be determined through an interrogation of failure data relating to the investigations, site visits and reporting requirements for each of the 218 failures between 2008 and 2011. Further information will be gathered from STW staff to account for the cost of remedial works to restore water quality (Question 6; Chapter 4).

The use of case study sites allows an in-depth analysis of a variety of data sources to try to identify weaknesses in the treatment or process management of WTWs for bacteriological quality. Question 5 uses two WTW sites which have experienced multiple failures to investigate the utility of advanced statistical tools in identifying root causes. The analyses include spot-sampled and monitor time-series data from the final monitoring point (Chapters 5 and 6), through-plant and weather stations (Chapter 6).

2.10. Statistical tools for analysing time-series data

Analysis of time-series data can perform two principal functions: 1) to show correlations among a variety of parameters at the time of an 'event', for example, the detection of indicator bacteria (water quality fingerprints); and 2) to identify a time lag between changes in one parameter and those in a second. In this section, statistical tools for both functions are explored.

2.10.1. Water quality fingerprints

Three clustering tools that could be used to show the water quality characteristics at the time of bacteriological non-compliances are detailed: Self-Organising Maps (SOMs), κ-means clustering and Principal Component Analysis (PCA).

SOMs are a type of artificial neural network that is trained using unsupervised learning. They were developed by Teuvo Kohonen (Kangas and Kohonen, 1996; Kohonen, 1998) and have been applied to a variety of disciplines, including economics (Deboeck and Kohonen, 1998), genetics (Tamayo *et al.*, 1999), climatology (Hewitson and Crane, 2002), engineering (Kohonen *et al.*, 1996) and water quality (Kalteh and Hijorth, 2008). SOMs enable the visualisation of high-dimensional input data in a low (usually two) dimensional output space. They are based on matrices of nodes. Each matrix contains sufficient nodes to match the number of data points in each parameter. The nodes of the base SOM are assigned random values between 0 and 1. The SOM algorithm first normalises the input data to between 0 and 1, then it introduces the first normalised data point to the matrix, and assigns it to the node that most closely matches its value. Each new normalised data point is introduced and assigned to its own closely matching node until all the nodes are filled. The generation of the map requires two sets of data matching runs: rough training to learn the global structure and fine training to complete the maps. The output space is colour-coded and refers to the original values of the input data. Additionally, labelled SOMs can be created using non-numeric data. These are clustered independently of a multi-parameter SOM but can be used to classify regions within it.

κ-means clustering partitions observations into clusters around the mean values. These clusters are used to characterise the dataset. κ-means clustering has been used in a variety of disciplines, including: genetics (Lam and Tsang, 2012), biometrics (Munir *et al.*, 2012), traffic management (Montazeri-Gh and Fotouhi, 2011) and robotics (Elango *et al.*, 2011).

PCA determines the underlying distribution of a complex dataset and re-expresses it linearly on the basis of its principal components (PCs). The PCs describe the variance of the dataset, with the first PC exhibiting the greatest variance. The second PC exhibits less variance and is un-correlated with the first PC (Shlens, 2003). PCA has been employed in many subject areas, including: health (Hoskins *et al.*, 2005; Babaoğlu and

Fındık, 2010), air pollution analyses (von Schneidemesser *et al.*, 2010) and financial assessments (Juneja, 2012).

2.10.2. Identifying a time lag

Cross-correlation, Auto-Regressive Integrated Moving Average (ARIMA) method and wavelet analysis are considered for the assessment of temporal similarity in the datasets.

Cross-correlation is a measure of the similarity of two variables (signals) as a function of a time lag between them (Bracewell, 1965). It achieves this by aligning peaks (or troughs) across the two signals at different lags and hence can be used to determine the time delay between two signals. Cross-correlation has been shown to be reasonably robust to sparse sampling frequencies (White and Peterson, 1994). It has relatively low memory and processing requirements (Miao *et al.*, 2005). Cross-correlation has been used for a wide variety of signal processing purposes, including: telecommunications (Beck, 1981); spectroscopy (Wong *et al.*, 2005); meteorology (Leese *et al.*, 1971) and earthquake detection (Shearer, 1997).

ARIMA is widely used in forecasting; for example of energy resources (Ediger and Akar, 2007; Zhu and Wei, 2013), stock prices (Pai and Lin, 2005), river water quality (Kurunç *et al.*, 2005; Faruk, 2010), and monsoon rains (Narayanan *et al.*, 2013). There are two key parts to the ARIMA method: auto-regression (AR) and moving average (MA). The AR component assumes that, subject to a time lag, it is possible to estimate future data in a time series. It describes the data in terms of a linear combination of past observations and a random error element. The MA component attempts to explain past errors that cannot be accounted for by AR. The integration of these two components enables the description of the underlying data patterns and can be used to extract time lags between input parameters (Ediger and Akar, 2007; Narayanan *et al.*, 2013). ARIMA is only recommended for datasets containing at least 50 observations (Khashei *et al.*, 2009; Christodoulos *et al.*, 2010). It is computationally expensive (Glantz and Mun, 2011).

Wavelet analysis, like cross-correlation, seeks to align peaks (or troughs) across two signals and can therefore be used to determine the time delay between two signals. Wavelet analysis separates the core signal from noise in the dataset using a pre-selected filter. It has been used in a variety of disciplines including: engineering (Ding *et al.*,

2011; Perpiñán and Lorenzo, 2011), water quality monitoring (Tsabaris and Prospathopoulos, 2011; Zhang *et al.*, 2012), population ecology (Cazelles *et al.*, 2008) and climate data analysis (Lau and Weng, 1995; Chellali *et al.*, 2010; Özger *et al.*, 2010). It is computationally expensive (Cooper, 2009).

3. Company Data Analysis[1]

3.1. Introduction

Severn Trent Water (STW) monitors coliform bacteria and *E. coli* on every sample collected for regulatory purposes and *C. perfringens* and Enterococci in accordance with identified risks in the raw water catchment or supply area. After a detection of indicator bacteria, investigatory samples are collected and all four bacteriological parameters are measured on these samples regardless of the initial testing criteria. The data presented in this Chapter refer only to the results from the first, regulatory sample.

Each time a sample fails to meet the bacteriological standards STW open a dedicated file to record the investigation and the remedial actions taken. These files are called Exception Reports and are used to enable accurate reporting to the Drinking Water Inspectorate. This chapter seeks to answer research questions 1 to 4:

1. What are the main causes of bacteriological non-compliances in UK water supplies?
2. Where in the water supply system do most bacteriological failures occur?
3. Which indicator organism is most frequently detected?
4. Is UK bacteriological compliance impacted by weather phenomena?

Three potentially suitable tools for developing water quality fingerprints were reviewed in Chapter 2. Of these, Self-Organising Maps (SOMs) were selected because of their intuitive output. Both κ-means clustering and Principal Components Analysis require translation in order to relate the outputs to the inputted data. Since the intention of these analyses was to inform operational practices it was desirable to use a tool that was clearly related to the analysed parameters. SOMs also allowed the analysis of non-numeric data using the labelled SOMs tool.

3.2. Methods

3.2.1. Severn Trent Water's sampling protocol

The following procedure is used by STW samplers when collecting routine water quality samples:

[1] This Chapter has been published in part in a chapter of 'The Significance of Faecal Indicators in Water: A Global Perspective', K Ellis *et al.*, 2012; and in the Water Science and Technology publication, K. Ellis *et al.*, 2013.

- The sample tap is flushed for a minimum of 2 min to ensure that the water is representative of water in supply.
- Aliquots of water are analysed for free and total chlorine using the diethyl-p-phenylene diamine (DPD) colorimetric standard method (Standing Committee of Analysts, 2010a). The water temperature is measured using a digital thermometer.
- The tap is turned off. Water treatment works (WTW) final and reservoir sample taps have simple spouts with no additional flow modifiers (pressurisers, sprinklers, etc.); if customers' taps have removable flow modifiers then they are taken off. The outer and inner surfaces of the tap are sprayed with 10,000 mg l^{-1} chlorine solution and a 2 min contact time is allowed for disinfection.
- The tap is flushed again for 2 min.
- A 500 ml bacteriological sample is collected in a sample bottle dosed with sufficient sodium thiosulphate to neutralise free or combined residual chlorine in concentrations not exceeding 5 mg Cl_2 l^{-1} (Standing Committee of Analysts, 2010a).
- At some WTWs and reservoirs, the sample tap is constantly running. When sampling at these sites, the flushing steps are omitted, the tap does not get turned off and only the outside of the tap can be disinfected.

Samples are transported in refrigerated containers to the laboratory and microbiological analyses occur within 24 h of collection. Total coliforms and *E. coli* are enumerated on membrane lactose glucoronide agar following the agar manufacturer's protocol (Oxoid, 2012), which conforms to Methods for the Examination of Water and Associated Materials (Standing Committee of Analysts, 2009). Enterococci are enumerated on membrane Enterococcus agar and *Clostridium perfringens* on membrane tryptose sulphite cycloserine agar (Standing Committee of Analysts, 2012; 2010b). At the end of the incubation period the number of colonies is counted and recorded as colony forming units (CFU) 100 ml^{-1}.

3.2.2. Company data collection

The following data were extracted from STW Exception Reports for all routine bacteriological non-compliances between 1st January 2008 and 31st December 2011:

- Date of failure;
- Sample point type: WTW final, reservoir, customer tap;
- Failure type: total coliforms, *E. coli*, *C. perfringens*, Enterococci;
- Number of colonies recorded;

- Chlorines: free and total, mg l^{-1};
- Water temperature, °C;
- Success of investigation to find the cause of failure: single cause identified, multiple potential causes identified, unknown cause. If a single cause was identified this was recorded;
- Tap type and location;
- Source water type: 100 % surface water (S), surface water > groundwater (S > G), surface water = groundwater (S = G), groundwater > surface water (G > S), 100 % groundwater (G).

3.2.2. Climate data collection and analysis

The following monthly weather data for the Midlands region were collected from the Met Office web-site (Met Office, 2012) for the period 1st January 2008 to 31st December 2011:

- Air temperature, °C: minimum, maximum and average;
- Total hours of sunshine, h;
- Rainfall, mm;
- Number of days with rainfall > 1 mm, d;
- Number of days with air frost, d.

The percentage failure rate was calculated using the total number of bacteriological samples per year, indicator organism, sample point type, free and total chlorine concentration range, water temperature range and source water type. Statistical analysis was conducted using Pearson rank correlation to determine potential correlations with climate data.

3.2.3. Self-Organising Maps

The analyses were carried out using the MATLAB® SOM Toolbox version 2.0 (Laboratory of Computer and Information Science, Finland). The default settings of linear initialisation and batch training were selected. Each variable is represented by a colour-coded rectangular plot called a component plane; a specific location in one plot is related to that same location in all corresponding component planes, enabling an understanding of how parameters change one with another.

A SOM was generated using the following parameters: year of failure (2008 – 2011), month of failure (January = 1 – December = 12), number of colonies recorded, colony forming units (CFU) 100 ml^{-1}, free and total chlorine concentration (mg l^{-1}) and water temperature (°C). Labelled SOMs were created for the following: sample point (F = WTW final; R = reservoir; T = customer tap), indicator organism (CO = total coliforms; EC = *E. coli*; CL = *C. perfringens*; EN = Enterococci), tap type (ST = STW standard; 2K = kitchen mixer tap, metal – with insert; 4K = kitchen single tap, metal – with insert), root cause identification (S = single cause; M = multiple potential causes; U = unknown cause), and source water type (S = 100 % surface water; G = 100 % groundwater; SG = blend S > G; E = equal blend; GS = blend G > S).

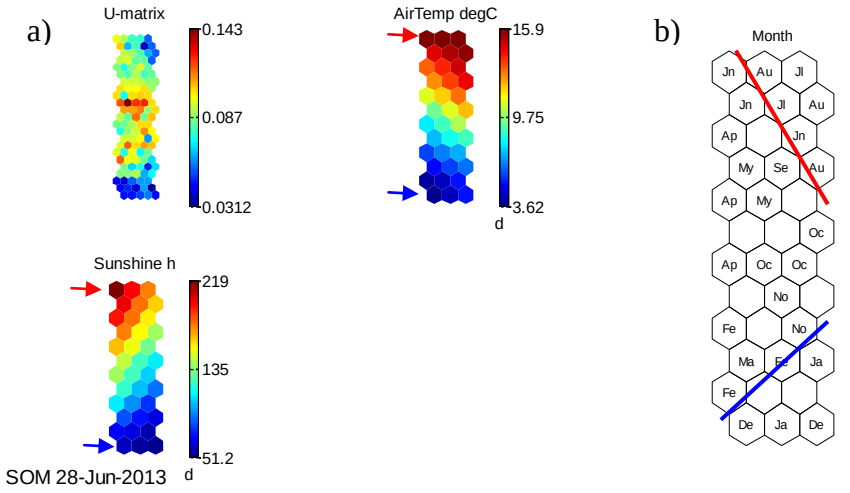

Figure 2: a) Self-organising map of average air temperature, °C, and number of hours of sunshine per month; b) labelled SOM of month.

As an example, using two datasets from the climate data, Figure 2a shows a SOM generated using number of hours of sunshine per month, h (n = 48), and average air temperature, °C (n = 48). The resultant U-matrix is the pattern of clusters recorded by the SOM algorithm. It can be observed that broadly speaking, the greater the number of hours of sunshine per month the warmer the average air temperature, and the smaller the number of hours of sunshine, the cooler the average air temperature, as would be expected. Looking at specific locations, it can be seen that the hottest air temperature (15.9 °C; dark red) was recorded during the months with the most hours of sunshine (219 h; dark red) (marked with →); however, the coldest air temperature (3.62 °C; dark blue) was recorded during months with approximately 80 h of sunshine (mid-blue) (marked with →) and not the least hours of sunshine (51.2 h; dark blue). Figure 2b shows the Labelled SOM of month from the same dataset (n = 48). It shows that

summer months are clustered in the top part of the Map (marked with —) and winter months are clustered in the bottom part (marked with —). The arrangement of the month data also shows that high air temperature is more characteristic of July and August than longer hours of sunshine and that fewer hours of sunshine are more characteristic of January and December than low air temperatures.

3.3. Results and Discussion

3.3.1. Overview of failures

Figure 3 provides an overview of the number of bacteriological failures recorded by STW between 2008 and 2011, as a percentage of the total number of analyses for indicator organisms and as absolute numbers. Across the four years 218 failures were detected representing 0.08 % of all bacteriological analyses. Between 2008 and 2010, the number of failures declined: 2008, 59 (0.091 % of analyses for indicator organisms that year); 2009, 43 (0.066 %); 2010, 42 (0.065 %); but 2011 saw an increase in the number of non-compliances to 74 (0.114 %; Figure 3a). In January 2008, the concentration of chlorine solution used to disinfect sample taps was increased from 1,000 mg l^{-1} to 10,000 mg l^{-1} (Standing Committee of Analysts, 2002). By comparing the number of failures for 2006 – 2007 and 2008 – 2009, it was shown that the number of failures was halved by the change in protocol (significant at $p < 0.05$; data not shown). The improvement in annual compliance from 2008 to 2010 was likely to be because of the new tap disinfection protocol and the increasing proficiency of samplers in its execution. The increase in 2011 could have been spurious; in 2012 there were 59 bacteriological failures, the same as in 2008. However, a new sampling protocol was introduced in April 2012 requiring the double disinfection of taps prior to collecting samples and this may have improved 2012's compliance.

Total coliform bacteria accounted for 188 failures (representing 0.160 % of analyses for that parameter), *C. perfringens* for 16 (0.171 %), *E. coli* for 13 (0.011 %), and Enterococci for a single failure (0.006 %; Figure 3b). The percentage failure rates for coliforms and *C. perfringens* were similar; the latter is monitored for less frequently than the former. For all four groups of bacteria, it was common for only one colony to be counted (Table 2); 52.75 % of all failures were caused by a single colony; 86.70 % of detections were for ten or fewer colonies.

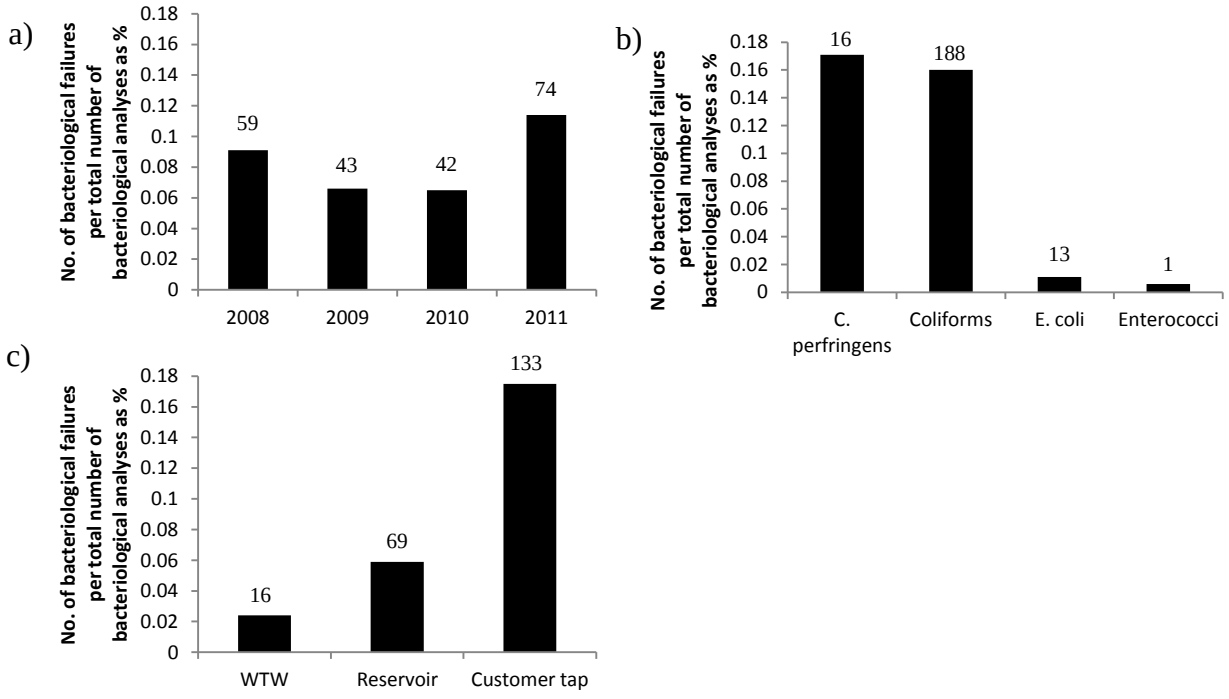

Figure 3: Percentage of bacteriological failures per total number of bacteriological analyses by a) year, b) organism, and c) sample point between 2008 and 2011. The number of failures per parameter is presented above each bar.

The number of bacteriological failures by sample point is shown in Figure 3c; customer taps accounted for 133 non-compliances (0.175 % of analyses for indicator organisms from those sample points), reservoirs for 69 (0.059 %) and WTW finals for 16 (0.024 %); over one third of non-compliances therefore were from company assets. Distributed water is at its highest quality at the point where it enters the distribution system – that is, as final water leaving the WTW. Water quality declines as it travels through the system as was observed with the increasing numbers of failures at reservoirs and customers' taps (Figure 3c). Failures in the final water may be the result of inadequate treatment or disinfection at the WTW (Blanch *et al.*, 2007) or localised contamination of the sample line or tap. Reservoirs and customers' taps may be affected by localised contamination of the sample line or tap, loss of residual chlorine, biofilms, microbial ingress (Levi, 2004) and long water residence times at the extremities of the distribution system (Srinivasan *et al.*, 2008). Whilst it is not possible for water companies to directly influence the maintenance and cleanliness of customers' taps, they are required to implement suitable management procedures with regard to asset sample lines and taps and turnover of water in the distribution system (World Health Organization, 2004; Srinivasan *et al.*, 2008).

Table 2: Number of bacteriological failures by organism and number of colonies enumerated between 2008 and 2011

Number of colonies	Organism			
detected	*C. perfringens*	Coliforms	*E. coli*	*Enterococci*
1	15	94	5	1
2 to 10	1	57	6	
11 to 25		8	1	
26 to 50		10		
51 to 75		9		
76 to 100		8	1	
>100		2		

3.3.2. Success of investigations to find the causes of failures

Identifying the root cause of a failure is vital for preventing a recurrence. A cause is assumed to have been identified if indicator organisms are found during re-sampling. If re-samples are compliant, they provide no indication as to the reason for the failing sample. Therefore, if, after reasonable efforts to identify a cause have been made, no cause has been identified, then the Exception Report is closed with the cause unknown. In reality, the detection of indicator organisms at a sample point could indicate a failure upstream of that location; for example, the cause of a customer tap failure could be contamination at the tap, but it could also have originated from its supplying WTW or service reservoir. Between 2008 and 2011, 53 failures had a single cause identified meaning that remedial action could be taken; nine had more than one potential cause (always ingress plus one other factor) and 156 had no cause identified (Figure 4a). Of the 156 failures with no cause identified, ten were from customers' taps and samplers were unable to re-enter the property to collect re-samples. For the 53 failures with a single cause identified, 43 were because the tap was dirty, eight because of bacteria in the plumbing or sample line, one due to the consequence of ingress to the distribution system, and one resulted from the failure of an upstream asset (an upstream asset is a WTW or reservoir that supplies water to other sample points) (Figure 4b). Non-compliances that are attributed to the tap or local pipe-work could be considered as false positives because the source of the indicator bacteria was not deemed to be the water or due to an ingress event or treatment failure.

The high proportion of re-samples that comply with the regulations may indicate that the bacteriological contamination was slight and transitory, or that greater care was taken when re-sampling. If no cause can be identified from the investigations, it is not possible to target remedial actions and thus the costs (which can be considerable) cannot be justified.

Customers whose taps have been shown to be the cause of a bacteriological failure are advised to use a mild chlorine solution to clean their taps inside and out to maintain them in a hygienic condition. Two of STW's taps also caused failures; whilst the taps are routinely flushed they are not cleaned inside and out as part of routine maintenance because of concerns of disturbing stable biofilms. Plumbing and sample lines in the vicinity of the sample tap were also identified as causes of non-compliance. For STW and their customers, remedying this cause means thoroughly disinfecting the service pipe-work or replacing it. STW has a rolling programme of sample line and tap replacement to ensure that samples are representative of the water from the WTW or reservoir and are not impacted by the quality of the sample line. This practice is recommended by the World Health Organization (2004). STW's response to non-compliances can interrupt the replacement programme and result in sites that were identified as 'at risk' being moved into the next year's replacement programme.

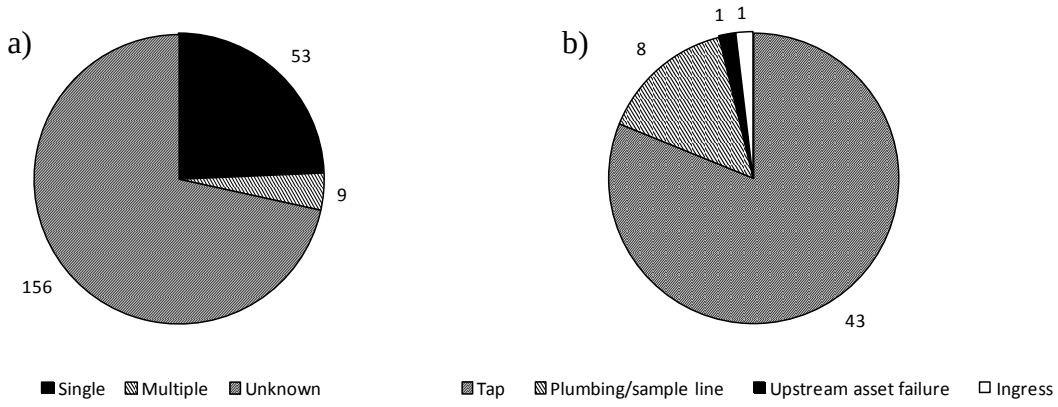

Figure 4: a) Number of bacteriological failures by success of investigation, and b) number of single cause failures divided by the causes identified between 2008 and 2011

3.3.3. Effect of tap type on compliance

Of the 218 failures between 2008 and 2011, 85 were from STW standard taps, which are found on WTWs or reservoirs, 79 were from kitchen mixer taps made from metal with an insert and the remaining 54 non-compliances may be classified as 'other', because of the much lower incidence of each of the individual tap types (Table 3).

There are several tap configurations used by STW, including the swan neck and 'Harris' type designs. A swan neck tap is a narrow elongated pipe with a curved spout and the 'Harris' tap has a narrow spout fitted with a screw cap and is the current standard for all new and replacement installations. When samples are collected from assets, samplers are not required to record the design of the tap. No cause was identified for 83.5 % of

STW standard taps, compared with 63.3 % for kitchen mixer taps made from metal with an insert, and 64.8 % for 'other' tap types.

The percentage failure rate for the different tap types was low and consistently below 1.0 %. The highest risk customer tap types and locations were single metal taps with inserts in downstairs cloak/bathrooms and plastic mixer taps with inserts from kitchens with 0.94 and 0.84 % failure rates respectively. Both configurations were sampled less frequently, which has increased the impact of the failures at each point.

Table 3: Number of bacteriological failures (both total and those with unknown causes) by tap type and tap location, and total number of samples collected from that combination of type and location between 2008 and 2011.

			Number of failures	
Tap type	Tap location	All sampled	Total	Unknown cause
Severn Trent Water standard	WTW or Reservoir	182292	85	71
Mixer tap - metal, without insert	Kitchen	8226	13	11
Mixer tap - metal, with insert	Kitchen	46040	79	50
Single tap - metal, without insert	Kitchen	5352	12	9
Single tap - metal, with insert	Downstairs Cloak/Bathroom	562	3	1
Single tap - metal, with insert	Kitchen	14539	17	11
Single tap - metal, with insert	Utility	319	1	0
Mixer tap - plastic, with insert	Kitchen	238	2	0
Supertap	Kitchen	444	2	2
Not recorded	Not recorded	2701	4	1

3.3.4. Impact of weather on failure incidence

Berry *et al.* (2006) and Pitkänen *et al.* (2008) observed that some weather phenomena impacted incidences of bacteria in drinking water. Visual assessment of plots of monthly rainfall and average temperature against numbers of failures per month appeared to support this view (Figure 5a and b). Correlations between these parameters were weak, however. Correlations with rainfall were stronger at 0 month shift than when time lags of one or two months were applied (Table 4). These results differ from the finding of Curriero *et al.* (2001) and Thomas *et al.* (2006) that bacteriological contamination was commonly detected up to two months after a rainfall event. Berry *et al.* (2006) and Pitkänen *et al.* (2008) stated that operators often did not adjust the treatment processes to account for heavy rainfall events. Heavy rainfall causes increased loading of nutrients and turbidity to surface water WTWs due to runoff. If the water treatment process does not adequately remove nutrients and turbidity, disinfection efficacy can be compromised (Sawyer *et al.*, 2003; Parsons and Jefferson, 2006; Farooq *et al.*, 2008; Wojcicka *et al.*, 2008). The stronger correlation between failures where no cause could be identified and total monthly rainfall (at 0 month shift) and number of

days with rainfall > 1 mm suggests that weather phenomena may have impacted STW's non-compliances. The strongest correlations indicate that cooler conditions tend to promote non-compliance: minimum temperature had a correlation coefficient of 0.26 and number of days with air frost had a coefficient of -0.28. It is worth noting that for hours of sunshine, rainfall and days with rainfall > 1 mm the correlations were slightly stronger for failures with no known cause. For the other parameters the reverse was the case.

Table 4: Pearson Correlation coefficients for monthly number of bacteriological failures (both total and unknown causes) and monthly data for each of the weather phenomena recorded between 2008 and 2011. Includes results for rainfall data with failure data correlated at one and two month shifts. Shaded results highlight those where correlations were stronger for failures with unknown causes.

	Bacteriological failures	
	Total	Unknown
Maximum air temperature, °C	0.21	0.17
Minimum air temperature, °C	0.26	0.24
Average air temperature, °C	0.23	0.20
Sunshine, h	-0.03	-0.09
Rainfall, mm (0 month shift)	0.17	0.21
Rainfall, mm (1 month shift)	0.14	-0.13
Rainfall, mm (2 month shift)	0.08	-0.03
Days with rain > 1mm, d	0.10	0.16
Days with air frost, d	-0.28	-0.26

3.3.5. Impact of residual chlorine concentration

Chlorine is an important bacteriological control parameter. STW's current chlorine management strategy states that the Water Quality Team should aim to achieve a concentration of 0.2 ± 0.1 mg l^{-1} free chlorine throughout the distribution system (Severn Trent Water Limited, 2011). Chlorination efficacy is impacted by water temperature and pH. Water temperature is measured via spot sampling, but spot-sampled pH measurements are rare.

Of the bacteriological failures with no known cause, 88 were observed from samples with free chlorine less than 0.2 mg l^{-1} (representing 0.229 % of analyses from samples with free chlorine below 0.2 mg l^{-1}; Figure 6). Mahto and Goel (2008), Francisque *et al.* (2009) and Wang *et al.* (2009) observed that 0.3 mg l^{-1} free chlorine controlled re-growth in the distribution system and offered some protection against bacteria that enter through ingress. The data demonstrate that 121 failures with unknown causes were detected in water with free chlorine less than 0.3 mg l^{-1} (0.276 %), and if a tolerance of $\pm$ 0.1 mg l^{-1} were applied, up to 142 non-compliances could be avoided (0.314 %).

Recommendations for total chlorine in the literature are harder to clarify since some WTW operators apply chlorination and others chloramination. Most of STW's treatment works apply chlorination to the final water and none of the non-compliant samples in this case study were from chloraminated systems. The data show that 96 failures were detected in samples with total chlorine less than 0.3 mg l^{-1} (0.382 %) and 146 where total chlorine was below 0.5 mg l^{-1} (0.476 %; Figure 6).

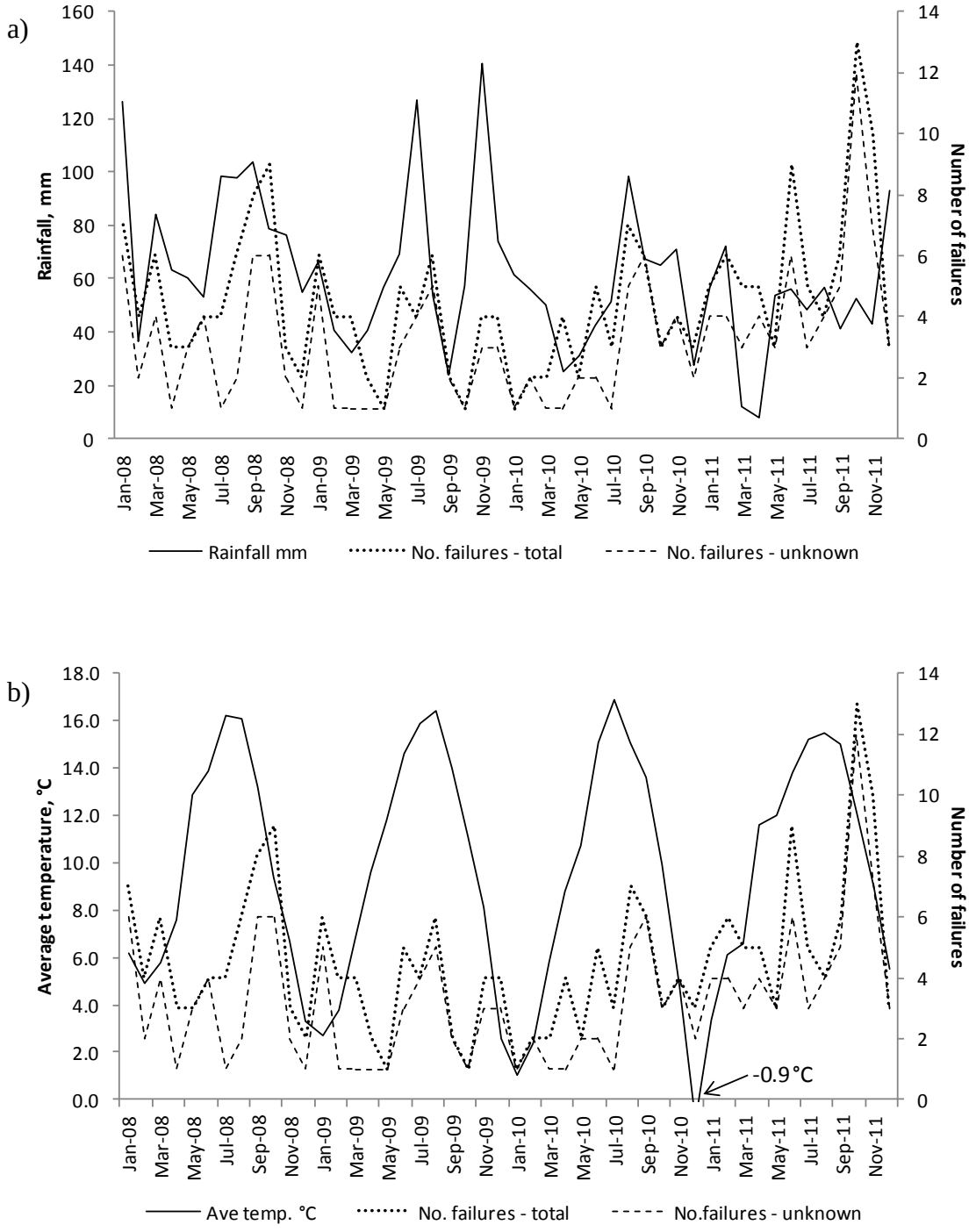

Figure 5: Monthly number of bacteriological failures (both total and those with unknown causes) plotted against a) total monthly rainfall and b) average monthly temperature between 2008 and 2011 (overleaf).

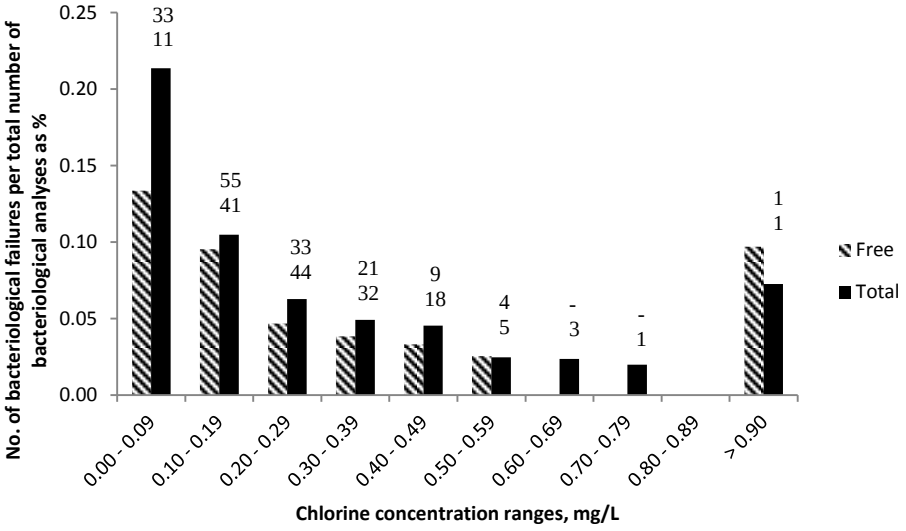

Figure 6: Percentage of bacteriological failures with no known cause per total number of bacteriological analyses grouped by free and total chlorine residual concentration between 2008 and 2011. The number of failures per parameter is presented above the bars, from top: Free, Total; - = no failures in this range.

When comparing the incidence of bacteriological failures before and after the change in sample tap disinfection protocol, the proportions of failures attributable to the different chlorine concentrations was similar (data not shown). Furthermore, non-compliances were evident even under conditions of 'adequate' disinfection; a finding echoed by Gouider *et al*. (2009). This suggests that bacteriological non-compliance cannot be controlled through improved chlorine management and sampling methods alone.

3.3.6. Impact of water temperature

Carter *et al.* (2000) demonstrated that higher water temperatures encouraged bacterial growth and Francisque *et al.* (2009) observed that counts of heterotrophic bacteria were greater above 18 °C. Sixty-five of STW's bacteriological failures were detected in water below 12 °C (0.154 % of analyses from samples with water temperature below 12 °C); nine in water above 18 °C (0.723 %); with the remaining non-compliances observed at water temperatures between 12.0 and 18.0 °C (0.075 %) (Figure 7). Chlorine's effectiveness as a disinfectant and its rate of decay increases with water temperature (Sawyer *et al.*, 2003; Crittenden *et al.*, 2005; Parsons and Jefferson, 2006). Faster chlorine decay is observed in warmer water conditions, and Francisque *et al.* (2009) demonstrated that when water temperatures were higher, increased residual free chlorine concentrations needed to be applied. Water temperatures were rarely above 18 °C in the STW region, which has skewed the percentage of failures for this temperature range. A larger number of failures were detected under cold and 'average'

conditions. Many chlorine dosing rigs are not operated in conjunction with direct temperature readings. Increasing and decreasing chlorine doses to improve water quality and palatability are carried out manually based on retrospective temperature trends.

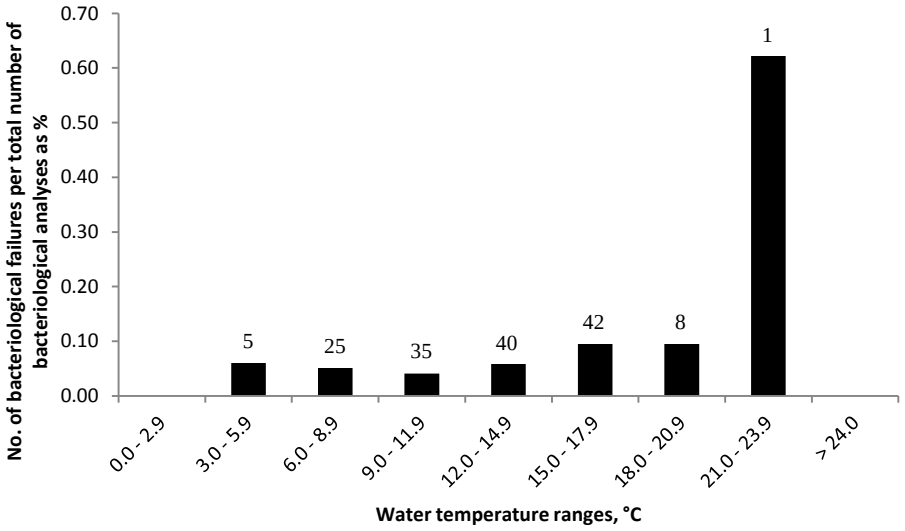

Figure 7: Percentage of bacteriological failures with no known cause per total number of bacteriological analyses grouped by water temperature between 2008 and 2011. The number of failures per parameter is presented above each bar.

3.3.7. Impact of source water type

Of the failures with no known cause, there were 62 from 100 % surface water sources (S; representing 0.067 % from this source water), 51 from 100 % groundwater sources (G; 0.045 %), 28 from blends with a greater proportion of surface water to groundwater (S > G; 0.056 %), 14 from blends where groundwater dominated surface water (G > S; 0.063 %), and one with an equal blend of surface- and ground-water (S = G; 0.063 %; Figure 8). STW has 18 100 % surface water WTWs, 123 100 % groundwater WTWs and seven mixed source WTWs. There were eight failures with no known cause from 100 % groundwater finals (0.018 %) and four from 100 % surface water finals (0.017 %). All surface water WTWs apply disinfection to their final water; groundwater WTWs apply disinfection at sites with lower raw water quality and marginal chlorination to high quality raw waters (marginal chlorination means dosing chlorine to meet the desired residual in supply, rather than dosing for disinfection; World Health Organization, 2004). Six of the eight 100 % groundwater WTW failures with no known cause were from sites with marginal chlorination.

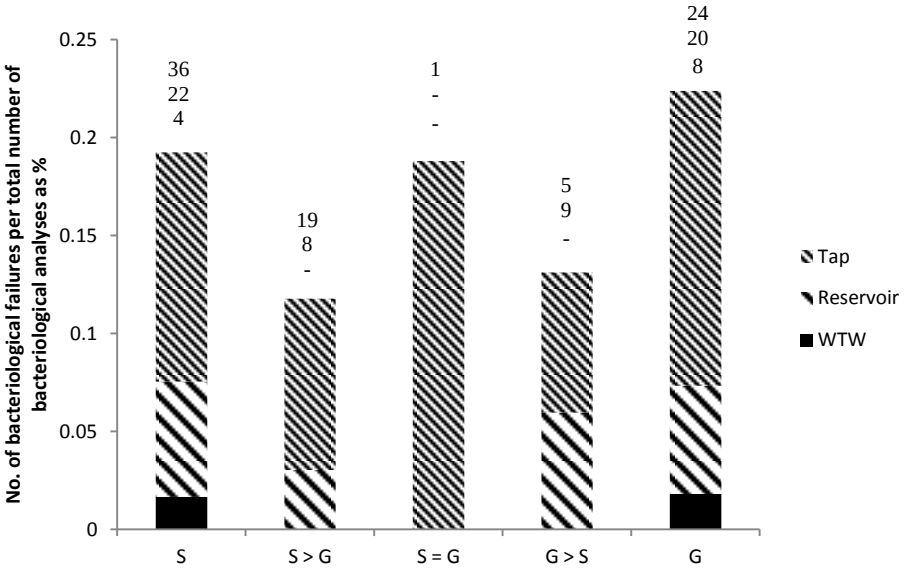

Figure 8: Percentage of bacteriological failures with no known cause grouped by source water type and divided by sample point between 2008 and 2011. The number of failures per parameter is presented above each bar, from top: Tap, Reservoir, WTW; - = no failures from that sample point.

Surface water treatment objectives include reduction in turbidity and organic matter; removal of metals such as aluminium, iron and manganese; as well as pesticides, nitrates, algae and bacteria. Groundwater resources are typically low in suspended solids, bacteria and organic compounds, but often require treatment for metals such as iron, manganese and arsenic (Parsons and Jefferson, 2006). Even after treatment, the chemical and biological composition of surface waters can pre-dispose them to changes in quality through the distribution system. The presence of carbon compounds in particular can encourage the growth of biofilms and the survival of planktonic bacteria even in the presence of residual disinfectants (LeChevallier *et al.*, 1987; Szewzyk *et al.*, 2000). Therefore, it is understandable that surface waters and surface water-dominated blends should represent a greater proportion of non-compliances. The presence of a high proportion of failures from 100 % groundwater sources has encouraged STW to re-investigate the catchments and the WTWs where increased raw water risks or deteriorations in final quality have been identified. These investigations have covered catchment management practices, borehole protection, and the treatment and disinfection requirements of the water to improve bacteriological quality.

3.3.8. Self-Organising Maps

Figure 9 shows that in 2008, 2010 and 2011 more failures were detected in winter months, whilst in 2009 more failures were observed in summer months. It also shows that the lowest chlorine residuals were found under the warmest water temperatures. Meanwhile, the highest chlorine residuals were recorded in the first half of each year,

when the water temperatures were cooler. Interestingly, the highest colony counts for detections of indicator organisms were also recorded under cooler water conditions. This suggests that although indicator organisms were present under a variety of chlorine concentrations, it is the temperature of the water that controls their numbers and that cooler water temperatures enhance their ability to survive disinfection. Figure 10 shows the Labelled SOMs. Each of these is independently clustered and they do not relate to one another.

In comparing the locations of the sample points (Figure 10a) it can be observed that WTW final (F) failures were more common in 2008, 2010 and 2011 and were limited to the cooler months (and water temperatures) of January, February, March and December. They had low colony counts. Failures were observed across the range of chlorine concentrations. This further highlights the need to manage water supplies better under cooler conditions, rather than focussing on the 'higher risk' warmer conditions. Service reservoir (R) failures were found throughout all years and at all water temperatures and chlorine concentrations. They also had low colony counts. Customer tap (T) failures were found under all conditions and accounted for all the higher colony counts recorded. The results show that total coliforms (CO) were found under all conditions and exhibited a variety of colony counts. *C. perfringens* (CL) were found predominantly in winter months and under cold to medium water temperatures. They were enumerated from water with low to medium chlorine concentrations. Colony counts were low. *E. coli* (EC) and Enterococci (EN) were not clustered in the labelled SOM due to their low incidence (Figure 10b). The observation that cooler water temperatures correlated with detections of indicator organisms contradicts received wisdom. The World Health Organization (2004) recommends maintaining water supplies below 15 °C to reduce bacterial growth in distribution. STW's supplies rarely exceeded 15 °C. Total coliforms are not strictly faecal in origin and their predominance at cooler water temperatures is therefore suggestive of environmental contamination. It is likely that the cooler temperatures impeded chlorine effectiveness and resulted in increased numbers of indicator organisms surviving disinfection. Furthermore, there is often more rainfall in the cooler months of the year and this could have flushed more bacteria into the source waters and presented a greater treatment challenge at the WTWs.

In terms of tap type (Figure 10c), the clusters of Severn Trent standard taps (ST) show that more assets failed in 2011, especially in the early part of the year. They had low

colony counts. They were found across the range of chlorine concentrations and water temperatures. Kitchen mixer tap, metal with insert (2K) failures were detected under all conditions. Kitchen single tap, metal with insert (4K) failures were observed in 2009 and 2010 between spring and autumn. They had low colony counts, low chlorine and medium to high water temperatures. Severn Trent standard taps and 2K taps represented one third each of the total distribution of tap types (Table 3).

The Labelled SOM for cause identification (Figure 10d) shows that single causes (S) tended to be identified in the first half of years 2009 to 2011. The failing samples had low colony counts, low chlorines and low to high water temperatures. Multiple potential causes (M) were observed in 2010 and 2011 between January and April. They also had low colony counts and low chlorines. Water temperatures were low to medium. Unknown causes (U) were recorded under all conditions.

In comparing the source water type (Figure 10e) it can be seen that surface water failures (S) were observed predominantly in 2008 and 2009, whilst groundwater failures (G) were mostly in 2010 and 2011. The highest colony counts were observed in blends of surface water > groundwater (SG). The highest chlorine residuals were recorded against groundwater (G) failures, which were also mostly found at cooler water temperatures. This suggests that at the groundwater sites, temperature was more important than chlorine residual in determining the effectiveness of disinfection.

It has been beneficial to draw together all the spot-sample data in the SOMs and observe how the parameters relate to one another. It has been especially valuable for its ability to include non-numeric data in the output. It does, however, generalise the data. This can be observed with regard to the *E. coli* and Enterococci results, which did not appear in the labelled SOMs. It is important to highlight this limitation. The outputs of these SOM analyses provide useful information for tackling the most prominent bacteriological parameter – total coliforms.

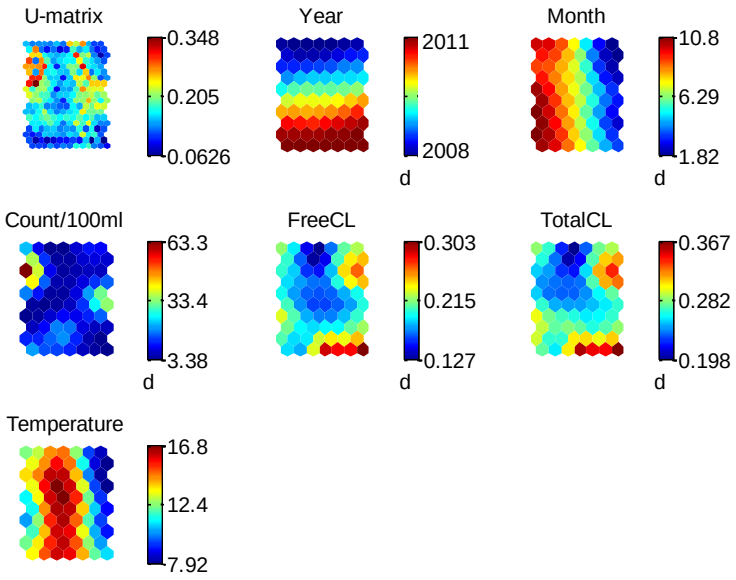

Figure 9: Self-organising map of year, month, colony count 100ml^{-1}, free and total residual chlorine and water temperature for all bacteriological failures January 2008 to December 2011.

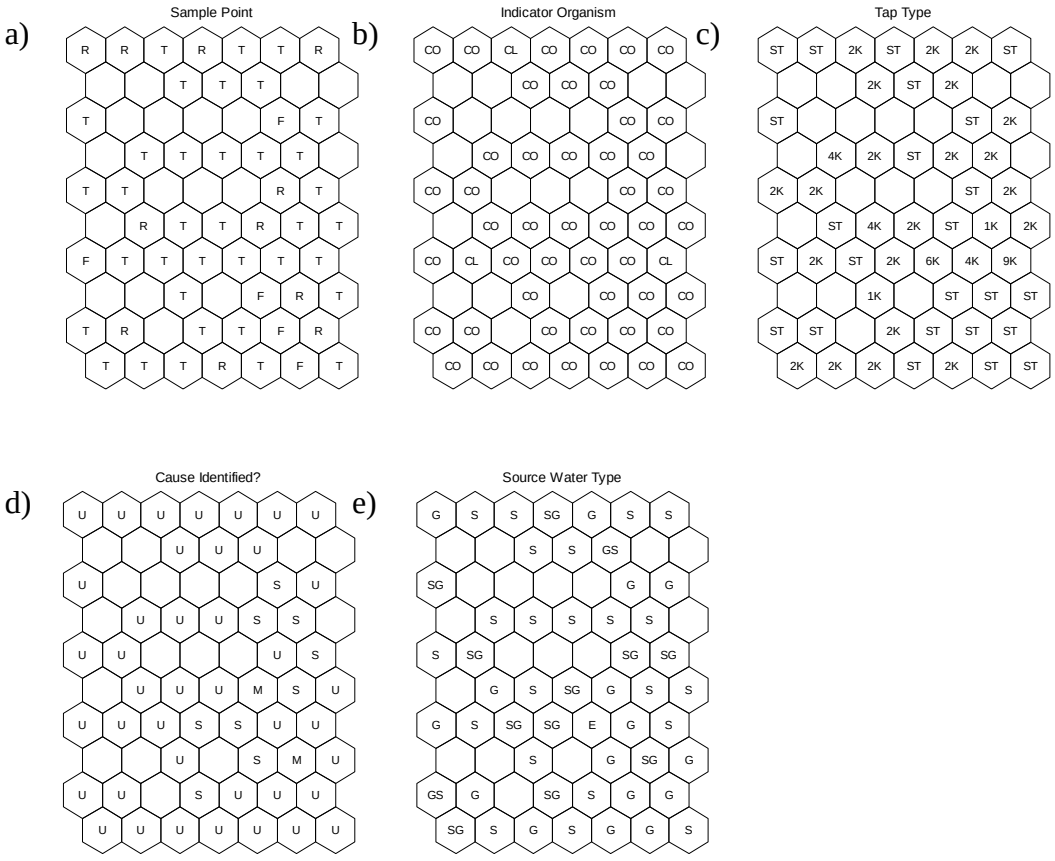

Figure 10: Labelled SOMs for a) sample point, b) indicator organism, c) tap type, d) success of root cause analysis and e) source water type.

3.4. Conclusions

- Water quality in the STW region is near excellent and exhibits high compliance with the regulations.
- Total coliforms were the indicator parameter that was identified most frequently.
- The majority of all detections were for fewer than 10 CFU 100 ml^{-1}.
- Whilst customer taps were the most vulnerable sampling point, failures were also identified in WTW finals and reservoirs which are within the control of STW and therefore provide an opportunity for focusing effort on reducing the number of failures. Furthermore, the impact of a failure at a customer's property is localised; indicator bacteria at a WTW or reservoir could expose a large number of consumers to potentially contaminated water.
- The cause of the majority of non-compliances was recorded as 'Unknown' because most of the failing sample points complied upon re-sampling.
- Samples from surface water supplies accounted for the highest number of failures, followed by groundwater supplies, with blended water having lower incidence of non-compliance. Surface water failures dominated in 2008 and 2009, whilst groundwater failures were more common in 2010 and 2011.
- WTW finals tended to fail under cooler water temperatures.
- Groundwater WTW finals failed more often than surface water WTW finals.
- STW's compliance under warmer water temperatures is good, but there is a need to focus on maintaining quality when the water is cooler.
- Single metal taps with inserts (4K) did not fail in winter. They failed when the water temperature was medium to high. Conversely, metal mixer taps with inserts (2K) failed all year round. This suggests that warming the tap during mixing can encourage bacterial growth.
- SOM analysis enabled the correlation of all the spot-sampled parameters for the 218 failures between 2008 and 2011. The loss of both Enterococci and *E. coli* from the labelled SOMs demonstrates both the value and weakness of using this tool: it focuses on the strongest relationships but it can lose important information about rarer events.

3.5. Recommendations

- It is suggested that an increased focus on compliance under 'normal' and cold water temperatures, in particular improved residual chlorine management, could reduce the frequency of failures. Whilst it is known that higher chlorine doses need to be

applied under warmer water temperatures to counteract the increased rate of chlorine decay (Sawyer *et al*., 2003; Parsons and Jefferson, 2006; Francisque *et al*., 2009), further research is required into managing the reduced efficacy of chlorine at lower water temperatures. This would benefit water companies in countries, including the UK, whose water temperatures rarely exceed the 15 °C recognised by the World Health Organization as promoting the growth of bacteria and increasing the decay rate of chlorine (World Health Organization, 2004).

- The greater number of failures from groundwater WTWs compared with surface water WTWs should encourage increased focus on water treatment processes to ensure continued compliance with bacteriological water quality parameters. It is also recommended that STW do not simply focus on one source type at a time – the observation that most surface water failures were detected in 2008 and 2009 and most groundwater failures in 2010 and 2011 suggests that this has happened in the past.
- Present strategies for maintaining sampling equipment do not allow the programme to continue in the face of un-planned work. This means that sites that are 'at risk' may not get their sample lines and taps replaced in a timely fashion, which perpetuates the problem of false positives – higher investment is recommended in this crucial preventive measure. Furthermore, this study suggests that greater focus should be given to pro-active maintenance of sample points at assets to improve compliance. For example, ensuring that sample points are kept in hygienic conditions and making regular site visits to identify and resolve potential risks to bacteriological quality.
- A larger dataset of failures would serve to strengthen the findings of this research. This could involve collecting the same data from other water companies that employ the same sample collection process or collecting more historical data from STW and accounting for the differing sampling protocols.

This company data review has answered the four research questions:

1. What are the main causes of bacteriological non-compliances in UK water supplies?

This study has shown that most bacteriological failures at STW have no cause identified. It concurs with the findings of UK Water Industry Research (2009). This makes it difficult for water companies to act upon non-compliances to improve performance. The research has highlighted the need for better investigative tools. Where causes were identified, the cleanliness of the tap was the principal reason.

2. Where in the water supply system do most bacteriological failures occur?

Most bacteriological failures were detected at customers' taps. Of the sites within the control of STW, the highest risk sample points were service reservoirs. Failures at service reservoirs and WTW finals require significant time and financial investment to investigate and remediate and this research should focus on these sample points.

3. Which indicator organism is most frequently detected?

Total coliforms were the most common failure parameter. These bacteria can be derived from environmental and faecal sources.

4. Is UK bacteriological compliance impacted by weather phenomena?

There was a weak correlation between weather phenomena and bacteriological failures, which concurs with the findings of Schets *et al.* (2005) and Pitkänen *et al.* (2008). With regard to rainfall, the relationship was further weakened by including a time lag of one or two months, which differed from the observations made by Curriero *et al.* (2001). Furthermore, the research has shown that failures are detected all year round at customers' taps and service reservoirs, but that those at WTW finals were more common under cooler water conditions. Thus it is necessary for greater efforts to be directed at improving bacteriological compliance at WTWs under cool water temperatures to ensure the quality of water in the distribution system.

This chapter has shown that none of the routinely measured parameters alone is a suitable predictor for bacteriological quality and that even with 'adequate' water quality and disinfectant concentrations at the time of sampling, non-compliances do still occur. It is thus important that research objectives in the future are based around the combined impacts of important water quality parameters (for example, chlorine residual, turbidity and water temperature) on bacterial survival.

4. Cost of Bacteriological Water Quality Failures

4.1. Introduction

To enable an assessment of the cost effectiveness of the outputs from this project it is important to develop a realistic estimate of the cost of bacteriological failures to Severn Trent Water (STW). This is the first time such a piece of work has been completed within STW and it answers research question 6:

6. What financial impact do bacteriological failures have on a UK water company?

4.2. Methods

The costs of investigation and remedial actions in response to bacteriological failures were determined for the 218 failures recorded between January 2008 and December 2011. Twelve of the 218 failures were from one sample with two indicator organisms detected. The investigations are based on failing samples, rather than parameters and thus there were 206 investigations conducted. The method for determining the costs of these investigations is summarised in Figure 11.

The following data were extracted from the relevant Exception Reports:

- Post code (customer tap only);
- Number of suites of analysis carried out and the time spent collecting these samples. A suite of analyses included on-site chlorines and temperature, heterotrophic plate counts at 22 and 37 °C, coliforms, *Escherichia coli, Clostridium perfringens* and Enterococci.

The post codes for assets were determined by extracting the x,y coordinates for the asset from "Sample Manager". These data were inputted into www.gridreferencefinder.com and the nearest post code function was used to obtain the result.

STW have two in-house microbiology laboratories: at Church Wilne and Shelton. Samples are sent to one of these laboratories based on their location within STW's region. A list of the water quality zones (WQZs) allocated to each laboratory was requested from the Scheduling team. WTWs and reservoirs are not included on the list, so the laboratories for these sampling locations were extrapolated. It was assumed that Quality Inspectors (samplers) went from and returned to the respective laboratories during the investigation. There are three Water Quality team offices: Little Eaton,

Frankley and Staverton. It was assumed that Water Quality staff departed from and returned to their bases during investigations. For the purposes of this study, it was assumed that Operations staff and Regulations and Fittings inspectors (inspectors of plumbing and pipe-work) were based at the same regional offices as the Water Quality team.

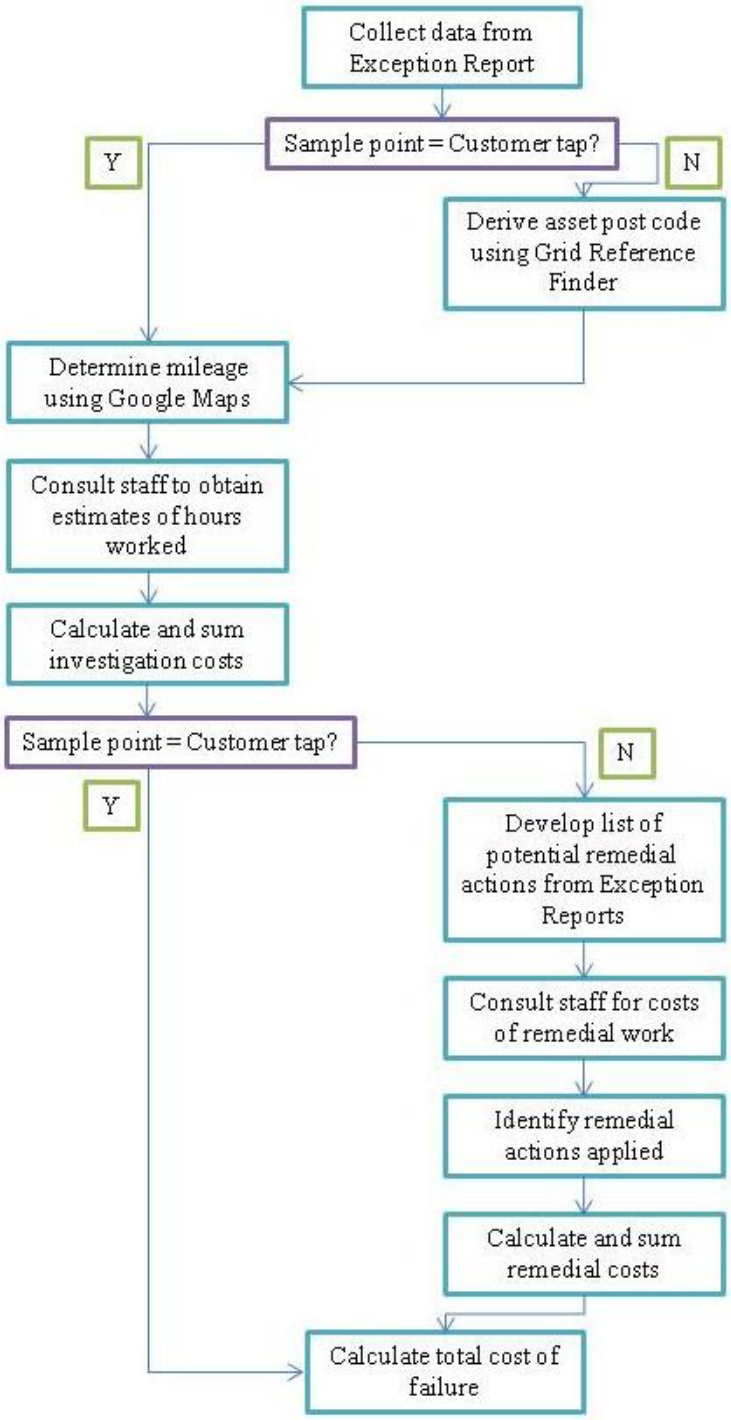

Figure 11: Flow chart of the process of deriving the total cost of bacteriological failures.

The number of miles driven by staff was derived from the post codes of the laboratories, the offices of the Water Quality team and the failure locations. The values were determined using Google Maps directions, taking the quickest route whilst avoiding toll roads.

Estimates of Quality Inspector hours were obtained based on the sample times in the Exception Report and rounding up to the nearest four hours, to include travel between sites and the laboratory. If the sampling time exceeded four hours it was assumed that more than one trip had been made to collect samples. This accounted for the additional travel time between sites.

The time for analysis includes media preparation, sample registration, plating samples, and reading the plates at the end of the incubation period; this was assumed to take twice the number of hours spent sampling.

The number of visits by Operations staff was estimated from the reports. Each visit was assumed to take four hours: two hours for travel and two hours on site.

The time spent by the Water Quality team investigating the failure was based on estimates provided by Jenny Surry and Roger Hinton (Water Quality Technicians, STW): five hours per customer tap and two days per asset (including one day on site). If the Exception Report showed that the investigation was complex, additional hours were allocated.

Where a Regulations and Fittings inspection was requested, a visit was assumed to take four hours; where the inspector attended but was not able to enter the property, this was allocated two hours (travel time).

Hours spent by the Public Health and Standards team were based on estimates provided by Shaun Dowen (Public Health and Standards Advisor, STW): one day for a customer tap; and, depending on the complexity of the investigation, two to four days per reservoir failure and two to five days per WTW failure.

Phil Gnych (Water Regulations Principal Advisor, STW) estimated that two hours was an appropriate average time spent per failure by the Reporting team.

Having determined the number of analytical suites, miles driven and hours worked, the following values were used in the calculation of the cost of investigating bacteriological failures:

- Analytical suite: £5.00 (for materials, electricity and maintenance of apparatus) – value approved by Karen Heaton (Microbiology Laboratory Manager, STW);
- Fuel price: £0.45 per mile (includes maintenance allowance) – figures for 2011/2012 (HM Revenue & Customs, 2012);
- Hourly rate: £26.50 (includes salary, training and pension) – value provided by Christopher Bridge (Good to Drink Project Leader, STW) and used for Price Review assessments.

The investigation costs were calculated using the following equation:

Cost of Failure Investigation = No. Analyses x Price per suite
+ Total No. Miles driven x Price per mile
+ Total No. Hours worked x Hourly rate

For some of the failures, specialist operations were conducted as part of the investigation, rather than during the remediation phase; for example, draining down and inspecting a reservoir. Where this was the case, the costs of these additional operations were applied to the respective investigations.

In addition to the investigation costs, the costs of remedial works were compiled.

It was assumed that the cost of all remedial works at customers' properties was borne by the customers. Furthermore, it was assumed that all remedial actions proposed for each WTW final and reservoir site were carried out. The potential actions were:

- Sample line replacement;
- Replacement reservoir;
- Reservoir cleaning;
- Replacing reservoir hatch seals;
- Replacing reservoir membranes;
- Disinfection kit;
- Rabbit-proof fencing;
- Enhanced monitoring.

Cost estimates for sample line replacement were provided by Charlotte Jordan (Water Quality Advisor, STW) and based on 2010 figures. The chosen cost was based on the description of the proposed remedial works in the Exception Report.

- Minimum cost: £1,000
- Maximum cost: £10,000
- Average cost: £5,126

Reservoir capacity and cost of construction data were supplied by Steve Hickman (Price Review 2014 estimator, STW), plotted and a power curve fitted to the points (R^2 = 0.9953). The equation for the curve was used to calculate the cost of constructing a new reservoir.

Cost of New Reservoir = 65093 x Capacity$^{0.4349}$

Where Capacity = reservoir capacity, m^3

Phil Robinson (Asset Creation Non-Infra Solutions Manager—West, STW) estimated the cost of isolating a reservoir (to de-commission it) at approximately £20,000.

Peter Williams (Price Review 2014 Non-Infrastructure Data Analyst) provided the following equation for the calculation of reservoir cleaning costs:

Cost of Reservoir Clean = (0.2501 x Capacity) + 1122.2

Where Capacity = reservoir capacity, m^3

Using data provided by Peter Williams, the average cost of replacement hatch seals was calculated as: £11,200.

Using data provided by Peter Williams, the average cost of replacing reservoir membranes was calculated as: £53,000.

Activities relating to chlorination equipment were assigned cost estimates provided by Amy Hazard (Water Quality Advisor, STW) and based on 2011/2012 figures:

- Relocating a chlorinator: £3,200
- Installing flow-control on a chlorinator: £500

- New booster chlorinator
    - Maximum cost: £8,000
    - Minimum cost: £6,000
    - Average cost: £6,800

One chlorinator required the installation of an automatic re-start function. It was assumed that this cost the same as installing flow-control.

Steve Gill (Capital Liaison Co-ordinator – Water Distribution, STW) obtained the costs of fitting rabbit-proof fencing to a reservoir site.
Mesh only: £5.50/m of perimeter. With overheads (at 20 %), £6.60/m
Mesh, post and rail: £8.50/m of perimeter. With overheads (at 20 %), £10.20/m
It was estimated that a team of four could install 500 m of fencing in four days (32 hours). Standard hourly rates were applied.

Enhanced monitoring was allocated a cost of £500.

It was assumed that all remedial activities recommended in the Exception Report were carried out at the assets. For each failure, the activities were listed and the respective costs calculated (as necessary) and then summed to give a final cost of remediation.

A number of assumptions were made throughout the process of determining the cost of failure:

- Quality Inspectors went from and returned to either Church Wilne or Shelton laboratory during the investigation.
- Operations staff and Regulations and Fittings inspectors were based at the same regional offices as the Water Quality team: Little Eaton, Frankley or Staverton. These staff went from and returned to their bases during the investigation.
- All journeys were the quickest available, whilst avoiding toll roads.
- Travel time from the base to the sample point was assumed to be one hour.
- Quality Inspectors spent four hours collecting samples in the majority of cases.
- The laboratory staff spent eight hours analysing samples in the majority of cases.
- Operations staff spent four hours visiting WTWs and reservoirs during site visits.
- The Water Quality team spent five hours working on customer tap failures and two days on asset failures in the majority of cases.

- Regulations and Fittings inspectors spent four hours carrying out their investigations.
- The Public Health and Standards team spent one day completing a customer tap Exception Report, two to four days on a Reservoir Report and two to five days on a WTW Final Report, depending on complexity.
- The Reporting team spent two hours compiling Drinking Water Inspectorate reports following each investigation.
- A suite of analyses cost £5.00.
- Fuel price was set at £0.45 per mile.
- The hourly rate was £26.50 for all personnel.
- Customers bore the cost of remedial works at their properties.
- All remedial actions proposed for each WTW final and reservoir site were carried out.

4.3. Results and Discussion

In total, STW spent £335,000 investigating bacteriological non-compliances between 2008 and 2011. Failures at WTW finals cost a total of £42,650; reservoirs cost £165,000; and customers' taps cost £125,000 (Figure 12a). The average cost per failure at each of the three sample points was £2,700 at WTW finals, £2,500 at reservoirs, and £1,000 at customers' taps (Figure 12b). The investigation of WTW final non-compliances includes analysis through the treatment process at the WTW as well as sampling from distribution; for these reasons, these failures are more costly to investigate. Customer tap failures typically require re-sampling at the original failing property and several neighbours in the same supply zone, resulting in much lower investigation costs. The previous cost assumption used within STW was £100 per investigation from all sample points.

Reservoir failures result in sampling from the WTW to the customer and other reservoirs in the same supply line. The average cost of investigating reservoir failures was similar to that of WTW finals partly because several reservoirs were drained down and inspected as part of the investigation, which inflated the cost.

In total, STW spent £2,900,000 remediating failures at WTW finals and reservoirs over the four year period. Remedial works at WTWs cost £65,550, whilst at reservoirs the total was considerably more at £2,800,000 (Figure 13a). The average cost of

remediating failures at each asset was £4,100 per WTW final and £42,400 per reservoir (Figure 13b).

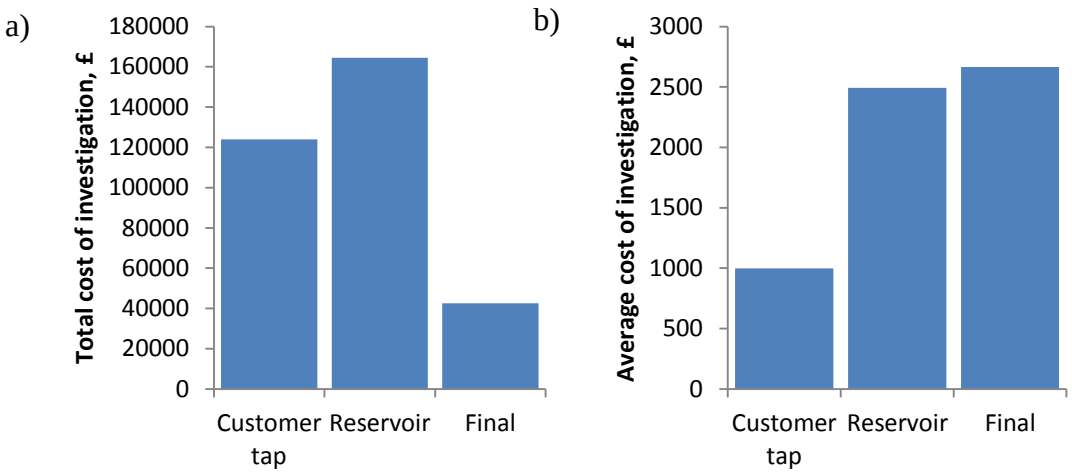

Figure 12: a) Total and b) average costs of investigating bacteriological failures.

The measures that can be taken at WTWs were limited to installing enhanced chlorination equipment and improving turbidity removal processes such as coagulation/flocculation. However, the interventions that were possible at reservoirs were more varied and often more extensive. For example, draining down and inspecting a reservoir frequently led to additional works, such as replacing hatch seals or membranes. In one instance, the reservoir was decommissioned and a new reservoir required.

Figure 14a shows the contribution that individual reservoir and WTW failures made to the total costs for assets. The decommissioning and replacement of one reservoir (North Malvern, shown in purple in Figure 14a) dominates the chart. In Figure 14b, that reservoir was excluded, and the average cost for reservoir remediation was reduced to £8,100 per failure.

The remedial costs for North Malvern reservoir have been deferred to Asset Management Period 6. A new reservoir will be built close to the site that has provided water to customers in North Malvern reservoir's zone since it was de-commissioned. Major reservoir construction projects were completed during the 2008 to 2011 time period. A new cell was added to an existing reservoir to increase capacity (Barby) and two new reservoirs were constructed: one to replace a reservoir at the end of its life (Coundon) and the other to replace a reservoir whose condition had deteriorated and

was at risk of intrusion (Mow Cop) (Brian Jones, Strategic Analyst—Distribution Strategies, STW).

Whilst North Malvern's replacement costs have been deferred, the fact that several major reservoir construction projects were completed in the four year period justifies the inclusion of the remediation costs in these calculations. Over the four year period, the total cost to STW for investigating and remediating failures was £3,235,000. Reservoir failures cost £2,965,000 and accounted for 92 % of the total. The total costs of failures from WTW finals and customers' taps were £108,200 and £125,000, respectively (Figure 15).

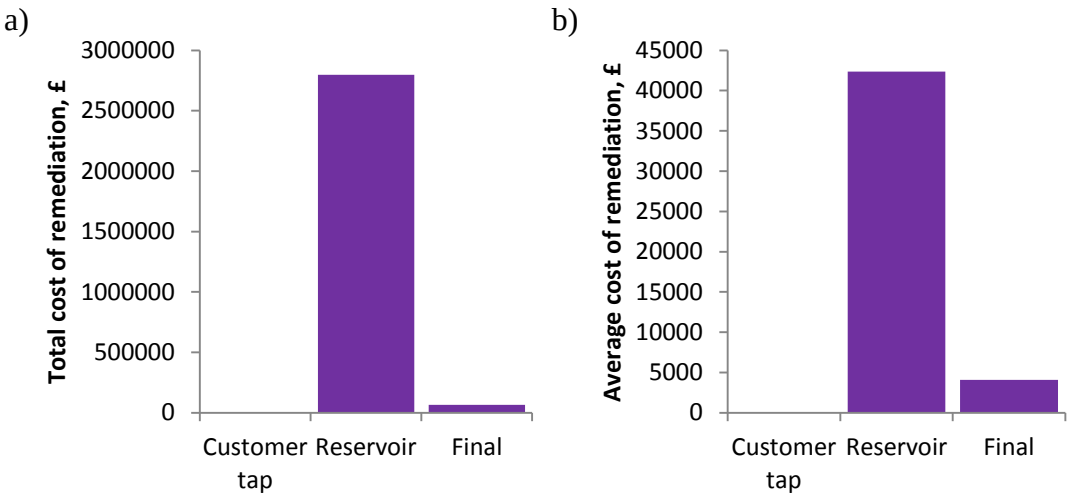

Figure 13: a) Total and b) average costs of remediating bacteriological failures.

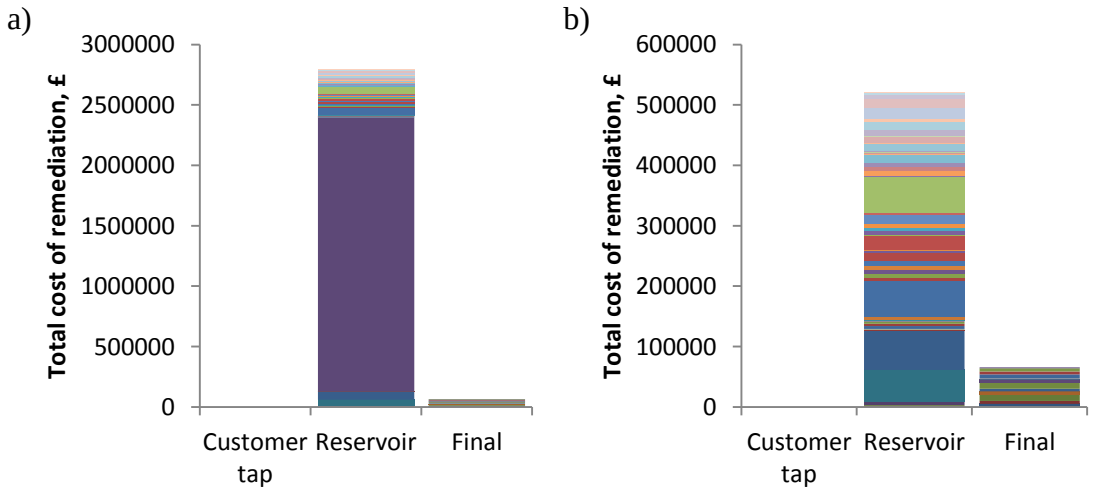

Figure 14: Individual contributions to the total cost of remediation made by each failure, a) including and b) excluding the replacement of North Malvern reservoir.

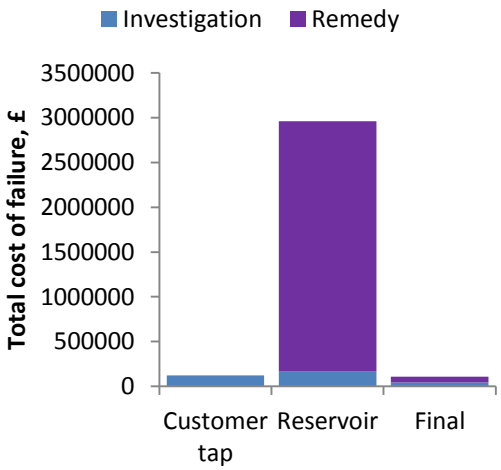

Figure 15: Total costs of investigating and remediating bacteriological failures.

To illustrate the process of determining the cost of non-compliance, three failures were selected: one WTW final, one reservoir and one customer tap. These were selected because they all failed for the same bacteriological parameter, were relatively simple investigations and the failures were all attributed to the sample tap or sample line (Table 5).

Investigating the coliform failure at Cosford WTW involved more staff hours, more analyses and an additional programme of enhanced monitoring. Lower Sweeney reservoir had less than half the investigation costs. This is largely because of a smaller re-sampling programme with consequent reductions in hours for Quality Inspectors and laboratory staff. The lowest investigation costs were attributed to the customer tap in Coalville Water Quality Zone. The investigation was localised and was completed with a single Quality Inspector visit: the original tap was sampled pre– and post-disinfection, an alternative tap at the property was sampled and five other properties in the same zone were visited, along with the upstream reservoir. For all investigations, indicator organisms were detected either on the tap swab or in the water samples.

In terms of remediation costs, STW sent a letter to the customer in Coalville WQZ advising them to clean their tap thoroughly. They were unable to provide further guidance because the Regulations and Fittings inspector had been unable to enter the property to assess the plumbing arrangements. Lower Sweeney reservoir required a new sample tap and Cosford WTW needed a replacement sample line (including the tap). These actions were carried out at the assets.

Table 5: Three case studies illustrating the calculation of the cost of bacteriological failures: one WTW final, one service reservoir and one customer tap.

Site Name	**Cosford WTW**	**Lower Sweeney Res**	**Coalville WQZ**
Year	2009	2010	2008
Sample Point	Final	Reservoir	Tap
Type of Failure	CO	CO	CO
Post code	TF11 9HY	SY10 9HT	LE672AW
No. Customer tap samples	26	7	8
No. Reservoir samples	6	21	1
No. WTW samples	41	0	0
No. of Analyses	73	28	9
Lab	Shelton	Shelton	Church Wilne
Miles to lab.	25.7	16.7	18.5
WQTeam office	Frankley	Frankley	n
Miles to WQ and Ops office	24.6	70	0
R&F office	n	n	Little Eaton
Miles to R&F office	0	0	28
Total miles	610.2	380.2	93.0
No. QI VISITS	9	3	1
No. QI HOURS	36	12	4
No. Scientist (Lab.) HOURS	72	24	8
No. Operations VISITS	2	1	0
No. Operations HOURS	8	4	0
No. Water Quality Team VISITS	1	1	0
No. Water Quality Team HOURS	28	24	5
No. Regs&Fittings VISITS	0	0	1
No. Regs&Fittings HOURS	0	0	2
No. PH&S HOURS	40	28	8
No. Reporting HOURS	2	2	2
Total staffing HOURS	186	94	29
Additional investigation actions	Enhanced monitoring	None	
Additional InvCosts, £	£ 500.00	£ -	£ -
COST to Investigate, £	£ 6,100.00	£ 2,800.00	£ 885.00
Failure cause	Sample line/tap	Tap	Tap
Recommended remedial works	Sample line replacement	Sample tap replacement	
COST to Remedy (STW), £	£ 5,130.00	£ 1,000.00	£ -
Recommendations acted on?	Y	Y	
Total Cost of Failure	**£ 11,230.00**	**£ 3,800.00**	**£ 885.00**

The customer tap failure in Coalville WQZ had the lowest overall cost, and was less than a quarter the cost of Lower Sweeney reservoir, which was approximately one third the cost of the failure at Cosford WTW.

It can also be seen from these case studies that the numbers of staff hours required to investigate each failure differed greatly. It took 186 h to complete the investigation into the failure at Cosford WTW, 94 h for Lower Sweeney reservoir and 29 h for the customer's tap in Coalville WQZ. Summarising the number of hours worked for all the failures between 2008 and 2011 shows that reservoirs accounted for the largest number of total hours worked: 4550 h; closely followed by customers' taps: 4250 h; WTW finals accounted for 1380 h (Figure 16a). The average number of hours shows that more hours were invested in WTW finals: 87 h; with 69 h for reservoirs; and 34 h for customers' taps (Figure 16b).

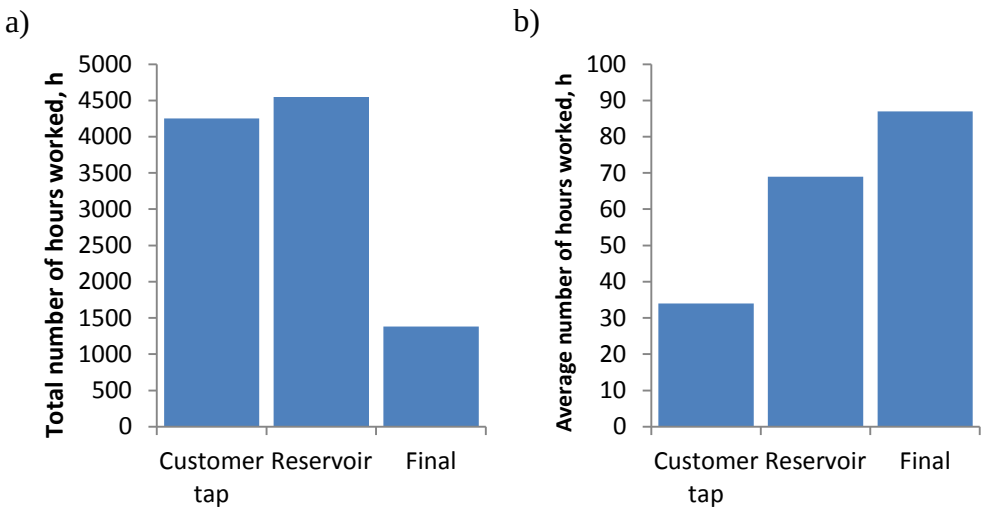

Figure 16: a) Total and b) average numbers of hours worked during investigations.

These investigation and remediation costs should be set within the context of the health benefits of monitoring for bacteriological quality. Not one of the failures between 2008 and 2011 was linked to reported waterborne illness. Whilst the costs are significant they represent good value for money in protecting the health of consumers.

4.4. Further Considerations

Aside from the costs quantified in this chapter, there are additional costs experienced by water companies when their performance falters, including loss of public confidence

and regulatory sanctions. Loss of public confidence is a difficult issue to account for. Unlike other services, it is not possible to change suppliers. This is why the regulatory sanctions are important: they ensure that the product cost represents the performance of the water company in the last financial period. This is administered by the UK Government's Office for Water (Ofwat).

Ofwat have two sets of serviceability indicators: one relates to the distribution pipes (Water Infrastructure) and the other to WTWs and reservoirs (Water Non-Infrastructure). The Infrastructure category covers numbers of burst mains, unplanned interruptions to supply, iron compliance at the customer tap, number of properties at risk of low water pressure, customer contacts for discolouration and combined compliance for turbidity, iron and manganese (Ofwat, 2009). Bacteriological parameters do not feature in the Infrastructure serviceability indicators. The Non-Infrastructure indicators cover coliform non-compliance at WTWs, coliform non-compliance at reservoirs (sanctions begin when >5 % of samples fail from a single site), turbidity at WTWs, number of enforcement actions considered for microbiological standards, and unplanned maintenance (through equipment failure or reduced asset performance) (Ofwat, 2009).

Where water companies fail to meet the serviceability agreements made at the start of each financial period, Ofwat has the power to impose sanctions. These can be up to 50 % of the present value of the capital maintenance expenditure for that indicator as detailed at the start of the financial period. There are several considerations made when determining the extent of the sanctions: whether the situation is marginally or seriously non-compliant, how far from the reference levels of stability the indicator parameter is, whether the company is able to demonstrate improvements in serviceability since the failure was recorded, and whether the failure has already resulted in legal interventions or failed service to customers (Ofwat, 2009).

These serviceability indicators show that bacteriological non-compliance at the customer tap does not result in sanctions, but that Ofwat penalise water companies for not properly maintaining their assets and assuring the quality of water from these sample points.

4.5. Conclusions

- This study has enabled the first realistic estimate of the cost of bacteriological failures to STW and, by inference, for UK water companies.
    - Since presenting this work to STW, these figures, and the accompanying method, have been adopted by STW for their regulatory reporting and future cost forecasting (Asset Management Plan 2014 Price Review).
- This study has highlighted the high costs of investigating and remediating failures from WTWs, reservoirs and customers' taps. Whilst the number of customer tap non-compliances was the highest, the low cost of individual investigations meant that overall their impact on STW was small. Likewise, the high cost of failures at WTWs combined with their rarity showed a similarly small impact on the Company. The high costs of investigating and remediating failures at reservoirs and the number of incidences over the four year period meant that they represented a significant proportion of the total costs.
- The total cost of 206 failing samples over the four year period was £3,235,000; of which 92 % was for failures at reservoir sites.
- When bacteriological failures are detected, water companies can also experience a loss of public confidence and face financial sanctions from Ofwat. These sanctions can be significant.

This data analysis has answered the research question:

6. What financial impact do bacteriological failures have on a UK water company?

The average costs of investigating bacteriological failures were £2,700 for WTWs, £2,500 for reservoirs and £1,000 for customers' taps. Remediating costs were, on average, £4,100 for WTWs and £42,400 (or £8,100 without North Malvern reservoir). The total cost for the 206 failing samples between 2008 and 2011 was £3,235,000.

The costs of bacteriological failures to a UK water company were calculated for the first time. The average costs were an order of magnitude larger than STW had been using in their financial forecasts. The use of accurate costs ensures realistic projections and prevents monetary losses from regulatory operations. The method that was employed has promise for use by other water companies and in other countries that have the same or similar investigatory requirements in the event of bacteriological failures.

5. Root Cause Analysis of Bacteriological Failures from Mythe WTW[2]

5.1. Introduction

In Chapter 3 it was observed that there were weak correlations between the presence of indicator organisms in drinking water samples and other data relating to spot samples: free and total chlorine and water temperature, amongst others. The reliance on spot-sampling data was a weakness of this study. Work by Codony *et al.* (2005) observed that discontinuous chlorination affected the efficacy of disinfection as demonstrated by heterotrophic plate counts (HPCs). Their work involved neutralising the chlorine in a test reactor for periods of several days. They observed that after each period of neutralised chlorine the effects of disinfection were reduced and counts of heterotrophic microorganisms increased. This work seeks to identify whether short-term variations in archived on-line residual free chlorine, turbidity and flow could have impacted bacteriological water quality in supplies at Severn Trent Water (STW). In order to determine the usefulness of on-line monitoring parameters it was necessary to select sites that not only had experienced bacteriological failures but also had several monitors. This excluded customer tap and reservoir failures.

This chapter seeks to answer research question 5:

5. Can improved analysis of on-line monitoring and spot-sample data be used to inform the root cause analysis of bacteriological failures?

The research focuses on a case study from Mythe WTW. Despite extensive investigations by STW, no causes were identified for the failures from this site. This is the outcome for approximately two thirds of all failure investigations (Chapter 3). Since no causes were identified, the failures from this site were selected for the data analysis in this research. The data analyses use cross-correlation and self-organising maps (SOMs). This study represents the first application of both tools to the analysis of the bacteriological quality of drinking water.

Mythe WTW had three coliform detections between March 2011 and November 2012. These were on the 31st March 2011, the 8th March 2012 and the 17th November 2012. Mythe WTW treats surface water from the River Severn. Mythe WTW produces 120 ML d^{-1} using the process outlined in Figure 17.

[2] This chapter has been published in part in the Procedia Engineering publication K. Ellis *et al.*, In Press.

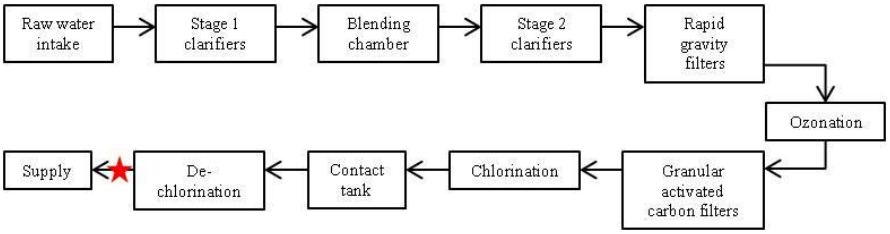

Figure 17: Process flow diagram for Mythe WTW; ★ marks the location of the on-line monitors and final spot-sampling point.

In Chapter 2, potentially suitable tools for identifying time lags in time-series data were reviewed. Cross-correlation was selected because it is reasonably robust to variable sampling frequencies and can be used for datasets with fewer than 50 observations. It is also less computationally expensive than either wavelet analysis or Auto-Regressive Integrated Moving Average method. Self-Organising Maps were used to develop water quality fingerprints for the reasons given in Chapter 3.

5.2. Methods

5.2.1. Data collection

Spot-sampling occurs daily at Mythe WTW final sampling point. The following results were extracted from STW's data handling software for the periods 1st January to 30th June 2011, 1st January to 30th June 2012 and 1st September 2012 to 28th February 2013: coliforms, colony forming units (CFU) 100 ml^{-1}; HPCs at 22 °C and 37 °C (HPC22 and HPC37), CFU ml^{-1}; free chlorine, mg l^{-1}; and water temperature, °C. In addition, for the same time periods, the following archived monitoring data for Mythe WTW final monitoring points were requested from STW's Asset Creation Data Team: free chlorine, mg l^{-1}, Sigrist AquaScat WTMA (Sigrist, Germany); turbidity, nephelometric turbidity units (NTU), Capital Controls® TVU/CC1930 (Severn Trent Services, Philadelphia); and flow, ML d^{-1}, Marsh Multi-Mag™ 285L (Marsh-McBirney Inc., Maryland). Free chlorine data were archived every 1 min and turbidity and flow data were archived every 15 min. The final sampling point and the on-line monitors are all situated after de-chlorination and before the storage tank from which water is pumped to supply (Figure 17).

Chemical, physical and bacteriological analyses were conducted by STW samplers and laboratory staff as detailed in Chapter 3.

5.2.2. Data manipulation

The datasets were saved in Microsoft® Excel (Microsoft Corporation, Washington) and any unnecessary columns from the on-line monitoring datasets were deleted (for example, monitor name) and column headers were deleted from all datasets. Using Excel's Remove Duplicates tool the date and time column was checked for duplicate entries and if any were found the first entry was retained and the other rows deleted. Because the on-line monitoring data was received as a .txt file the date and time column was not formatted correctly. These columns were classified as containing date and time data of the format 'DD/MM/YYYY hh:mm'. Each prepared dataset was saved as a .csv file.

All datasets were imported into MATLAB® R2012a Student Version (The MathWorks Inc., Massachusetts). The following code details the import process and the conversion of the formatted date and time column to MATLAB's date-number (datenum) format:

```
file_1='Dataset1'; %Specifies the name of the file to import

filename1 = strcat(file_1,'.csv'); %Specifies the .csv extension

count=0;
    fid1=fopen(filename1, 'r+');
    if (fid1~=-1) %If file found, start import
        data = textscan(fid1, '%s%n','delimiter',',',...
'Whitespace','\tb','commentStyle', '"');
        dates=datenum(data{1}, 'dd/mm/yyyy HH:MM');
        parameter1=data{2};
        samples=size(dates,1);
        count=count+1;
        fclose(fid1);
    else %If file not found, display alert
        disp('no file present')
        cd('..')
    end
```

Before conducting any data analysis, it was necessary to ensure that all columns had the same number of rows. To prepare datasets for interpolating and zero-padding, they were specified as datasets and their columns were named, using the following code:

```
Data1=dataset(dates, parameter1, 'VarNames',{'Date'...
      'Parameter1'});
```

The individual files were combined to form a single dataset using functions to join, interpolate, or fill as necessary. These functions all retain the column names as defined in the previous step. Where parameters were sampled at the same interval, for example final coliforms and final HPC bacteria, these files were joined using the 'join' function:

```
Data3 = join(Data1,Data2,'key','Date','Type','outer',...
   'MergeKeys',true); %Joins files with one Date field in the output
```

Linear interpolation was applied to data from turbidity monitor, flow monitor, spot-sampled chlorine and temperature spot data, using the date-number field from chlorine monitor data (Wyer *et al.*, 2010). Linear interpolation was selected because it does not extrapolate beyond the input data.

```
interpolation1 = interp1(Data5.Date, Data5.Parameter5, ...
      Data4.Date, 'linear', 'extrap'); %Uses Date4.Date as a template
```

Zero-padding was used for all the bacteriological parameters from the Mythe datasets. Zero-padding ensures that when colonies were recorded, the results remained as integers. The column to be zero-padded is joined to the template dataset. In this process, if a cell contains no data MATLAB records it as 'not a number' (NaN). The zero-padding converts the NaNs to 0's, as detailed below.

```
Data8 = join(Data6,Data7,'key','Date','Type','outer',...
        'MergeKeys', true); %Joins new column to template dataset

Data8.NewColumn(isnan(Data8.NewColumn)) = 0; %Replace NaN with 0
```

These processes resulted in three Mythe datasets which were time-aligned at 1 min intervals.

5.2.3. Cross-Correlation

Twenty-seven cross-correlations were applied to each joined dataset for Mythe, as detailed in
Table 6. Where there is an 'x' in the diagram, it represents the cross-correlation between the first parameter (down the side) and the second parameter (across the top).

The un-biased XCORR function in MATLAB was applied in each case, as follows:

```
CrossCor1= xcorr(DataAll.Parameter1, DataAll.Parameter2);
```

In addition, a plot of each cross-correlation was generated. This made it possible to assess the veracity of the next step: selecting the strongest correlation and identifying the appropriate time lag.

```
figure, plot(CrossCor1);
        hold on %Enables inclusion of title, labels and legend
        title('Plot of XCORR result - Parameter1 and Parameter2);
        xlabel('Lags')
        ylabel('Correlation Coeff')
        legend('XCORR result')
        hold off
```

Table 6: Cross-correlations applied to joined Mythe datasets for 2011, 2012a and 2012b; x = cross-correlation applied between Parameter 1 (down the side of the table) and Parameter 2 (across the top).

	Final free chlorine monitor	Final turbidity monitor	Final free chlorine spot	Final HPC37	Final coliforms
Final chlorine monitor			x	x	x
Final flow	x	x	x	x	x
Final turbidity monitor	x		x	x	x
Final water temperature spot	x	x	x	x	x
Final free chlorine spot				x	x
Final HPC22				x	x
Final HPC37					x

The highest cross-correlation result (strongest correlation) produces the tallest peak in the plot. The location of the highest cross-correlation result relative to the mid-point of all the cross-correlation results indicates whether Parameter1 could have affected Parameter2 and by what time-frame. The XCORR function produces (2n)-1 results because it scans forwards and backwards from the peaks in Parameter1 relative to those in Parameter2. The process of determining the time lags is detailed below:

```
% CrossCor1
[lagcCrossCor1, indexCrossCor1] = max(CrossCor1); %Locate tallest peak
lagmaxCrossCor1 = (size(CrossCor1,1))+1; %Find number of rows, add 1
lagmidCrossCor1 = lagmaxCrossCor1/2; %Find mid-point of lagmax
this_lagCrossCor1 = lagmidCrossCor1 - indexCrossCor1; %Calc. lag, mins
time_lag_in_hrCrossCor1 = this_lagCrossCor1/60; %Convert from min to h
```

The results were grouped into an output table.

```
XCORRname = {'CrossCor1';'CrossCor2'}; %Names of cross-correlations
MaxXCORR = [lagc1801; lagc1802]; %Height of tallest peak
TimeLagHr = [time_lag_in_hr1801; time_lag_in_hr1802]; %Time lags, h

xcorrRES = dataset(XCORRname, MaxXCORR, TimeLagHr, 'VarNames', ...
      {'Cross_CORR', 'MaxXCORR', 'TimeLagHr'}); %Compile into table
```

A subset of this dataset was created containing only the cross-correlations where the time lags were both positive and <24 h. Positive time lags mean that peaks in the first parameter occurred before peaks in the second parameter and could have impacted them. A time lag of <24 h was selected because the spot sampling was conducted daily.

```
xcorrBEST = xcorrRES(xcorrRES4.TimeLagHr >=0 & xcorrRES4.TimeLagHr...
      <=24,:); %Identify applicable results
xcorrBEST(:,{'Cross_CORR','MaxXCORR','TimeLagHr'}); %Label output
```

The results were then exported from MATLAB as text files and were then imported into Excel. This was achieved using the MATLAB export function:

```
export(xcorrRES);
```

Cross-correlations were conducted on the full datasets for Mythe and also for the week of the failure. The rows corresponding to the respective time period were extracted from the full dataset and the whole process repeated on this sub-set.

```
Fail1 = DataAll(1:1440,:);
```

MATLAB code for the six month data analyses can be viewed in full in Appendix 1.

5.2.4. Self-Organising Maps

The SOM is an artificial neural network model which draws inspiration from biological processes. The Map evolves localised response patterns to input vectors. The prototype vectors are positioned on a regular low-dimensional grid in a spatially ordered fashion helping to improve visualisation. SOMs can aid in the identification of correlations among more than two parameters, thereby building on the results from the cross-correlations and accounting for the fact that several factors may be involved at once in bacteriological compliance. Complex datasets can be clustered and the output is a visual representation of the statistical pattern found by the SOM algorithm (Kangas and Kohonen, 1996; Kohonen, 1998). SOMs have been used for analysis and modelling of water resources as reviewed in Kalteh and Hijorth (2008). Mounce *et al*. (2012) proposed their use in data mining microbiological and water quality data from a pilot-scale pipe rig. This work is the first use of SOMs in the analysis of bacteriological compliance data from real WTWs.

The analysis was carried out using the MATLAB® SOM Toolbox version 2.0 (Laboratory of Computer and Information Science, Finland). The SOM algorithm first normalised the datasets and conducted rough training on these to learn the global structure; then fine training was completed before producing the SOM plots. Each parameter (such as turbidity) is represented by a colour-coded rectangular plot called a 'component plane'; a point in one component plane is related to the same location in all corresponding plots in the SOM output enabling an understanding of how parameters change one with another.

For the Mythe datasets, eight parameters were analysed using SOMs: chlorine monitor, turbidity monitor, flow monitor, chlorine spot, temperature spot, HPC22, HPC37 and coliforms. The default settings of linear initialisation and batch training were selected. The Mythe SOMs were conducted on the full six month datasets, on each week within the datasets and on each day from the week of failure.

5.2.5. Records of monitor interventions

STW's Research and Development team had mentioned that some work had been conducted previously which suggested that un-scheduled monitor interventions, for example re-calibrating a monitor, could be correlated with bacteriological failures. When operators make un-scheduled adjustments to equipment a record is made. These records can be used to check whether changes in data trends are genuine or the result of an intervention. In light of this, the monitor intervention records (from Works Management Master Log, 'WIMS') pertaining to final turbidity and free chlorine monitors at Mythe WTW were requested from operational staff.

These data were received as screen shots. An Excel file was created containing the date and time of each intervention and a '1' recorded in the 'result' column. When this was imported into Excel it was zero-padded, as detailed above, and subjected to cross-correlation analysis with the Mythe coliform detections only.

5.3. Results

5.3.1. Cross-correlation

There were 81 cross-correlations conducted on the Mythe datasets for both six month and weekly time periods. From the six month datasets 22 yielded positive time lags between 0 and 24 h (Table 8). Where the results were 0 h, this showed that the two

parameters changed respective to one another and there was no time lag between them. This was true for all three datasets for the following cross-correlations: chlorine monitor x chlorine spot, flow monitor x chlorine spot, temperature spot x chlorine monitor, and temperature spot x chlorine spot. These results provide confirmation of good chlorine monitoring by both on-line monitors and samplers and also confirm the variation of chlorine with temperature. However, the variation of chlorine spot data with flow monitor data shows that chlorine concentration rises and falls with flow rate. Mythe's chlorine dosing is related to flow rate, however, this should not affect the resulting concentration but rather the (unmeasured) rate of disinfectant addition. This suggests that the performance of the chlorine dosing rig should be examined.

The cross-correlations of turbidity monitor with chlorine monitor and chlorine spot produced interesting results. In 2011, a time lag was identified for both correlations: 5 h for chlorine monitor and approximately 16.3 h for chlorine spot. This suggests that changes in turbidity impacted the chlorine concentration of the water. The difference in time lag could be a function of the different sampling frequencies for the two sets of chlorine data. In 2012a, the cross-correlation between turbidity monitor and chlorine spot showed a time lag of 0 h; and between turbidity monitor and chlorine monitor the result did not meet the positive criterion. This means that peaks in turbidity occurred after peaks in chlorine monitor data and could not be considered causative. In 2012b, there was an applicable time lag for both correlations: 0.2 h for chlorine monitor and 0 h for chlorine spot. Temperature spot and turbidity resulted in time lags of 0 h in 2012a and 2012b, but in 2011, the time lag was both negative and >24 h. HPC22 and HPC37 had a time lag of 0 h in 2012a, but in 2011 and 2012b, the time lags were both negative and >24 h. Chlorine spot data x HPC22 and chlorine spot data x HPC37 only resulted in applicable results in 2012b, in 2011 and 2012a the time lags were negative and >24 h. For changes in chlorine spot data, there was a time lag of 23.4 h before a detection of HPC22 and 0 h before a detection of HPC37. None of the applicable results includes a correlation with coliform detections for the six month datasets. It is most likely that the absence of coliforms from the cross-correlation results is because of the size of the dataset relative to the number of detections.

Table 8: Cross-correlation results that were positive and between 0 and 24 h for the six month datasets: Mythe 2011, 2012a and 2012b.

Cross-correlation inputs		Year		
Parameter 1	Parameter 2	2011	2012a	2012b
Chlorine monitor	Chlorine spot	0.0	0.0	0.0
Flow monitor	Chlorine spot	0.0	0.0	0.0
Turbidity monitor	Chlorine monitor	5.0	-	0.2
Turbidity monitor	Chlorine spot	16.3	0.0	0.0
Temperature spot	Chlorine monitor	0.0	0.0	0.0
Temperature spot	Turbidity monitor	-	0.0	0.0
Temperature spot	Chlorine spot	0.0	0.0	0.0
HPC22	HPC37	-	0.0	-
Chlorine spot	HPC22	-	-	23.4
Chlorine spot	HPC37	-	-	0.0

Table 7: Cross-correlation results that were positive and between 0 and 24 h for the week of the failure for datasets Mythe 2011, 2012a and 2012b. Shaded rows highlight applicable cross-correlations with coliforms.

Cross-correlation inputs		Year		
Parameter 1	Parameter 2	2011	2012a	2012b
Chlorine monitor	Chlorine spot	0.0	0.0	0.0
Flow monitor	Chlorine monitor	0.0	0.0	0.0
Flow monitor	Chlorine spot	0.0	0.0	0.0
Flow monitor	Turbidity monitor	0.0	0.0	0.0
Flow monitor	Coliforms	19.1	-	12.3
Turbidity monitor	Chlorine monitor	1.0	0.0	0.0
Turbidity monitor	Chlorine spot	0.0	0.0	0.0
Turbidity monitor	Coliforms	7.9	-	-
Temperature spot	Chlorine monitor	0.0	0.0	0.0
Temperature spot	Chlorine spot	0.0	0.0	0.0
Temperature spot	Turbidity monitor	0.0	0.0	0.0
Chlorine monitor	Coliforms	-	-	22.7
Chlorine spot	HPC37	-	-	9.1
HPC37	Coliforms	-	-	23.0

Of the 81 cross-correlations conducted on the week of failure datasets, 33 yielded positive time lags between 0 and 24 h (Table 7). Time lags of 0 h were observed across the three weekly datasets for the following cross-correlations: chlorine monitor x chlorine spot, flow monitor x chlorine monitor, flow monitor x chlorine spot, flow monitor x turbidity monitor, turbidity monitor x chlorine spot, temperature spot x chlorine monitor, temperature spot x chlorine spot and temperature spot x turbidity monitor. These results concur with the findings from the full datasets with regard to the variation of chlorine with both temperature and flow rate. At this time-scale, the data show that flow rate impacts turbidity.

Turbidity monitor x chlorine monitor showed a lag time of 1.0 h for 2011's dataset, but for the two 2012 datasets the two parameters changed one with another. In 2012b, changes in chlorine spot data correlated with changes in HPC37 results with a time lag of 9.1 h. Interestingly, at this time-scale, coliforms appear in the cross-correlation results (highlighted in Table 7). There were no consistent relationships across the three datasets. In 2011 and 2012b, there were time lags between changes in flow rate and the coliform results, of 19.1 h and 12.3 h respectively. Turbidity monitor x coliforms returned an applicable result in 2011 of 7.9 h. Changes in chlorine monitor data and coliforms in 2012b had a time lag of 22.7 h. The day before the coliform detection in 2012b, HPC37s had been enumerated, with a lag time of 23.0 h. The HPC37 results had been impacted by the chlorine spot data in this particular dataset.

Figure 18 shows the data trends for 2011's week of failure. It shows that flow rate peaked and dropped off (from 40 to 34 ML d^{-1}) almost a day before the coliform detection; it also highlights the peak in turbidity that occurred approximately 8 h beforehand (from 0.05 to 0.60 NTU). Figure 19 shows that turbidity spiked in the 24 h prior to the coliform detection in 2012a. Figure 20 shows an unclear trend with flow rate in 2012b, but that there were HPC37 bacteria detected less than 24 h before the coliform failure and a fluctuation in chlorine concentration (peaking at 1.3 mg l^{-1} and falling to 0.55 mg l^{-1}). These Figures corroborate the findings of the cross-correlations and indicate that changes in final turbidity and unstable chlorine concentrations impact the survival of coliforms.

5.3.2. Self-Organising Maps

The SOMs for 2011, 2012a and 2012b are presented in Figure 21. There are two parts to the SOM output. They are the summary U-matrix and the component planes for the individual parameters. The U-matrix allows examination of the overall cluster patterns in the input dataset after the model has been trained. In the component planes for each parameter, the colouring corresponds to actual numerical values for the parameters as shown in the scale bars next to each plot. Blue shades show low values and red shades correspond with high values. The ranges for the bacteriological parameters have been adjusted by the algorithm as a result of the zero-padding; the SOM output is blue where the result was 0 CFU ml^{-1}/100 ml^{-1}; for the maximum results the output colour is red. The three datasets are discussed simultaneously. The purpose of these analyses is to

identify common features for the three failures to aid operators in preventing future non-compliances.

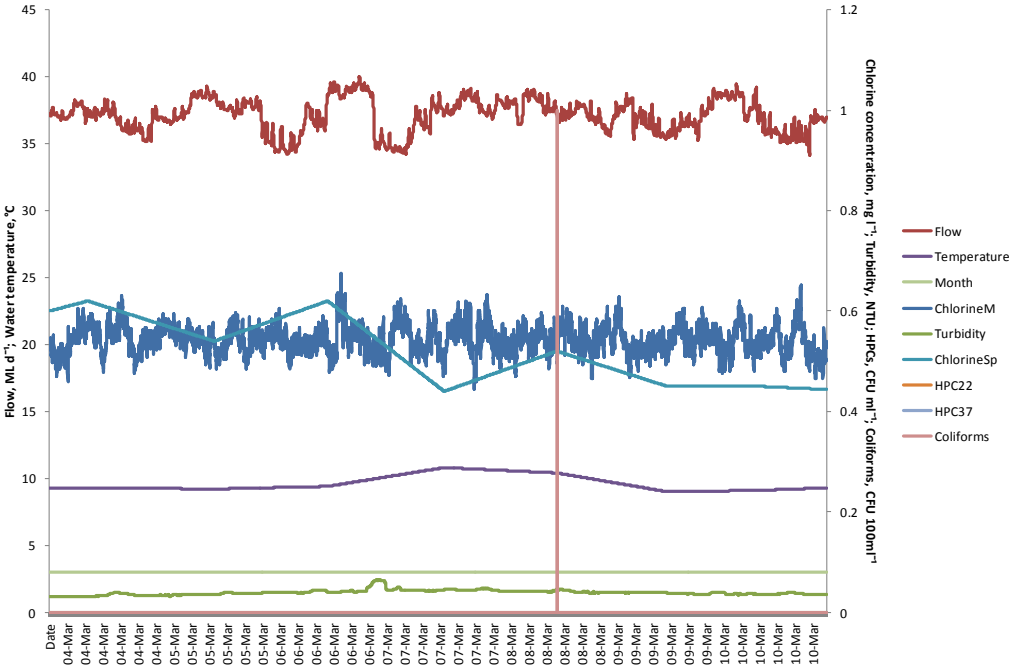

Figure 18: Plot of data from the week of failure at Mythe, 2011.

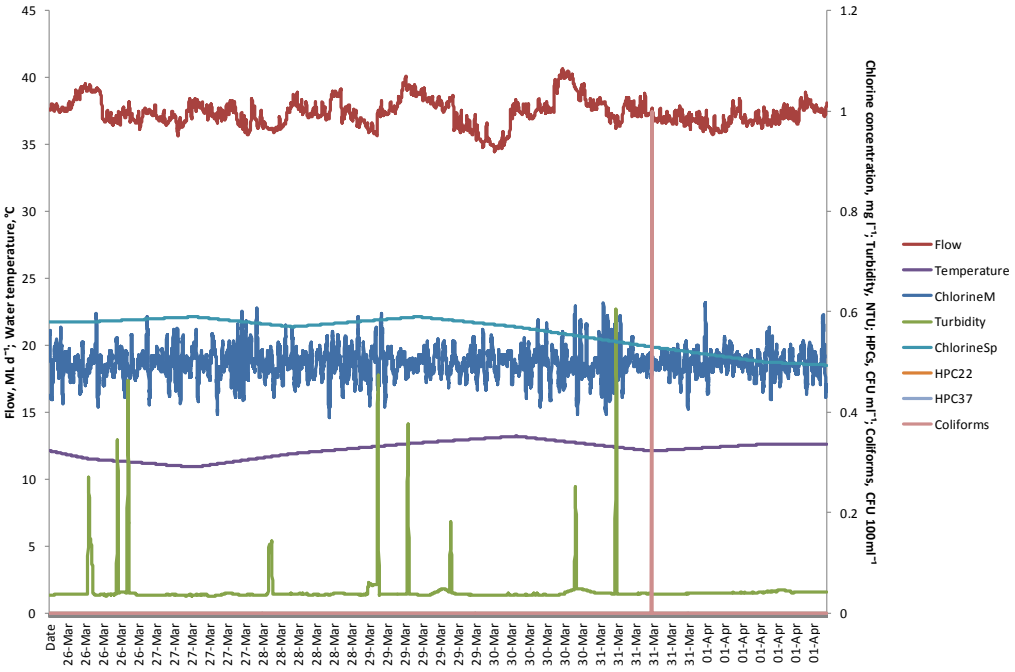

Figure 19: Plot of data from the week of failure at Mythe, 2012a.

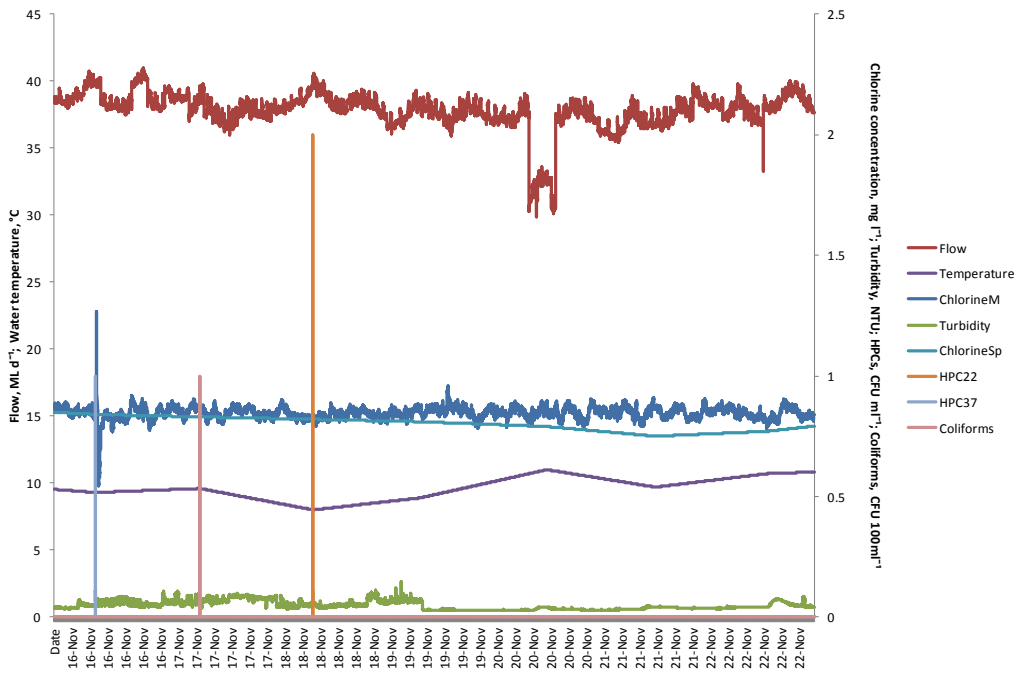

Figure 20: Plot of data from the week of failure at Mythe, 2012b.

The temperature ranges noted for the three datasets were: 2011, 4.8 – 18.9 °C; 2012a, 4.2 – 20.0 °C; and 2012b, 4.8 – 16.8 °C. Each of the component planes is dominated by low-medium water temperatures (Figure 21).

The flow plot for 2011 shows a spread of flow rates with medium rates (35.5 – 38.4 ML d^{-1}) dominating. In the dataset for 2012a, high flow rates were most prevalent (36.2 – 38.6 ML d^{-1}). The 2012b dataset was dominated by medium-high flow rates (34.9 – 40.0 ML d^{-1}) (Figure 21).

The turbidity plots also differ in their patterns. In 2011, the turbidity monitor recorded predominantly low (0.03 – 0.08 NTU) values with two patches of high (0.13 – 0.18 NTU) turbidity. Results for 2012b were similar (low, 0.03 – 0.06 NTU; high, 0.08 – 0.11 NTU). In comparison, the plot for 2012 showed a spread of low-medium turbidity values (0.02 – 0.05 NTU) (Figure 21).

Chlorine monitor data showed the majority of readings were medium-high in 2011 (0.47 – 0.57 mg l^{-1}) with a patch of low chlorines (0.42 – 0.47 mg l^{-1}). Conversely, 2012a results were dominated by low-medium results (0.51 – 0.66 mg l^{-1}) with a patch of high chlorines (0.66 – 0.74 mg l^{-1}). Chlorine concentrations were variable in 2012b, with a spread of values across the full range (0.82 – 0.86 mg l^{-1}) (Figure 21).

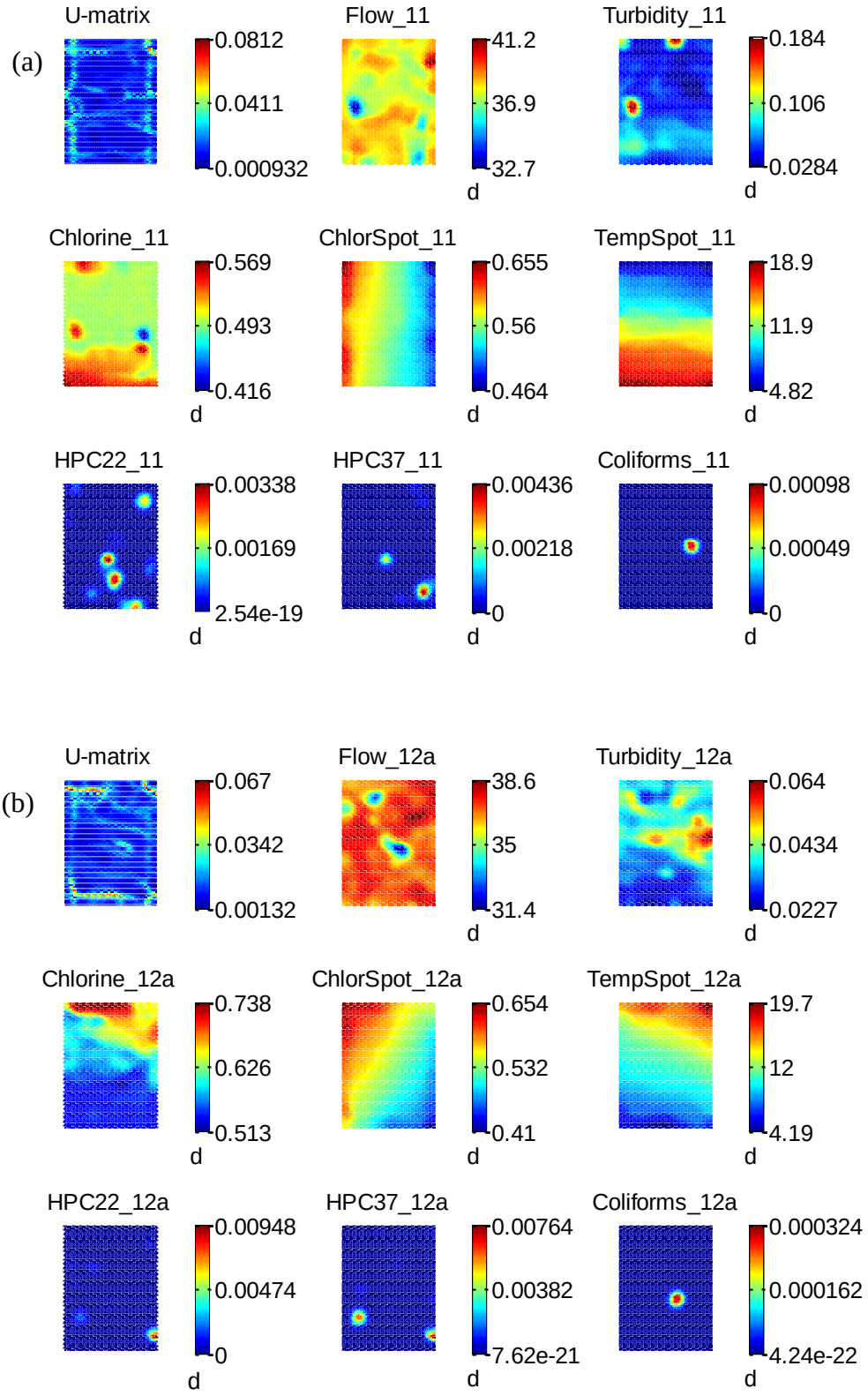

Figure 21: Self-organising maps for (a) 2011, (b) 2012a and (c) 2012b (overleaf) – six month datasets.

(c)

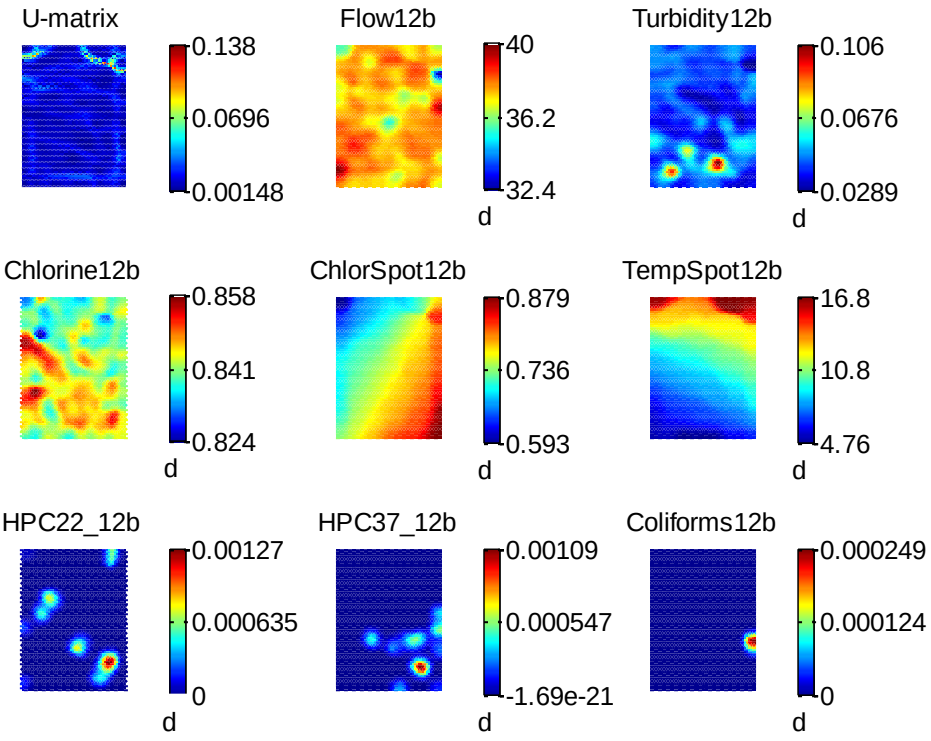

Table 9: Mythe final SOM results showing parameter ranges for HPCs (upper) and coliforms (lower) – six month datasets.

HPCs at 22 and 37 degC	Year		
	2011	2012a	2012b
Flow, ML d^{-1}	32.7 - 41.2	36.2 - 38.6	34.9 - 40.0
Turbidity, NTU	0.03 - 0.08	0.02 - 0.03	0.03 - 0.0.6
Chlorine monitor, mg l^{-1}	0.47 - 0.57	0.51 - 0.59	0.82 - 0.86
Chlorine spot, mg l^{-1}	0.46 - 0.59	0.41 - 0.57	0.59 - 0.88
Water temperature, °C	4.8 - 18.9	4.2 - 9.4	4.8 - 16.8

Coliforms	Year		
	2011	2012a	2012b
Flow, ML d^{-1}	32.7 - 38.4	31.4 - 33.8	37.5 - 40.0
Turbidity, NTU	0.03 - 0.08	0.03 - 0.05	0.03 - 0.06
Chlorine monitor, mg l^{-1}	0.42 - 0.47	0.51 - 0.59	0.83 - 0.84
Chlorine spot, mg l^{-1}	0.46 - 0.52	0.41 - 0.49	0.78 - 0.88
Water temperature, °C	9.5 - 14.2	4.2 - 9.4	4.8 - 8.0

The spot-sampled chlorine plot for 2011 shows the chlorine concentrations in approximately vertical stripes. The concentrations run low (0.46 – 0.52 mg l^{-1}) to high (0.59 – 0.66 mg l^{-1}) from left to right. In 2012a and 2012b the ranges are arranged diagonally top left to bottom right with 2012a going from high (0.57 – 0.65 mg l^{-1}) to low (0.41 – 0.49 mg l^{-1}) and 2012b from low (0.59 – 0.69 mg l^{-1}) to high (0.78 – 0.88 mg l^{-1}) (Figure 21).

The numbers of HPC bacteria at 22 and 37 °C varied between the two years. In 2011, there were 19 detections of HPC22 ranging from 1 – 15 CFU ml^{-1}; in 2012a, there were 10 detections ranging from 1 – 22 CFU ml^{-1}; and in 2012b there were 11 detections ranging from 1 – 3 CFU ml^{-1}. In 2011, there were ten detections of HPC37 ranging from 1 – 5 CFU ml^{-1}; in 2012a, there were nine detections ranging from 1 – 18 CFU ml^{-1}; and in 2012b there were 11 detections ranging from 1 – 2 CFU ml^{-1}. The HPC results have variable fingerprints across the three years (Figure 21 and Table 9). In 2011, detections tended to occur across low-high flow rates (32.7 – 41.2 ML d^{-1}), low turbidity (0.03 – 0.08 NTU), medium to high chlorine monitor values (0.47 – 0.57 mg l^{-1}), low to medium chlorine spot values (0.46 – 0.59 mg l^{-1}) and low-high water temperature (4.8 – 18.9 °C). When these results were compared with the raw data for HPC22 it was observed that the majority of detections occurred between May and June. In 2012a, detections tended to occur with high flow rates (36.2 – 38.6 ML d^{-1}), low turbidity (0.02 – 0.03 NTU), low chlorine monitor values (0.51 – 0.59 mg l^{-1}), low-medium spot-sampled chlorine values (0.41 – 0.57 mg l^{-1}) and low water temperature (4.2 – 9.4 °C). The raw data showed that these detections were mostly between March and April. In 2012b, detections tended to occur with medium-high flow rates (34.9 – 40.0 ML d^{-1}), low turbidity (0.03 – 0.06 NTU), low-high monitor chlorine values (0.82 – 0.86 mg l^{-1}), low-high spot-sampled chlorines (0.59 – 0.88 mg l^{-1}) and low-high water temperature (4.8 – 16.8 °C). The raw data showed that these detections were mostly between November and December. There were no correlations between HPC results and coliform detections.

One coliform CFU 100 ml^{-1} was detected in each time period. The detections were all plotted centre-right in their respective component planes (Figure 21). The coliform results produced variable fingerprints over the three datasets (Table 9). In 2011 and 2012a, the detections occurred with low monitor chlorine values (0.42 – 0.47 mg l^{-1}, 2011; 0.51 – 0.59 mg l^{-1}, 2012a) and low chlorine spot values (0.46 – 0.52 mg l^{-1}, 2011; 0.41 – 0.49 mg l^{-1}, 2012a). In 2012b, monitor chlorine was medium (0.83 – 0.84 mg l^{-1}) and spot-sampled chlorine was high (0.78 – 0.88 mg l^{-1}). In 2011 and 2012b the coliform detections correlated with low temperature (4.8 – 9.5 °C, 2011; 4.8 – 8.0 °C, 2012b) whilst in 2012a the failure corresponded to medium water temperature (8.0 – 12.1 °C). In 2011, the flow rate was low-medium (32.7 – 38.4 ML d^{-1}) and turbidity was low (0.03 – 0.08 NTU); in 2012a, the flow rate was low (31.4 – 33.8 ML d^{-1}) and the

turbidity medium (0.03 – 0.05); in 2012b, the flow rate was high (37.5 – 40.0 ML d^{-1}) and the turbidity low (0.03 – 0.06 NTU).

Across the three datasets, it can be seen that the coliform detections occurred when the turbidity was low (<0.08 NTU) and monitor chlorine low-medium (<0.60 mg l^{-1} in 2011 and 2012a; <0.84 mg l^{-1} in 2012b). Coliforms were not detected under high water temperature conditions.

During the week of the coliform failure in 2011, the coliform detection correlated with medium flow rate (36.9 – 38.5 ML d^{-1}), low turbidity (0.04 – 0.12 NTU), low monitor and spot-sampled chlorines (0.44 – 0.48 mg l^{-1} and 0.50 – 0.53 mg l^{-1}, respectively) and medium water temperature (11.7 – 12.4 °C). There were no HPCs enumerated during that week (Figure 22 and Table 10).

The week of 2012a's coliform detection showed the coliform failure corresponding to medium flow rate (36.2 – 37.7 ML d^{-1}), low turbidity (0.03 – 0.04 NTU), medium monitor and spot-sampled chlorines (0.53 – 0.56 mg l^{-1} and 0.50 – 0.56 mg l^{-1}, in that order) and high water temperature (10.1 – 10.7 °C). There were no HPCs enumerated over that time period (Figure 22 and Table 10).

In 2012b, the coliform detection correlated with high flow (36.7 – 39.1 ML d^{-1}), medium turbidity (0.05 – 0.07 NTU), medium monitor chlorine (0.84 – 0.86 mg l^{-1}), high spot-sampled chlorine (0.81 – 0.83 mg l^{-1}) and medium water temperature (9.1 – 10.0 °C). HPCs did not correlate with coliforms, but they were found under the same conditions for flow, monitor and spot-sampled chlorine. HPCs corresponded to low-medium turbidity (0.03 – 0.07 NTU) and medium-high water temperature (9.1 – 11.0 °C) (Figure 22 and Table 10).

At the weekly time-scale, coliforms were found when the flow rate was medium-high (>36.0 ML d^{-1}), turbidity was low-medium (<0.12 NTU), monitor and spot-sampled chlorines were low-medium (0.44 – 0.56 mg l^{-1} in 2011 and 2012a and 0.80 – 0.86 mg l^{-1} in 2012b) and water temperature was between 9.0 and 11.0 °C (Figure 22). These results agree with the findings from the six month datasets.

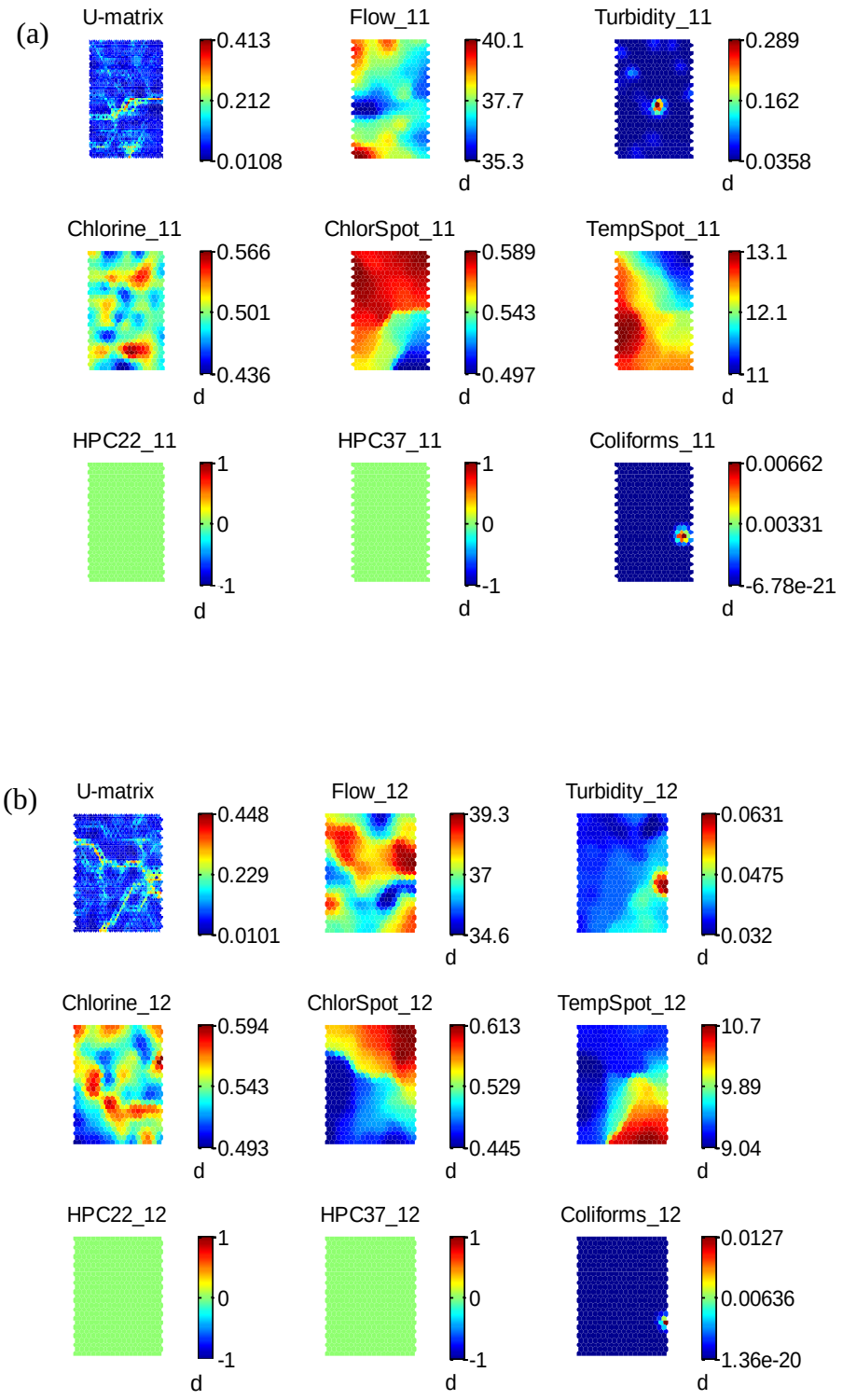

Figure 22: Self-organising maps for (a) 2011, (b) 2012a and (c) 2012b (overleaf) – weekly datasets.

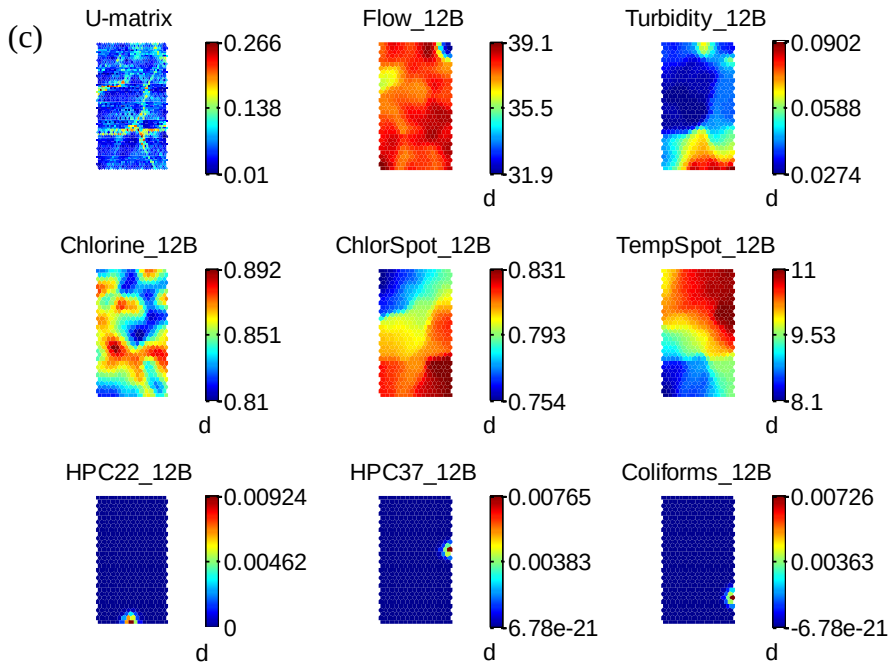

Table 10: Mythe final SOM results showing parameter ranges for HPCs (upper) and coliforms (lower) – weekly datasets.

HPCs at 22 and 37 degC	Year		
	2011	2012a	2012b
Flow, ML d^{-1}	-	-	36.7 - 39.1
Turbidity, NTU	-	-	0.03 - 0.07
Chlorine monitor, mg l^{-1}	-	-	0.84 - 0.86
Chlorine spot, mg l^{-1}	-	-	0.81 - 0.83
Water temperature, °C	-	-	9.1 - 11.0

Coliforms	Year		
	2011	2012a	2012b
Flow, ML d^{-1}	36.9 - 38.5	36.2 - 37.7	36.7 - 39.1
Turbidity, NTU	0.04 - 0.12	0.03 - 0.04	0.05 - 0.07
Chlorine monitor, mg l^{-1}	0.44 - 0.48	0.53 - 0.56	0.84 - 0.86
Chlorine spot, mg l^{-1}	0.50 - 0.53	0.50 - 0.56	0.81 - 0.83
Water temperature, °C	11.7 - 12.4	10.1 - 10.7	9.1 - 10.0

When SOMs were used to assess the day of the failure, they showed that across the three failure days the flow rate was approximately 37.0 ML d^{-1}; turbidity was less than 0.13 NTU (and less than 0.07 NTU in both 2012 datasets); and water temperature was between 9.0 and 12.0 °C. There were no HPCs enumerated on any of the failure days. In 2011 and 2012a the monitor and spot-sampled chlorines were 0.48 – 0.52 mg l^{-1} and in 2012b the range was 0.83 – 0.86 mg l^{-1} (Figure 23 and Table 11).

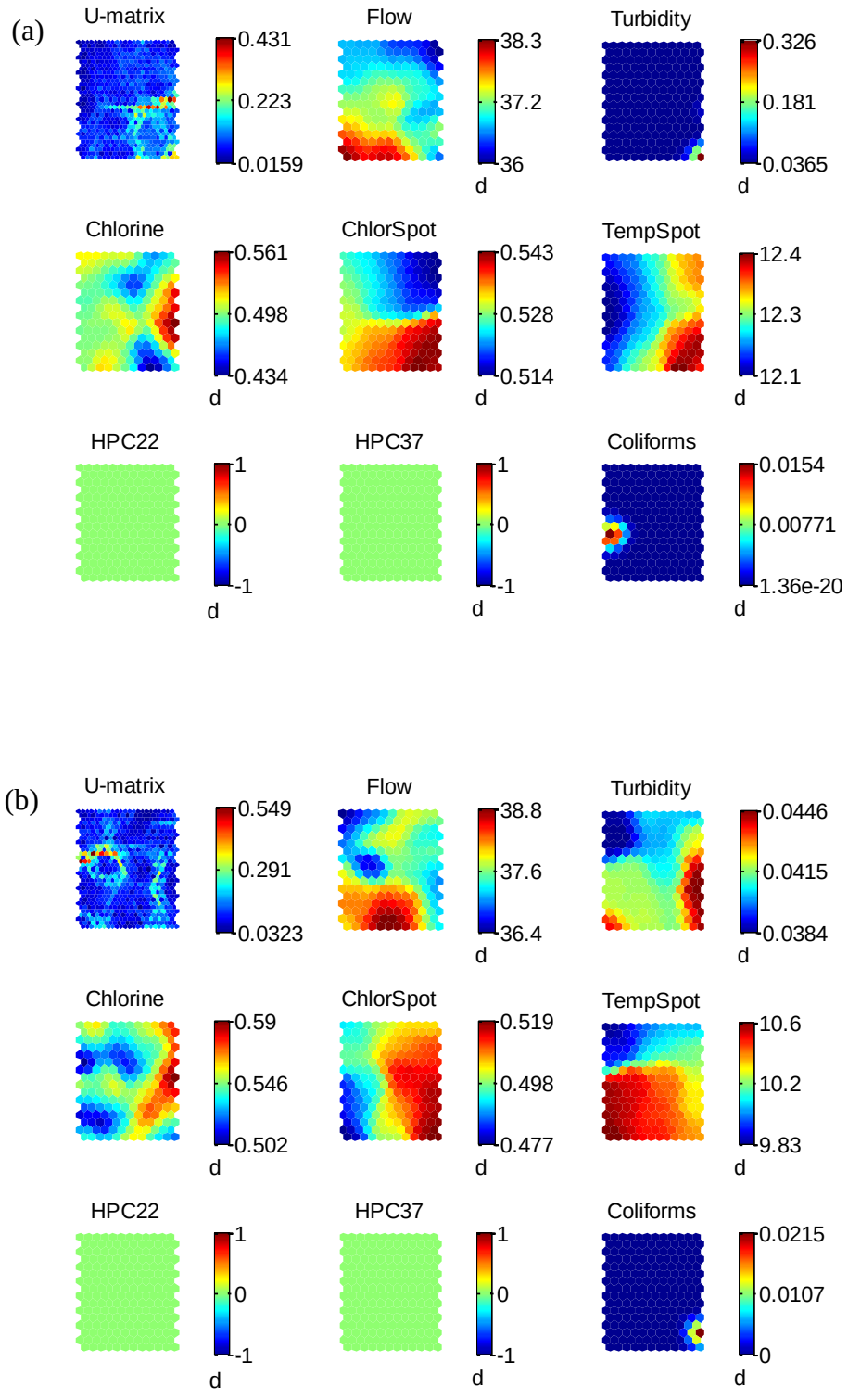

Figure 23: Self-organising maps for (a) 2011, (b) 2012a and (c) 2012b (overleaf) – daily datasets.

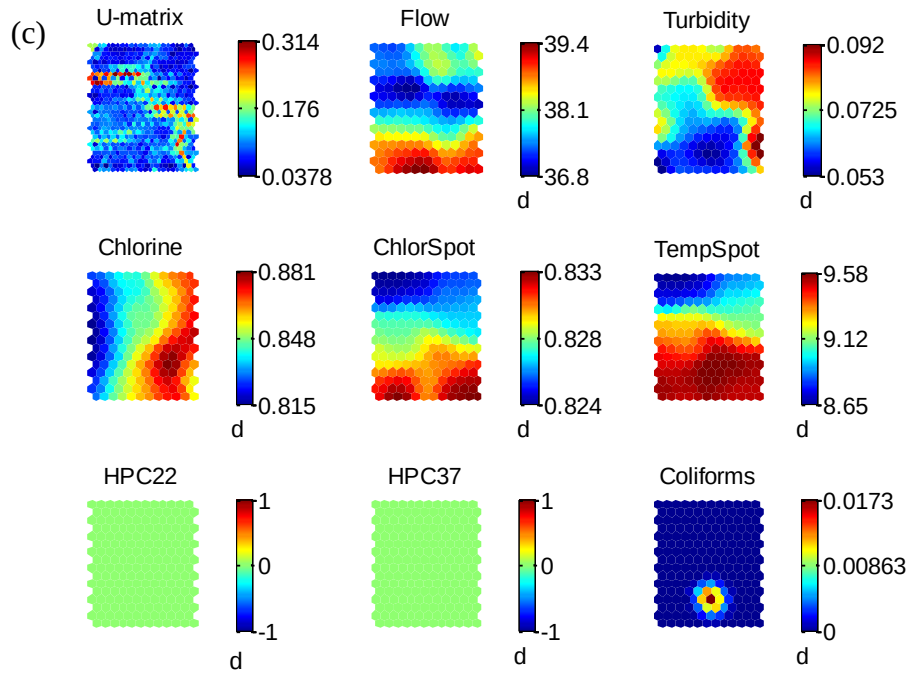

Table 11: Mythe final SOM results showing parameter ranges for coliforms – daily datasets.

Coliforms	Year		
	2011	2012a	2012b
Flow, ML d^{-1}	36.8 - 37.5	36.4 - 37.2	37.7 - 39.4
Turbidity, NTU	0.04 - 0.13	0.04	0.05 - 0.07
Chlorine monitor, mg l^{-1}	0.48 - 0.52	0.53 - 0.56	0.84 - 0.86
Chlorine spot, mg l^{-1}	0.52 - 0.53	0.51 - 0.52	0.83
Water temperature, °C	12.1 - 12.2	10.3 - 10.6	9.3 - 9.6

5.3.3. Cross-correlation and SOM results

Few of the cross-correlation results that met the selection criteria also had observable correlations in the SOMs. Flow monitor x chlorine spot showed no clear patterns in the SOMs for any of the six month datasets. There was approximate agreement with chlorine monitor x chlorine spot in 2012a, but not in 2011 and 2012b. Likewise, there was approximate agreement with temperature spot x chlorine spot in both of the 2012 datasets, but not in 2011. The cross-correlations for temperature spot x chlorine monitor yielded agreement for both of the 2012 datasets and an approximate agreement for 2011: these show that in 2011 and 2012a when temperature increased, the applied dose of chlorine increased, but in 2012b the applied dose decreased. At the weekly-scale, the majority of findings from cross-correlation bore no resemblance to the outcomes of the SOM analyses. There were approximate relationships between the cross-correlations

and SOMs for the following: flow x chlorine monitor, 2011; flow x chlorine spot, 2012a; and temperature x chlorine spot, 2012b. In 2012a, the SOM showed a relationship between temperature spot and turbidity, with turbidity increasing with decreasing temperature.

5.3.4. Monitor interventions

The WIMS reports for the chlorine monitor showed re-calibration to be the most common action taken, and one incidence where the sample line broke and had to be repaired. The majority of the turbidity reports commented on erratic readings or high alarms and the principal action taken was to increase the flow through the monitor to achieve a more stable reading. In 2011, there were four chlorine monitor interventions and 20 jobs logged for the turbidity monitor; in 2012a there were seven and ten interventions, respectively; and in 2012b there were ten and 37 jobs logged, correspondingly. The cross-correlation of the dates and times of these interventions with the detections of coliforms yielded time lags of between 4,344 h (181 days) prior to and 2,162 h (90 days) after the event. None of the time lags was between 0 and 24 h. These results show that monitor interventions are not a useful predictive tool for coliform failures at Mythe WTW.

5.4. Discussion

5.4.1. Comparison of the results from cross-correlation and Self-Organising Maps

Cross-correlation aims to provide a time lag between the changes in two selected parameters. The way these results have been assessed in this method means that only the strongest correlations are considered viable. From the six month datasets 27 % of cross-correlations yielded results that met the selection criteria: time lags that were both positive and <24 h; at the weekly scale, this increased to 41 %. This tool cannot determine whether a rise or a fall in the first parameter affected the second. The SOM analysis incorporates all the data and shows how one parameter relates to another; it has no time element. The use of both methods was intended to provide useful information to operators in managing the bacteriological quality of treated water at Mythe.

Turbidity negatively impacts chlorine residual and thus its disinfection efficacy (LeChevallier *et al*., 1981; Sawyer *et al*., 2003). The cross-correlation results showed that these parameters changed one with another; the SOM results did not clearly reflect this. The occurrence of coliforms with both low-medium chlorines and low-medium

turbidities suggests that the relationship among chlorine, turbidity and indicator organisms is more complex than 'turbidity affects disinfection efficacy'. Particle size and particle type can be important parameters in influencing the effectiveness of disinfection processes (Templeton *et al*. 2008). Deborde and von Gunten's review (2008) observed that there was a difference in the impacts of inorganic and organic turbidities on chlorine stability. Farooq *et al*. (2008) found that disinfection was more effective in the presence of inorganic turbidity in comparison with organic turbidity. They also noted a weak inverse correlation between chlorine residual and coliforms in drinking water. The results from Mythe WTW concur with this observation; however, the turbidities were low in both datasets. Particle size and type and turbidity composition are not routinely determined in drinking water. Chlorine concentrations were correlated with water temperature in the six month datasets; this may have had a greater effect than the low amount of turbidity.

Both methods showed that there was no relationship between HPCs and coliforms. This observation was also noted in Chapter 3 for the whole STW region. It is generally accepted that HPCs represent an overview of the bacteriological quality of drinking water (Standing Committee of Analysts, 2012; McCoy and Olson, 1986; Francisque *et al*., 2009), i.e. the greater the number of HPCs the higher the likelihood of detecting indictor organisms. The lack of correlation between the numbers of HPCs and the detection of indicator organisms suggests this may only be true in cases of acute contamination. At Mythe WTW, the physical, chemical and microbiological data surrounding the coliform detections were not exceptional and the failures were for 1 CFU 100 ml^{-1} in each case. Cross-correlation results meeting the selection criteria and including coliform detections were only noted at the weekly scale and showed impacts from flow rate, turbidity, monitor chlorine and HPC37 detections.

5.4.2. Raw data and data manipulation

The spot-sampled data, apart from the coliform detections, were not marked as being exceptional. Variation was observed in the on-line flow, turbidity and chlorine data, as would be expected at their sampling frequencies. The WIMS datasets were the weakest inputs to the analyses. The database records the time that the intervention is logged. The operators did not always record the actual time (or date) of their work. The results from this analysis may not be a true representation of the relevance of monitor interventions to the occurrence of bacteriological failures.

To conduct these analyses it was necessary to ensure that all parameters contained the same number of rows. The application of linear interpolation and zero-padding makes assumptions about what is happening with the parameters between samples. This is of especial concern with regard to the spot-sampled parameters, where most of the analysed dataset is constructed of assumed data. Monitors exist for the chemical and physical parameters investigated in this study and these are used by operators to modify treatment parameters at Mythe WTW. The greatest unknown is what is happening with the bacteriological parameters.

The week of failure time frames for the cross-correlations were extracted on a loop selecting 10,080 rows at a time (representing the number of minutes per week). These same selections were applied to the SOMs. Using this method, the day of the failure occurred at different points within the week and in the third dataset, the failure day was Day 1. This would have impacted the results of the cross-correlations, in particular, as it was not possible to analyse 24 h in advance of the failure.

5.4.3. Operational value of the results from the two methods

Both methods are useful for identifying relationships among a variety of water quality parameters. Cross-correlation provides a simple time lag output; however, the tendency for qualifying results to be 0 h merely highlights the tendency for parameters to change respective to one another. Correlations with coliform data were only observed at the weekly time-scale. The SOMs provide a broader understanding of water quality at the final sampling point under all given conditions. They can therefore help in the development of a water quality fingerprint that results in a coliform failure.

Earlier versions of the six month dataset SOM analyses included month number in the component planes. When the third dataset was introduced, inclusion of the month number resulted in SOMs which were difficult to read on account of the month numbers being 9, 10, 11, 12, 1, and 2. The month numbers were removed from the 2011 and 2012a datasets for continuity. Following this it was observed that some of the findings no longer held. In particular, it was shown that all three time-scales, six month, weekly and daily, now agreed; previously, the daily datasets had presented a different water quality fingerprint. This demonstrates the importance of carefully selecting the parameters for analyses using SOMs.

Neither method is directly useful to operators on a day-to-day basis as their outputs need interpretation prior to use. It is beneficial to be able to see the general water quality factors that led to coliform detections; the cross-correlation results alone show a lack of time lag in which to act upon changes in water quality to prevent a failure. In order to enable the use of these tools it is important to find parameters that give a time lag sufficient for preventive action to be taken (for example by collecting on-line monitoring data from alternative locations within the WTW) and to develop simpler outputs from the analytical tools.

5.5. Conclusions

Cross-correlation and SOMs were used to determine whether on-line water quality monitoring data could be used to inform the root cause analysis of bacteriological failures identified during spot-sampling at Mythe WTW. Three datasets were examined. They represented six months of monitoring data from January to June in 2011 and 2012 and from September 2012 to February 2013. There was a single coliform detection in each six month period.

Cross-correlation results that were considered for further analysis were positive and <24 h. Twenty-two of the 81 cross-correlations met both criteria from the six month datasets, the following four had time lags of 0 h for all three datasets: chlorine monitor x chlorine spot, flow monitor x chlorine spot, temperature spot x chlorine monitor, and temperature spot x chlorine spot. Of the 81 cross-correlations conducted on the weekly datasets 33 met the selection criteria and the following had 0 h lags for all three datasets: chlorine monitor x chlorine spot, flow monitor x chlorine monitor, flow monitor x chlorine spot, flow monitor x turbidity monitor, turbidity monitor x chlorine spot, temperature spot x chlorine monitor, temperature spot x chlorine spot, and temperature x turbidity monitor. These results show good chlorine monitoring by on-line monitors and samplers and also confirm the variation of chlorine with temperature. The variation of chlorine spot data with flow monitor data suggests that chlorine concentration could rise and fall with flow rate.

The six month SOMs for the HPC results showed that the following conditions correlated with their detection at Mythe WTW:

- Low-high flow: 32.7 – 41.2 ML d^{-1}
- Low-high water temperature: 4.2 – 18.9 °C

- Low-medium turbidity: 0.02 – 0.08 NTU
- Low-high residual chlorine: 0.47 – 0.86 mg l^{-1} (monitor) and 0.41 – 0.88 mg l^{-1} (spot sample).

The detection of coliform bacteria at Mythe was not correlated with HPC22 or HPC37. They were correlated with the following conditions under all time-scales:

- Low-high flow: 31.4 – 40.0 ML d^{-1}
- Low-medium water temperature: 4.2 – 14.2 °C
- Low turbidity: 0.03 – 0.08 NTU
- Low-medium residual free chlorine: 0.42 – 0.59 mg l^{-1}/0.83 – 0.84 mg l^{-1} (monitor) and 0.45 – 0.54 mg l^{-1}/0.78 – 0.88 mg l^{-1} (spot-sampled).

There was no evidence to suggest that monitor interventions preceded bacteriological failures at Mythe within any meaningful time-frame.

The analysis of data from Mythe WTW has shown that high turbidity did not relate to bacteriological failures. 'High' turbidity in this case study ranged from 0.06 – 0.60 NTU across the selected time periods (as shown in the trend plots). The Water Supply (Water Quality) Regulations 2000 specify that turbidity at the final monitoring point must be below 1.00 NTU to prevent it impacting disinfection (Her Majesty's Stationery Office, 2000); thus it is unlikely that the high turbidities at Mythe resulted in reduced chlorination efficacy.

Coliform detections were associated with fluctuations in monitor chlorine data; whilst this did not involve a cessation of disinfection as in the work by Codony *et al.* (2005), it does demonstrate the importance of a stable concentration. The SOM results show that when the chlorine dose was low-medium there was a risk of coliform detections. It is important to note that this was low-medium for the range of residual concentrations at the two times of year featured. This implies that the target residuals should be revised upwards at Mythe WTW.

Coliform detections occurred under low-medium water temperatures, and were consistently below the 15.0 °C recommended by the World Health Organization (2004). Low-medium water temperature would exacerbate the impact of the fluctuations in

monitor chlorine which were observed and may have contributed to the non-compliances at Mythe.

The research question asked whether improved analysis of on-line and spot-sample data could be used to inform the root cause analysis of bacteriological failures. Using data from the final monitoring point alone has provided information on risk factors at Mythe WTW and these add to the root cause analysis for this WTW.

This Chapter has shown the first application of cross-correlation and SOMs for the analysis of bacteriological quality using spot-sampled and on-line monitoring data from a WTW. The need for equal numbers of rows in the analysed dataset by both tools and the nature of the raw data meant that a significant portion of the analyses were based upon assumed (interpolated or zero-padded) data. The results show that SOMs enabled an understanding of the prevailing water quality at the time of the coliform detections at Mythe WTW. However, deriving a time lag to enable operators to act to prevent a future failure was more difficult. It is likely that this is because all the monitoring data were taken from the final sampling point at the WTW.

5.6. Recommendations for the management of bacteriological quality at Mythe WTW

- Mythe's chlorine dosing is related to flow rate, however, this should not affect the resulting concentration but rather the (unmeasured) rate of disinfectant addition. Since the cross-correlations indicated that chlorine concentration was impacted by flow rate, the dosing rig should be examined and repaired/replaced as necessary.
- All three of the coliform detections occurred when both the chlorine concentration and water temperature were low-medium. It is therefore recommended that the dose and/or the contact time be increased when disinfecting water at Mythe under low-medium temperature conditions.

5.7. Further work

- In order to increase confidence in the conditions leading to a bacteriological failure, more historical data needs to be collected and examined using the same protocols. For Mythe, this should involve collecting the data for the same parameters for historical bacteriological non-compliances. These tools can serve to aid in the setting of water quality parameters (chlorine concentration, turbidity, etc.) for other

sites, companies and within other countries by highlighting high risk combinations of parameters.

- Sampling at a higher frequency for bacteriological parameters would greatly aid the ability of operators to act to ensure final water is compliant. Greater investment in the development of on-line monitoring tools is recommended. Research conducted by Berney *et al.* (2008) and Hammes *et al.* (2008) has already demonstrated that flow cytometry (FCM) is useful for monitoring microbiological quality. Once data have been collected using an on-line system, they can be analysed using cross-correlation and SOMs such that acceptable limits of FCM readings can be prepared and used to protect water quality in the distribution system.
- A set of tools that can aid operators in their work to maintain water quality should be the aim of future work. One of the key requirements would therefore be to develop an output that recommends timely interventions, for example, 'increase chlorine residual concentration by X mg l^{-1}' or 'reduce flow rate through WTW by X ML d^{-1}' within a suitable time-frame. Such a system could be based on an artificial neural network which uses lagged time-series monitoring signals (with time-lags identified by cross correlation) for predicting operational conditions.
- To increase the time lag available between a change in water quality and the detection of a bacteriological failure, it would be beneficial to test data from earlier in the WTW process train. Collecting data from after the rapid gravity filters or the granular activated carbon filters (Figure 17) may provide greater insight into the complex relationships between the different parameters under examination.
- The bacteriological quality of water is known to decline with distance from the WTW (Levi, 2004). Using the cross-correlation and SOM tools to determine whether actions at the WTW could have prevented a failure at a service reservoir would be valuable.

6. Root Cause Analysis of Bacteriological Failures from Strensham WTW

6.1. Introduction

In Chapter 5 it was observed that by working only with data from the Final monitoring point of a WTW the majority of parameters change one with another and do not allow time for operators to act on changing conditions. In order to assess whether having data from throughout the treatment process would enable a successful root cause analysis, a further site was selected. This Severn Trent Water (STW) site also treats surface water from the River Severn: Strensham WTW. It produces 160 ML d^{-1} using the process outlined in Figure 24. There are three outlets from Strensham and coliforms were detected from two of them between January and May 2013. This work focuses on River Severn Aqueduct (RSA) 1, because this is the outlet from which regulatory samples are collected. RSA 1 experienced one coliform detection on the 29th March 2013 and an Enterococcus detection on the 16th May 2013. It also had three coliform detections from 1 L samples in the weeks following the regulatory coliform detection: 14th March, 1st April and 12th April 2013. Because of performance problems in 2011, Strensham was having frequent through-plant spot sampling in addition to the routine Raw and Final monitoring. This makes the Strensham case study especially interesting.

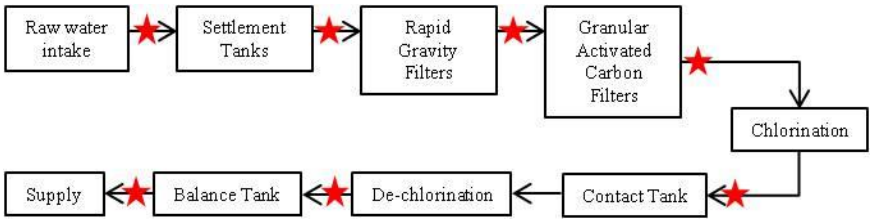

Figure 24: Process flow diagram for Strensham WTW; ★ marks the location of the on-line monitors and through-plant spot-sampling locations.

This chapter seeks to provide further insight into research questions 4 and 5:

4. Is UK bacteriological compliance impacted by weather phenomena?
5. Can improved analysis of on-line monitoring and spot-sample data be used to inform the root cause analysis of bacteriological failures?

This chapter will also assess the utility of this Recommendation from Chapter 5:

- To increase the time lag available between a change in water quality and the detection of a bacteriological failure, it would be beneficial to test data from earlier in the WTW process train.

6.2. Methods

6.2.1. Data collection

Results were collected from STW's data handling software for the period 1st January to 31st May 2013. These data were for coliforms, colony forming units (CFU) 100 ml^{-1}; 1 L coliforms, CFU 1 L^{-1}; *E. coli*, CFU 100 ml^{-1}; non-coliforms, CFU 100 ml^{-1}; 1 L non-coliforms, CFU 1 L^{-1}; Enterococci, CFU 100 ml^{-1}; HPCs at 22 °C and 37 °C (HPC22 and HPC37), CFU ml^{-1}; pH, pH units; turbidity, nephelometric turbidity units (NTU); free and total chlorine, mg l^{-1}; and water temperature, °C. The sampling points from which these results were derived are detailed in Table 12. There are four sets of Settlement Tanks (A, B, C and D), each with their own sampling point. There are four sets of Rapid Gravity Filters (RGFs) (A, B, C and D), but there are only two sampling points: ABC combined and D. Raw water Enterococci and *C. perfringens* analyses were conducted monthly, other Raw water and through-plant analyses up to and including Granular Activated Carbon (GAC) Filters were conducted every two to four days and Contact Tank, Balance Tank and Final water samples were collected daily. In addition, data for daily air temperature, °C and weekly rainfall, mm were received from Met Office Hadley Centre for Climate Change (2013) and STW's Water Resources Strategy team, respectively.

Chemical, physical and bacteriological analyses were conducted by STW samplers and laboratory staff as detailed in Chapter 3.

Table 12: Strensham spot-sampling data and the processes from which these data were collected; x = analyses conducted (down the side of the table) on samples collected from specific sample points (across the top).

	Raw	Settlement Tank	RGFs	GAC Filters	Contact Tank	Balance Tank	Final
Coliforms 100 ml^{-1}	x	x	x	x	x	x	x
Coliforms 1 L^{-1}							x
E. coli	x	x	x	x	x		x
Non-coliforms 100 ml^{-1}	x	x	x	x	x		x
Non-coliforms $1L^{-1}$							x
Enterococci	x						x
HPC22					x		x
HPC37					x		x
pH	x	x	x		x	x	x
Turbidity	x	x	x		x	x	x
Free chlorine					x	x	x
Total chlorine					x	x	x

For the same time period, the following archived on-line monitoring data were received from STW's Asset Creation Data Team: Raw pH, pH units and Raw temperature, °C, ABB AX400 (ABB Ltd., UK); GAC pH, pH units, ABB AX400 (ABB Ltd., UK); Final free chlorine, mg l^{-1}, Capital Controls® TVU/CC1930 (Severn Trent Services, Philadelphia); Final flow, ML d^{-1}, Kent Veriflux VTC (Elster Metering Ltd., UK); and Final turbidity, NTU, Sigrist AquaScat WTMA (Sigrist, Germany). Chlorine and turbidity data were archived every 1 min and the other data were archived every 15 min.

Further on-line monitoring data were received from STW's Asset Creation Data Team for monitor turbidity: RGF Filter Blocks A, B and C, NTU, Hach 1720E (Hach Lange, UK) and Filter Block D, formazin turbidity units (FTU), Hach 1720E (Hach Lange, UK) and GAC Filters, NTU, Sigrist AquaScat WTMA (Sigrist, Germany). Nephelometric and formazin turbidity units measure different phenomena in water and results can vary greatly for the same water samples. Nephelometry measures the scattering of light by particulates and the formazin method the interference to light passage in a straight line (Sawyer *et al.*, 2003).

6.2.2. Data manipulation

The data were manipulated following the protocols detailed in Chapter 5; of necessity, some differences in method were made and these are detailed below.

It was intended that the Strensham datasets would be interpolated on the basis of the Final chlorine monitor data, as was done with the Mythe dataset. However, it was found that data had not been archived at each of the anticipated time points. Instead, a separate input file was constructed formed only of date and time data at 1 min intervals between 1st January 2013 and 31st May 2013. This was then used as the interpolation template for all Raw water parameters, all Settlement Tank parameters, all RGF parameters, all GAC parameters, Contact Tank, Balance Tank and Final free and total chlorine, turbidity and pH, Final flow and Final chlorine monitor data.

As before, the Final bacteriological data were zero-padded, as were bacteriological data from the Contact Tank and Balance Tank. From these sampling points bacteria were found less often and many of the results were 0 CFU ml^{-1}/100 ml^{-1}.

These processes resulted in one Strensham dataset which was time-aligned at 1 min intervals.

A separate Filter dataset was constructed using the same methods and principally containing turbidity and bacteriological data to enable the analysis of the RGF Filter Block and GAC Filter turbidity data. This dataset was also time-aligned at 1 min intervals using the date and time template created for the first Strensham dataset.

6.2.3. Cross-correlation

The Strensham dataset resulted in 2,204 cross-correlations, as shown in Table 13a and b. Table 13 is used in the same way as
Table 6 in Chapter 5.

Cross-correlations were conducted on the full dataset for Strensham and also for the failure weeks. The Mythe analyses used MATLAB to divide the six month datasets into weeks. This process led to the day of the failure being in different locations within the failure week. To ensure this was not the case with the Strensham analyses, the week datasets were determined based on three days either side of the failure day. The rows corresponding to the respective time periods for the coliform, first, second and third 1 L coliform and Enterococcus failures were extracted from the full dataset and the whole process repeated on these sub-sets.

The Filter dataset resulted in 684 cross-correlations. Rainfall and Raw water turbidity were cross-correlated with the monitor turbidity from the individual RGF Filter Blocks and the GAC Filters. Monitor turbidity from the RGFs and GAC Filters were then correlated with spot-sampled turbidity and bacteriological parameters from their treatment stage, GAC Filters (RGFs only), Contact Tank and Balance Tank and Final monitor turbidity and bacteriological parameters.

6.2.4. Self-Organising Maps

The Self-Organising Map (SOM) analyses were conducted on each unit process through Strensham WTW, working from the Raw water through to the Final. The climate parameters were subjected to analysis with the bacteriological parameters from the Final sampling point: coliforms 100 ml^{-1}, coliforms 1 L^{-1}, non-coliforms 1 L^{-1} and Enterococci 100 ml^{-1}. These analyses were conducted on the full five month dataset and

on the weeks of each of the failures. Furthermore, the data for through-plant coliforms and turbidity were analysed. The turbidity analyses included the monitor data from the individual RGF Filters and the GAC Filters.

Table 13a: Cross-correlations applied to joined Strensham dataset; x = cross-correlation conducted between Parameter 1 (down the side of the table) and Parameter 2 (across the top).

	Raw *E. coli*	Raw non-coliforms	Raw *C. perfringens*	Raw Enterococci	Raw turbidity	Raw pH Spot	Raw pH Monitor	Raw water temperature	Settlement tank coliforms	Settlement tank *E. coli*	Settlement tank non-coliforms	Settlement tank turbidity	Settlement tank pH	RGF coliforms	RGF *E. coli*	RGF non-coliforms	RGF turbidity	RGF pH	GAC coliforms	GAC *E. coli*	GAC non-coliforms	GAC pH	Contact tank coliforms	Contact tank HPC22	Contact tank HPC37
Raw coliforms	x	x	x	x	x	x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Raw *E. coli*		x	x	x	x	x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Raw non-coliforms	x		x	x	x	x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Raw Enterococci																									
Raw turbidity	x	x	x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Raw pH Spot	x	x	x	x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Raw pH Monitor	x	x	x	x	x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Raw water temperature	x	x	x	x	x	x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Settlement tank coliforms										x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Settlement tank *E. coli*									x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Settlement tank non-coliforms									x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	x
Settlement tank turbidity									x	x	x		x	x	x	x	x	x	x	x	x	x	x	x	x
Settlement tank pH									x	x	x	x		x	x	x	x	x	x	x	x	x	x	x	x
RGF coliforms															x	x	x	x	x	x	x	x	x	x	x
RGF *E. coli*														x		x	x	x	x	x	x	x	x	x	x
RGF non-coliforms														x	x		x	x	x	x	x	x	x	x	x
RGF turbidity														x	x	x		x	x	x	x	x	x	x	x
RGF pH														x	x	x	x		x	x	x	x	x	x	x
GAC coliforms																				x	x	x	x	x	x
GAC *E. coli*																			x		x	x	x	x	x
GAC non-coliforms																			x	x		x	x	x	x
GAC pH																			x	x	x		x	x	x
Contact tank coliforms																								x	x
Contact tank HPC22																							x		x
Contact tank HPC37																							x	x	
Contact tank free chlorine																							x	x	x
Contact tank total chlorine																							x	x	x
Contact tank turbidity																							x	x	x
Contact tank pH																							x	x	x
Balance tank coliforms																									
Balance tank free chlorine																									
Balance tank total chlorine																									
Balance tank turbidity																									
Balance tank pH																									
Final free chlorine monitor																									
Final flow																									
Final turbidity monitor																									
Final coliforms 100 ml																									
Final Enterococci																									
Final HPC22																									
Final HPC37																									
Final coliforms 1 L																									
Final non-coliforms 1 L																									
Final free chlorine Spot																									
Final total chlorine																									
Final turbidity Spot																									
Final pH																									
Air temperature	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x
Rainfall	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x

Table 13b: Cross-correlations applied to joined Strensham dataset; x = cross-correlation conducted between Parameter 1 (down the side of the table) and Parameter 2 (across the top).

	Contact tank free chlorine	Contact tank total chlorine	Contact tank turbidity	Contact tank pH	Balance tank coliforms	Balance tank free chlorine	Balance tank total chlorine	Balance tank turbidity	Balance tank pH	Final free chlorine monitor	Final flow	Final turbidity monitor	Final coliforms 100 ml	Final Enterococci	Final HPC22	Final HPC37	Final coliforms 1 L	Final non-coliforms 1 L	Final free chlorine Spot	Final total chlorine	Final turbidity Spot	Final pH	Air temperature
Raw coliforms			x	x	x			x	x		x	x	x	x	x	x	x	x			x	x	
Raw *E. coli*			x	x	x			x	x		x	x	x	x	x	x	x	x			x	x	
Raw non-coliforms			x	x	x			x	x		x	x	x	x	x	x	x	x			x	x	
Raw Enterococci														x									
Raw turbidity	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Raw pH Spot	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Raw pH Monitor	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Raw water temperature	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Settlement tank coliforms	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Settlement tank *E. coli*	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Settlement tank non-coliforms	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Settlement tank turbidity	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Settlement tank pH	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
RGF coliforms	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
RGF *E. coli*	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
RGF non-coliforms	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
RGF turbidity	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
RGF pH	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
GAC coliforms	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
GAC *E. coli*	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
GAC non-coliforms	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
GAC pH	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Contact tank coliforms	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Contact tank HPC22	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Contact tank HPC37	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Contact tank free chlorine		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Contact tank total chlorine	x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Contact tank turbidity	x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Contact tank pH	x	x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Balance tank coliforms						x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Balance tank free chlorine					x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Balance tank total chlorine					x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Balance tank turbidity					x	x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Balance tank pH					x	x	x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	
Final free chlorine monitor											x	x	x	x	x	x	x	x	x	x	x	x	
Final flow										x		x	x	x	x	x	x	x	x	x	x	x	
Final turbidity monitor										x	x		x	x	x	x	x	x	x	x	x	x	
Final coliforms 100 ml										x	x	x		x	x	x	x	x	x	x	x	x	
Final Enterococci										x	x	x	x		x	x	x	x	x	x	x	x	
Final HPC22										x	x	x	x	x		x	x	x	x	x	x	x	
Final HPC37										x	x	x	x	x	x		x	x	x	x	x	x	
Final coliforms 1 L										x	x	x	x	x	x	x		x	x	x	x	x	
Final non-coliforms 1 L										x	x	x	x	x	x	x	x		x	x	x	x	
Final free chlorine Spot										x	x	x	x	x	x	x	x	x		x	x	x	
Final total chlorine										x	x	x	x	x	x	x	x	x	x		x	x	
Final turbidity Spot										x	x	x	x	x	x	x	x	x	x	x		x	
Final pH										x	x	x	x	x	x	x	x	x	x	x	x		
Air temperature	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	
Rainfall	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x

The default settings of linear initialisation and batch training were selected, but a change was required in the 'SOM make' line of code:

```
% SOM1
TRAIN_CORE =[DataAll.Parameter1 DataAll.Parameter2 ...
DataAll.Parameter3 DataAll.Parameter4 DataAll.Parameter5];
                                    %Specify data to include
   sData=som_data_struct(TRAIN_CORE);

   sData=som_normalize(sData,'range'); %Normalises data for analysis
   sM = som_make((sData),'msize',[60 40]);
                %Make SOM, use specified component plane dimensions
sM.comp_names{1}='Parameter1'; %Label the component plane
sM.comp_names{2}='Parameter2';
sM.comp_names{3}='Parameter3';
sM.comp_names{4}='Parameter4';
sM.comp_names{5}='Parameter5';

figure, som_show(sM); %Show SOM plot
```

This modified line of code was required to overcome a quirk in the SOM Toolbox that allows some sets of component planes to have a 3:2 aspect ratio and others to have 10:1 despite being based on the same number of input values (Figure 25).

Because of the size and complexity of the Strensham dataset, once it had been compiled a line of code was added to remove the unnecessary Workspace variables that had been accrued during its construction (to free-up memory).

```
clearvars -except DataAll*; %Remove unnecessary variables, keep
                            %DataAll dataset
```

The cross-correlation figures for Strensham were constructed so that each one contained three plots. A command was introduced to clear the figures each time ten had been generated.

```
close all; %Delete open plots
```

Furthermore, the allowable number of rows of code in MATLAB Editor was exceeded. This meant that the cross-correlations had to be split into five sections, with 600 in each of the first four Editor files. The results were then brought together into an Excel file for subsequent analyses.

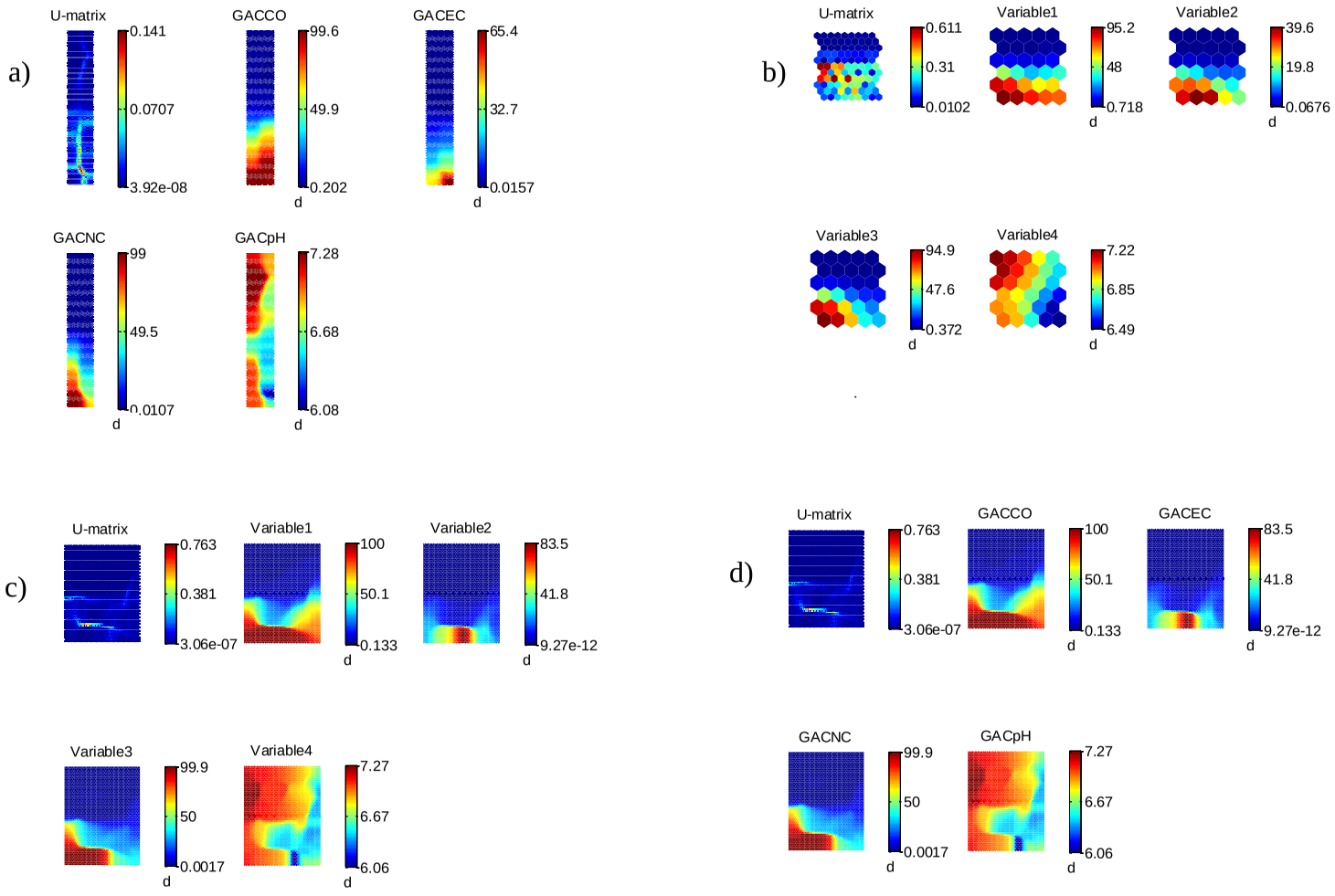

Figure 25: a) Initial SOM output, b) trial one, c) trial two, and d) correctly labelled and correctly sized.

6.3. Results

6.3.1. Cross-correlation

The results from the cross-correlations can only be identified as significant if the length of time water spends in Strensham WTW is considered. These times are presented in Table 14. Since it cannot be known which Settlement Tank affected water from the RGFs and beyond, the average time range in this treatment process is 2.2 – 2.6 h.

Table 14: Time, h, that water spends in each treatment stage of Strensham WTW at maximum and minimum output. Maximum output values were provided and assume 100 % efficiency; times for minimum output have been calculated based on the minimum flow rate and assume the same proportions.

	Intake	Settlement Tank		RGF Filters	GAC Filters	Contact Tank
Maximum flow (131 ML d^{-1})	0.5	A	2.2	1.1	0.9	2.0
		B	2.2			
		C	2.0			
		D	2.4			

	Intake	Settlement Tank		RGF Filters	GAC Filters	Contact Tank
Minimum flow (113 ML d^{-1})	0.6	A	2.6	1.2	1.0	2.3
		B	2.5			
		C	2.3			
		D	2.8			

The cross-correlation analysis of Strensham's data showed that the majority of results were both positive and between 0 and 24 h (Table 15). No cross-correlations were conducted between *C. perfringens* and the other datasets because of the sporadic nature of monitoring for this parameter (approximately monthly) and the fact that none were recorded in the Final water. Likewise, Enterococci were only cross-correlated with Final Enterococci, but the result did not meet the criteria of being both positive and between 0 and 24 h. The rainfall and air temperature datasets (Table 16 and Table 17) showed that most of the qualifying results for all parameters were for 0 h. This was the case for the majority of applicable results across all analyses. Therefore, after looking at the full cross-correlation results for the climate parameters, the other results tables will focus on cross-correlations with results > 0 h. The full tables of qualifying results are in Appendix 2 and important features from these shall be referred to in this Chapter. The cross-correlation results will be explored in stages working progressively through the WTW from Raw water to Final. Where appropriate, the full five month dataset and the five failure weeks will be discussed simultaneously, with the tables divided into sections by parameter. In the tables for rainfall and air temperature, where results for all five failure weeks, sometimes with the inclusion of the five month dataset, were in

agreement, these rows have been highlighted. In the subsequent tables (excluding the individual RGF and GAC Filter turbidity results), only the results that referred to the failure parameters (coliforms, Enterococci and 1 L coliforms) have been highlighted. The table for the RGF and GAC Filter results highlights the rows where all the failure weeks agree (including/excluding the full five month dataset) and results that referred to failure parameters have been marked with a box.

6.3.1.1. Rainfall cross-correlations

Of the 414 cross-correlations conducted between rainfall and the WTW datasets and air temperature, 198 met the selection criteria (Table 15 and Table 16). Of the applicable results, all except one were 0 h; that was rainfall x GAC coliforms in the dataset for the third 1 L coliform detection, with a time lag of 7.2 h. There were no correlations with rainfall for Final coliforms, Enterococci or 1 L coliforms.

Rainfall x Raw coliforms and rainfall x Raw turbidity changed one with another during the weeks of the coliform, Enterococci, and first and third 1 L coliform detections (Table 16). The trends over the respective weeks show that increased rainfall resulted in increased numbers of coliforms and higher turbidity (graphs not shown). Rainfall x Raw non-coliforms resulted in consistent results; the trend charts show that colony counts rose with increasing rainfall. Raw *E. coli* and Raw *C. perfringens* changed with rainfall in the week of the Enterococcus failure and the first and third 1 L coliform detections. During these weeks, the trends show *E. coli* increasing with rainfall; there was no clear trend for the other failure weeks. During the week of the Enterococcus failure and the third 1 L coliform detection, numbers of *C. perfringens* rose with rainfall and for the first 1 L coliform detection the reverse was the case. Raw Enterococci changed with rainfall around the time of the first and third 1 L coliform failures and the trends show this was a slight decline; furthermore, the sporadic monitoring for this parameter means that the dataset is heavily reliant on interpolation. Broadly speaking, these analyses show that numbers of coliforms (and other bacteria) entering the WTW were influenced by rainfall in the catchment. Bacteria and particulate matter are washed into rivers from the watershed during rainfall events which increases the loading received at a WTW (Schets *et al.*, 2005; Pitkänen *et al.*, 2008). In the Raw water, changes in rainfall consistently correlated with changes in pH, both monitored and spot-sampled, for the five failure weeks. For the coliform, Enterococcus and first and second 1 L coliform detections spot-sampled pH fell and monitor pH rose with increasing rainfall for these

datasets. Over the week of the third 1 L coliform failure rainfall decreased and so too did monitor and spot-sampled pH. Finally, the raw water temperature changed with rainfall for the Enterococcus detection and the three 1 L coliform failures. Water temperature changed inversely with amount of rainfall and thus increased during the week of the third 1 L coliform detection and decreased in the other weeks.

Table 15: Number of cross-correlations conducted on each Parameter and the number that were both positive and between 0 and 24 h.

Parameter 1	No. Cross-correlations	No. +ve and 0-24 h
RawCO	342	244
RawEC	342	284
RawNC	342	251
RawCLOS	0	-
RawEN	1	0
RawTurb	342	259
RawpHSpot	342	321
RawTemp	342	320
RawpHMon	342	299
ASettCO	222	147
ASettEC	222	131
ASettNC	222	147
ASettTurb	222	153
ASettpH	222	159
BSettCO	222	131
BSettEC	222	130
BSettNC	222	143
BSettTurb	222	154
BSettpH	222	159
CSettCO	222	145
CSettEC	222	132
CSettNC	222	138
CSettTurb	222	146
CSettpH	222	162
DSettCO	222	137
DSettEC	222	127
DSettNC	222	143
DSettTurb	222	160
DSettpH	222	161
ABCFiltCO	192	125
ABCFiltEC	192	111
ABCFiltNC	192	117
ABCFiltTurb	192	121
ABCFiltph	192	132
Rainfall	414	198

Parameter 1	No. Cross-correlations	No. +ve and 0-24 h
DFiltCO	192	124
DFiltEC	192	119
DFiltNC	192	119
DFiltTurb	192	112
DFiltpH	192	132
GACCO	162	87
GACEC	162	11
GACNC	162	69
GACpH	162	95
CONCO	138	0
CONHPC22	138	2
CONHPC37	138	3
CONFreeCL	138	83
CONTurb	138	82
CONpH	138	86
CONTotalCL	138	85
BALCO	96	2
BALFreeCL	96	59
BALTurb	96	57
BALpH	96	60
BALTotalCL	96	95
FINCLMon	66	33
FINFlow	66	34
FINTurbMon	66	34
FINCO	66	0
FINEN	66	0
FINHPC22	66	1
FINHPC37	66	0
FINCO1L	66	1
FINNC1L	66	3
FINFreeCL	66	35
FINTurb	66	35
FINpH	66	35
FINTotalCL	66	36
AirTemp	414	212

All four Settlement Tanks are housed within buildings. It is unlikely that their water quality was directly impacted by rainfall, which is what a 0 h time lag suggests. Settlement Tank A coliforms changed with rainfall during the weeks of the coliform, Enterococcus and third 1 L coliform detections (Table 16). The trends show that coliform numbers increased with rainfall over these periods (graphs not shown). *E. coli* correlated with rainfall during the Enterococcus and the second and third 1 L coliform failures. Non-coliforms changed with rainfall during the weeks of the Enterococcus and second 1 L coliform detections. In Settlement Tank B, coliforms, *E. coli* and non-coliforms changed (increased) with rainfall during the weeks of the coliform and Enterococcus failures, with a further correlation with *E. coli* during the third 1 L coliform detection. *E. coli* and non-coliforms changed with rainfall during the week of the coliform and Enterococcus failures for Settlement Tank C. The coliforms in this Tank were observed to change (increase) with rainfall only during the Enterococcus failure. Meanwhile, in Settlement Tank D, coliforms changed (increased) with rainfall during the coliform, Enterococcus and third 1 L coliform failures; *E. coli* correlated with rainfall during the Enterococcus and third 1 L coliform failures and the trends show their numbers increased; and non-coliforms changed (increased) with rainfall during the coliform and Enterococcus detections. The apparent direct impact (0 h time lag) of rainfall on bacteriological quality from the Settlement Tanks despite them not being exposed to the elements may be an effect of the sporadic bacteriological monitoring or of the unknown distance between the rainfall monitors and Strensham WTW.

In Settlement Tanks B and C, turbidity correlated with rainfall during the week of the coliform detection (rose with increasing rainfall); and also the first and third 1 L coliform and Enterococcus failures (fell with increasing rainfall) (Table 16). In Settlement Tanks A and D, the settled water turbidity correlated with rainfall for the Enterococcus and first and third 1 L coliforms, but the trends showed an inconsistent response to changes in rainfall. It is unclear why Tank A performed differently to Tanks B and C; Tank D may have functioned differently because it is on a different treatment stream.

The pH in Settlement Tanks B and C did change with rainfall for all five failure weeks; but this was not true for Settlement Tanks A and D. Settlement Tank D is on a separate process stream to A, B and C and this could be why it has a different response;

however, Tank A is part of the ABC stream and would be expected to perform similarly to the other two.

RGF Filter Blocks A, B and C are uncovered and could have been directly impacted by rainfall. Coliforms coming off Filter Block ABC changed (increased) with rainfall for all five failure weeks (Table 16). *E. coli* numbers also changed (increased) with rainfall at the time of the coliform and Enterococcus detections. The non-coliforms from Filter Block ABC changed (increased) with rainfall for both the coliform and the third 1 L coliform failures. Turbidity coming off the filters did not change consistently with rainfall. In Filter Block ABC, turbidity changed (rose) during the weeks of the coliform and Enterococcus failures; it changed (fell) during the second and third 1 L coliform detections. The pH changed (rose) with rainfall for the coliform and Enterococcus failures; and changed (fell) during the weeks of the first and third 1 L coliform failures. RGF Filter Block D is housed within a building and rainfall cannot have directly impacted the quality of water from this Block as indicated by the 0 h time lags.

The GAC Filters are all housed within buildings. It is unlikely that rainfall would have directly impacted the quality of water at this treatment stage, which is what the 0 h time lags imply. GAC coliforms responded to rainfall during the week of the third 1 L coliform failure – with a time lag of 7.2 h. This is approximately 1.5 times the length of time it takes for water to be treated to post-GAC standard (4.7 – 5.5 h). The trend shows that coliform numbers increased with decreasing rainfall. The location of the rainfall monitor in relation to Strensham WTW is unknown and may account for the 2 – 3 h time delay on the treatment time to this stage. This viable time lag indicates that rainfall can affect the bacteriological performance of the GAC Filters. Therefore, monitoring rainfall levels could provide some warning of coliforms passing through this process. These suppositions will be studied in more detail with reference to GAC Filter turbidity (Table 29).

There were no qualifying results for cross-correlations between rainfall and bacteriological parameters beyond the GAC Filters (Table 16). However, consistent results exist for rainfall correlations with Contact Tank pH, Final free and total chlorine and Final pH. With the pH results, it is likely that the rainfall's impact on the raw water pH was carried all through the WTW. Air temperature changed (increased) with rainfall

during the Enterococcus and first and second 1 L coliform detections; it also changed (inversely) with rainfall during the week of the third 1 L coliform failure.

6.3.1.2. Air temperature cross-correlations

Of the 414 cross-correlations conducted between air temperature and the WTW datasets and rainfall, 212 met the selection criteria (Table 17). Of the applicable results, all except five were 0 h. Four of these occurred during the week of the coliform failure. They were for air temperature with: Raw turbidity, 19.0 h; Raw water temperature, 7.3 h; Settlement Tank C pH, 23.2 h; and, Final flow rate, 8.9 h. The fifth one occurred in the week of the third 1 L coliform detection and related to air temperature x Contact Tank HPC22, 8.2 h. Applicable cross-correlation results for the Enterococcus failure and the first and second 1 L coliform detections were numerous. There were no correlations with air temperature for Final coliforms, Enterococci or 1 L coliforms, but Final non-coliforms did feature.

Raw water temperature was impacted by air temperature during all five failure weeks and throughout the five month dataset. The trends show that Raw water temperature increased with increasing air temperature (graphs not shown). The correlation of (increasing) Raw water indicator bacteria with air temperature is likely to be a result of air temperature affecting water temperature. Since water temperature change lagged behind air temperature change, it would be expected that Contact Tank HPC22 numbers would lag behind too (8.2 h). However, Raw water temperature x Contact Tank HPC22 did not yield cross-correlation results that were positive and between 0 and 24 h (Table 18b).

The total chlorine concentration in the Contact Tank consistently correlated with air temperature, including the five month dataset. It is likely that this is as a result of the air temperature influencing the Raw water temperature; water temperature is a factor in determining the required chlorine dose (Crittenden *et al.*, 2005). Final monitor free chlorine was similarly affected.

Table 16: Cross-correlation results for rainfall at Strensham. Shaded rows highlight cross-correlations that were both positive and between 0 and 24 h for all five failure weeks and, where applicable, the five month dataset.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
Rainfall	RawCO	-	0.0	0.0	0.0	-	0.0
Rainfall	RawEC	-	-	0.0	0.0	-	0.0
Rainfall	RawNC	-	0.0	0.0	0.0	0.0	0.0
Rainfall	RawCLOS	-	-	0.0	0.0	-	0.0
Rainfall	RawEN	-	-	-	0.0	-	0.0
Rainfall	RawTurb	-	0.0	0.0	0.0	-	0.0
Rainfall	RawpHSpot	-	0.0	0.0	0.0	0.0	0.0
Rainfall	RawTemp	-	-	0.0	0.0	0.0	0.0
Rainfall	RawpHMon	-	0.0	0.0	0.0	0.0	0.0
Rainfall	ASettCO	-	0.0	0.0	-	-	0.0
Rainfall	ASettEC	-	-	0.0	-	0.0	0.0
Rainfall	ASettNC	-	-	0.0	-	0.0	-
Rainfall	ASettTurb	-	-	0.0	0.0	-	0.0
Rainfall	ASettpH	-	0.0	0.0	0.0	-	0.0
Rainfall	BSettCO	-	0.0	0.0	-	-	-
Rainfall	BSettEC	-	0.0	0.0	-	-	0.0
Rainfall	BSettNC	-	0.0	0.0	-	-	-
Rainfall	BSettTurb	-	0.0	0.0	0.0	-	0.0
Rainfall	BSettpH	-	0.0	0.0	0.0	0.0	0.0
Rainfall	CSettCO	-	-	0.0	-	-	0.0
Rainfall	CSettEC	-	0.0	0.0	-	-	-
Rainfall	CSettNC	-	0.0	0.0	-	-	-
Rainfall	CSettTurb	-	0.0	0.0	0.0	-	0.0
Rainfall	CSettpH	-	0.0	0.0	0.0	0.0	0.0
Rainfall	DSettCO	-	0.0	0.0	-	-	0.0
Rainfall	DSettEC	-	-	0.0	-	-	0.0
Rainfall	DSettNC	-	0.0	0.0	-	-	-
Rainfall	DSettTurb	-	-	0.0	0.0	-	0.0
Rainfall	DSettpH	-	0.0	0.0	0.0	-	0.0
Rainfall	ABCFiltCO	-	0.0	0.0	0.0	0.0	0.0
Rainfall	ABCFiltEC	-	0.0	0.0	-	-	-
Rainfall	ABCFiltNC	-	0.0	-	-	-	0.0
Rainfall	ABCFiltTurb	0.0	0.0	0.0	-	0.0	0.0
Rainfall	ABCFiltpH	-	0.0	0.0	0.0	-	0.0
Rainfall	DFiltCO	-	0.0	0.0	0.0	-	0.0
Rainfall	DFiltEC	-	0.0	0.0	-	-	0.0
Rainfall	DFiltNC	-	0.0	-	-	-	0.0
Rainfall	DFiltTurb	-	-	0.0	-	-	0.0
Rainfall	DFiltpH	-	0.0	0.0	0.0	-	0.0
Rainfall	GACCO	-	-	0.0	-	-	7.2
Rainfall	GACNC	-	-	0.0	-	-	-
Rainfall	GACpH	-	0.0	0.0	0.0	-	0.0
Rainfall	CONFreeCL	-	0.0	0.0	0.0	-	0.0
Rainfall	CONTurb	-	0.0	0.0	-	-	0.0
Rainfall	CONpH	-	0.0	0.0	0.0	0.0	0.0
Rainfall	CONTotalCL	-	0.0	0.0	0.0	-	0.0
Rainfall	BALFreeCL	-	0.0	0.0	0.0	-	0.0
Rainfall	BALTurb	-	0.0	0.0	-	-	0.0
Rainfall	BALpH	-	0.0	0.0	0.0	-	0.0
Rainfall	BALTotalCL	-	-	0.0	0.0	-	0.0
Rainfall	FINCLMon	0.0	-	0.0	0.0	-	0.0
Rainfall	FINFlow	-	-	-	0.0	0.0	0.0
Rainfall	FINTurbMon	-	0.0	0.0	-	-	0.0
Rainfall	FINFreeCL	-	0.0	0.0	0.0	0.0	0.0
Rainfall	FINTurb	-	-	0.0	0.0	-	0.0
Rainfall	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
Rainfall	FINTotalCL	-	0.0	0.0	0.0	0.0	0.0
Rainfall	AirTemp	-	-	0.0	0.0	0.0	0.0

Table 17: Cross-correlation results for air temperature at Strensham. Shaded rows highlight cross-correlations that were both positive and between 0 and 24 h for all five failure weeks and, where applicable, the five month dataset.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
AirTemp	RawCO	-	-	0.0	0.0	0.0	0.0
AirTemp	RawEC	-	-	0.0	0.0	0.0	0.0
AirTemp	RawNC	-	-	0.0	0.0	0.0	0.0
AirTemp	RawCLOS	0.0	0.0	0.0	-	0.0	0.0
AirTemp	RawEN	-	0.0	-	-	0.0	0.0
AirTemp	RawTurb	-	19.0	0.0	0.0	0.0	0.0
AirTemp	RawpHSpot	0.0	-	0.0	-	0.0	0.0
AirTemp	RawTemp	0.0	7.3	0.0	0.0	0.0	0.0
AirTemp	RawpHMon	0.0	-	0.0	0.0	0.0	0.0
AirTemp	ASettCO	-	-	0.0	-	0.0	0.0
AirTemp	ASettEC	-	-	0.0	-	0.0	0.0
AirTemp	ASettNC	-	-	0.0	-	0.0	0.0
AirTemp	ASettTurb	-	0.0	0.0	-	0.0	0.0
AirTemp	ASettpH	0.0	-	0.0	-	0.0	0.0
AirTemp	BSettCO	-	-	0.0	-	0.0	0.0
AirTemp	BSettEC	-	-	0.0	-	-	0.0
AirTemp	BSettNC	-	-	0.0	-	0.0	0.0
AirTemp	BSettTurb	0.0	-	0.0	-	0.0	0.0
AirTemp	BSettpH	0.0	-	0.0	-	0.0	0.0
AirTemp	CSettCO	-	-	0.0	-	-	0.0
AirTemp	CSettEC	-	-	0.0	-	-	-
AirTemp	CSettNC	-	-	0.0	-	-	0.0
AirTemp	CSettTurb	0.0	-	0.0	-	0.0	0.0
AirTemp	CSettpH	0.0	23.2	0.0	-	0.0	0.0
AirTemp	DSettCO	-	-	0.0	-	0.0	0.0
AirTemp	DSettEC	-	0.0	0.0	-	-	0.0
AirTemp	DSettNC	-	-	0.0	-	0.0	0.0
AirTemp	DSettTurb	0.0	-	0.0	0.0	0.0	0.0
AirTemp	DSettpH	0.0	-	0.0	-	0.0	0.0
AirTemp	ABCFiltCO	0.0	-	0.0	-	0.0	0.0
AirTemp	ABCFiltEC	-	-	0.0	-	-	0.0
AirTemp	ABCFiltNC	-	-	0.0	-	0.0	0.0
AirTemp	ABCFiltTurb	-	-	0.0	-	0.0	0.0
AirTemp	ABCFiltpH	0.0	-	0.0	-	0.0	0.0
AirTemp	DFiltCO	0.0	0.0	0.0	-	0.0	0.0
AirTemp	DFiltEC	-	-	0.0	-	-	0.0
AirTemp	DFiltNC	-	-	0.0	-	0.0	0.0
AirTemp	DFiltTurb	-	-	0.0	-	0.0	0.0
AirTemp	DFiltpH	0.0	0.0	0.0	-	0.0	0.0
AirTemp	GACCO	-	-	0.0	-	0.0	-
AirTemp	GACNC	-	-	0.0	-	-	-
AirTemp	GACpH	0.0	-	0.0	-	0.0	0.0
AirTemp	CONHPC22	-	-	-	-	-	8.2
AirTemp	CONFreeCL	0.0	-	0.0	0.0	0.0	0.0
AirTemp	CONTurb	-	-	0.0	-	0.0	0.0
AirTemp	CONpH	0.0	-	0.0	-	0.0	0.0
AirTemp	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
AirTemp	BALFreeCL	0.0	-	0.0	0.0	0.0	0.0
AirTemp	BALTurb	-	-	0.0	-	-	0.0
AirTemp	BALpH	0.0	0.0	0.0	-	0.0	0.0
AirTemp	BALTotalCL	0.0	-	0.0	0.0	0.0	0.0
AirTemp	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
AirTemp	FINFlow	-	8.9	0.0	-	0.0	0.0
AirTemp	FINTurbMon	-	-	0.0	-	-	0.0
AirTemp	FINNC1L	-	0.0	-	-	-	-
AirTemp	FINFreeCL	0.0	-	0.0	-	0.0	0.0
AirTemp	FINTurb	-	-	0.0	-	-	0.0
AirTemp	FINpH	0.0	0.0	0.0	-	0.0	0.0
AirTemp	FINTotalCL	0.0	-	0.0	-	0.0	0.0
AirTemp	Rainfall	-	-	0.0	0.0	0.0	0.0

Table 18: Raw water cross-correlations where at least one of the results had a time lag >0 h. Shaded results highlight applicable cross-correlations with Final coliforms or Final 1 L coliforms.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
RawCO	RawTurb	21.4	0.0	0.0	0.0	0.0	0.0
RawCO	ASettEC	3.9	0.0	0.0	0.0	0.0	0.0
RawCO	CSettEC	0.8	0.0	0.0	0.0	0.0	0.0
RawCO	ABCFiltEC	0.1	0.0	0.0	0.0	0.0	0.0
RawCO	DFiltEC	1.5	0.0	0.0	0.0	0.0	0.0
RawCO	GACEC	-	-	-	10.7	-	-
RawCO	BALTurb	4.0	0.0	0.0	0.0	5.4	0.0
RawCO	FINHPC37	21.8	-	-	-	-	-
RawCO	FINNC1L	-	-	-	-	23.7	-
RawEC	RawCO	0.0	4.6	0.0	0.0	0.0	0.0
RawEC	RawNC	2.2	11.8	0.0	0.0	0.0	0.0
RawEC	RawEN	22.9	0.0	-	0.0	0.0	0.0
RawEC	RawTurb	1.6	0.0	0.0	0.0	0.0	0.0
RawEC	ASettCO	12.2	1.4	0.0	0.0	0.0	0.0
RawEC	ASettEC	13.9	0.0	0.0	-	0.0	0.0
RawEC	BSettCO	-	3.3	0.0	-	0.0	0.0
RawEC	BSettEC	4.2	-	0.0	-	0.0	0.0
RawEC	CSettEC	17.8	15.2	0.0	-	0.0	-
RawEC	DSettCO	8.1	10.5	0.0	-	0.0	0.0
RawEC	DSettEC	0.8	0.0	0.0	0.0	0.0	0.0
RawEC	ABCFiltEC	4.7	3.8	0.0	-	0.0	0.0
RawEC	DFiltCO	0.1	0.0	0.0	0.0	0.0	0.0
RawEC	DFiltEC	5.7	5.3	0.0	0.0	0.0	0.0
RawEC	CONTurb	-	0.9	0.0	0.0	0.0	0.0
RawEC	FINTurbMon	-	14.0	-	0.0	0.0	0.0
RawEC	FINCO	-	20.3	-	-	-	-
RawEC	FINCO1L	-	-	-	-	12.3	-
RawEC	FINFreeCL	2.0	0.0	0.0	0.0	0.0	0.0
RawNC	ASettEC	5.0	0.0	0.0	-	0.0	0.0
RawNC	BSettEC	6.5	0.0	0.0	-	0.0	0.0
RawNC	CSettEC	7.7	0.0	0.0	-	0.0	0.0
RawNC	ABCFiltCO	1.7	0.0	0.0	0.0	0.0	0.0
RawNC	DFiltCO	1.2	0.0	0.0	0.0	0.0	0.0
RawNC	GACCO	-	-	0.0	-	-	0.1
RawNC	GACNC	-	0.0	0.0	-	-	5.3
RawNC	CONTotalCL	0.1	0.0	0.0	0.0	0.0	0.0
RawNC	FINFlow	8.7	0.0	0.0	0.0	0.0	0.0
RawNC	FINFreeCL	8.1	0.0	0.0	0.0	0.0	0.0
RawNC	FINTotalCL	3.5	0.0	0.0	0.0	0.0	0.0
RawTurb	FINCO	-	20.3	-	-	-	-
RawTurb	FINNC1L	-	-	-	-	23.7	-
RawpHSpot	RawTurb	17.3	0.0	0.0	0.0	0.0	0.0
RawpHSpot	BSettEC	3.9	0.0	0.0	0.0	0.0	0.0
RawpHSpot	BSettNC	6.1	0.0	0.0	0.0	0.0	0.0
RawpHSpot	DFiltTurb	10.9	0.0	0.0	0.0	0.0	0.0
RawpHSpot	GACCO	-	0.0	0.0	0.0	0.0	0.6
RawpHSpot	CONHPC37	-	-	23.7	-	-	-
RawpHSpot	FINTurbMon	7.4	0.0	0.0	0.0	0.0	0.0
RawpHMon	ASettEC	0.0	0.0	1.6	0.0	0.0	0.0
RawpHMon	CSettEC	0.0	0.0	3.3	0.0	0.0	0.0
RawpHMon	DFiltTurb	16.4	0.0	0.0	0.0	0.0	0.0
RawpHMon	GACCO	-	0.0	0.0	0.0	0.0	0.3
RawpHMon	GACEC	-	-	-	0.0	-	15.0
RawpHMon	GACNC	-	0.0	0.0	0.0	0.0	17.9

Table 18b: Raw water cross-correlations where at least one of the results had a time lag >0 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
RawTemp	ASettEC	-	0.0	3.4	0.0	0.0	0.0
RawTemp	BSettEC	-	9.5	0.0	0.0	0.0	0.0
RawTemp	BSettNC	-	10.3	0.0	0.0	0.0	0.0
RawTemp	CSettEC	-	-	5.8	0.0	0.0	0.0
RawTemp	DSettEC	-	9.0	0.0	0.0	0.0	0.0
RawTemp	DFiltTurb	17.2	6.2	0.0	0.0	0.0	0.0
RawTemp	CONTurb	11.6	0.0	0.0	0.0	0.0	0.0
RawTemp	BALTurb	4.0	0.0	0.0	0.0	0.0	0.0

6.3.1.3. Raw coliform cross-correlations

Of the 342 cross-correlations conducted with Raw coliforms, 244 resulted in positive time lags between 0 and 24 h (Table 15). Whilst most of the results were 0 h, several time lags were identified (Table 18a and b). From the five month dataset, the following correlations resulted in a time lag: Raw turbidity, 21.4 h; Settlement Tank A *E. coli*, 3.9 h; Settlement Tank C *E. coli*, 0.8 h; Filter Block ABC *E. coli*, 0.1 h; Filter Block D *E. coli*, 1.5 h; Balance Tank turbidity, 4.0 h; and Final HPC37, 21.8 h. Furthermore, during the first 1 L coliform failure, Raw coliforms produced a time lag with GAC Filter *E. coli*, 10.7 h; and during the second 1 L coliform failure, positive time lags were observed for Balance Tank turbidity, 5.4 h and Final 1 L non-coliforms, 23.7 h.

Bacteriological cross-correlations for Raw water coliforms met the selection criteria across all datasets for the following parameters: Raw non-coliforms and *C. perfringens*; Settlement Tanks A, B, C and D coliforms, *E. coli* and non-coliforms; Filter Blocks ABC and D coliforms, *E. coli* and non-coliforms (Appendix 2). The time lags relating to downstream coliforms were all 0 h; but viable time lags were identified with *E. coli*. The time lag between Raw coliforms and Settlement Tank A *E. coli* was 0.7 – 1.2 h longer than the time taken for water to be treated to this stage in the WTW (Table 14). Conversely, the time lags for Tank C and Filter Blocks ABC and D *E. coli* were too short. The time lag for GAC Filter *E. coli* was approximately double the time required to treat water to this stage. It is assumed that this is because of the sampling frequency for bacteriological parameters. Unless there was a problem with the operation of the Settlement Tanks (something which has not been identified) water would be expected to pass through them at approximately the same rate at any given time. It appears that the performance of the different Settlement Tanks is variable. These peaks or troughs in the *E. coli* data are not related to the peaks or troughs in the Raw water coliforms against which they have been compared. It demonstrates that the bacteriological quality of both

the Raw water and the treatment stages fluctuate, and in such a manner that they appear to change contiguously.

There was a time lag of 21.4 h between a change in the Raw coliforms and that of Raw turbidity in the full five month dataset (Table 18a). It suggests that peaks or troughs in Raw coliform data preceded those of turbidity by almost a day.

6.3.1.4. Raw *E. coli* cross-correlations

Of the 342 cross-correlations conducted with Raw *E. coli*, 284 resulted in positive time lags between 0 and 24 h (Table 18a). The majority of the results were for 0 h and consistently applicable time lags were identified for Raw *E. coli* correlated with the following bacteriological parameters: Raw coliforms, non-coliforms and *C. perfringens*; Settlement Tank A coliforms and non-coliforms; Settlement Tank D *E. coli*; Filter Block ABC coliforms; and Filter Block D coliforms and *E. coli* (Appendix 2). Twenty-five of the cross-correlations resulted in time lags. From the five month dataset, these were for Raw *E. coli* with: Raw non-coliforms, 2.2 h; Raw Enterococci, 22.9 h; Raw turbidity, 1.6 h; Settlement Tank A coliforms, 12.2 h and *E. coli*, 13.9 h; Settlement Tank B *E. coli*, 4.2 h; Settlement Tank C *E. coli*, 17.8 h; Settlement Tank D coliforms, 8.1 h and *E. coli*, 0.8 h; Filter Block ABC *E. coli*, 4.7 h; Filter Block D coliforms, 0.1 h and *E. coli*, 5.7 h; and Final spot-sampled free chlorine, 2.0 h. It is interesting to note the repeated appearance of *E. coli* within the results. There were no *E. coli* recorded post-GAC in the raw data and this shows that *E. coli* were effectively controlled through chlorination throughout the time period under study. Time lags were observed from the week of the coliform detection too, these were for Raw *E. coli* with: Raw coliforms, 4.6 h; Raw non-coliforms, 11.8 h; Settlement Tank A coliforms, 1.4 h; Settlement Tank B coliforms, 3.3 h; Settlement Tank C *E. coli*, 15.2 h; Settlement Tank D coliforms, 10.5 h; Filter Block ABC *E. coli*, 3.8 h; Filter Block D *E. coli*, 5.3 h; Contact Tank turbidity, 0.9 h; Final monitor turbidity, 14.0 h; and Final coliforms, 20.3 h. The trend for the week of the coliform detection shows that it was a peak in Raw water *E. coli* that preceded the bacteriological failure. Finally, in the second 1 L coliform failure, there was a time lag of 12.3 h between a change in the Raw *E. coli* loading and the collection of the failing 1 L coliform sample. This result further suggests a potential link between Raw *E. coli* and Final coliforms and highlights a potential problem with the disinfection protocol at Strensham regarding the survival of coliforms.

The results show that Raw water coliforms and non-coliforms during the week of the coliform failure were impacted by a change in the numbers of Raw water *E. coli*. The trend showed that coliforms and non-coliforms continued to increase after *E. coli* numbers had peaked and were in decline. Since coliforms and non-coliforms come from a variety of sources and are not necessarily faecal in origin they will be affected differently by the environmental and catchment conditions. It is likely that these bacteria are found in greater numbers in the environment than the strictly faecal indicators (i.e. *E. coli*, *C. perfringens* and Enterococci).

From the five month dataset, Raw *E. coli* yielded time lags with *E. coli* from all four Settlement Tanks and both Filter Blocks. It takes 2.5 – 3.4 h for water to pass the Settlement Tanks and 3.6 – 4.6 h for water to leave the RGF Filter Blocks. The time lags recorded against Settlement Tanks A and C were 4.3 – 5.1 and 6.1 – 7.1 times the length of time required to treat water to this level. For Settlement Tank B the time lag was at least 1.0 h longer that the treatment time; whilst Tank D's time lag was insufficient. Although the Settlement Tank time lags do not agree with the treatment time, the Filter Block time lags were closer (Blocks ABC and D: 3.8 – 4.4 h).

The Contact Tank parameters consistently correlated with Raw *E. coli* and a time lag of 0.9 h was observed with turbidity during the week of the coliform failure; this time lag is insufficient for the water to have passed through the treatment works to this stage.

Of interest are the appearance of time lags for coliforms, 20.3 h and 1 L coliforms, 12.3 h during the weeks of the coliform detection and the second 1 L coliform failure, respectively. Throughout the cross-correlation of the *E. coli* data, both coliforms and *E. coli* have been recurring features of results with viable time lags. *E. coli* results were not found after the GAC Filters across the six datasets. This strongly suggests that, at the very least, the disinfection strategy is not optimised to kill/inactivate coliforms, but is effective against *E. coli*. It is important to note that coliforms were not present in the raw data from the Contact Tank or Balance Tank during the failure weeks, which would imply that some of them were damaged but not killed during disinfection and started to recover beyond the Balance Tank.

6.3.1.5. Raw non-coliform cross-correlations

Of the 342 cross-correlations conducted with Raw non-coliforms, 251 met the criteria of being both positive and between 0 and 24 h (Table 18a). The majority of these results were for 0 h and consistent results were obtained with the following bacteriological parameters: Raw coliforms and *C. perfringens*; Settlement Tank A coliforms and non-coliforms; Settlement Tank D *E. coli* and non-coliforms; and Filter Blocks ABC and D coliforms, *E. coli* and non-coliforms (Appendix 2). Time lags were observed for a variety of parameters. From the five month dataset, Raw non-coliform numbers changed ahead of the following parameters: Settlement Tank A *E. coli*, 5.0 h; Settlement Tank B *E. coli*, 6.5 h; Settlement Tank C *E. coli*, 7.7 h; Filter Block ABC coliforms, 1.7 h; Filter Block D coliforms, 1.2 h; Contact Tank total chlorine, 0.1 h; Final flow rate, 8.7 h; Final spot-sampled free chlorine, 8.1 h; and Final total chlorine, 3.5 h. The time lags observed for the Settlement Tanks are two to three times longer than the time required for water to be treated to this stage; the time lags derived for the Filter Bocks, Contact Tank and Final total chlorine are too short. Two parameters in the third 1 L coliform failure resulted in viable time lags: GAC Filter coliforms and non-coliforms, 0.1 h and 5.3 h, respectively. The GAC Filter coliform time lag is shorter than the time required for treatment to this level, but the non-coliform result suggests that Raw non-coliforms are related to GAC Filter non-coliforms. The trend shows that GAC Filter non-coliforms increased after an increase in Raw non-coliforms.

6.3.1.6. Raw turbidity cross-correlations

Of the 342 cross-correlations conducted with raw turbidity, 259 met the criteria of being both positive and between 0 and 24 h (Table 18a). The majority of the results were 0 h and consistent results were obtained for the following parameters: Raw coliforms, *E. coli*, non-coliforms and *C. perfringens*; Settlement Tank A coliforms; Settlement Tanks A, B and C turbidity and pH; Settlement Tank D coliforms, *E. coli* and pH; Filter Blocks ABC and D coliforms, non-coliforms, turbidity and pH; GAC Filter pH; Contact Tank and Balance Tank free and total chlorines and pH; Final monitor free and spot-sampled free and total chlorines, flow, monitor and spot-sampled turbidity and pH (Appendix 2). Two results had viable time lags: Final coliforms during the week of the coliform failure, 20.3 h and Final non-coliforms in the dataset for the second 1 L coliform detection, 23.7 h (Table 18a). These time lags are approximately three times the length of time required to fully treat water. There were no data provided for the length of time that water may spend in the Balance Tank prior to being discharged, but

it is unlikely to be 14 h. Raw water turbidity across the five failure weeks had a range of 5.22 – 27.52 NTU. The trends showed that turbidity fluctuated gently during the weeks of the coliform and second and third 1 L coliform failures; the week of the Enterococcus failure saw turbidity remain low and then rise from 5.22 – 16.39 NTU in the last two days of that period; turbidity during the first 1 L coliform failure rose steadily from 7.94 – 27.52 NTU. The trends did not show any turbidity spikes in the failure weeks. The maximum recorded in the five month dataset was 225.00 NTU, which shows that the Raw water turbidities that were effective during the failure weeks were relatively low. These results show Raw coliforms, *E. coli*, non-coliforms and *C. perfringens* consistently correlated with Raw turbidity and that correlations with coliforms persisted through Settlement Tanks A and D and Filter Blocks ABC and D and that time lags were derived for Final coliforms and non-coliforms.

6.3.1.7. Raw water pH cross-correlations

There were 342 cross-correlations conducted on both the spot-sampled and monitor raw water pH. For spot-sampled pH, 321 correlations were positive and between 0 and 24 h and for monitor pH, 320 cross-correlations met the criteria (Table 15). Most of the results were for 0 h from both sets of results (Table 18a and Appendix 2).

Time lags were observed from the spot-sampled pH dataset for the following parameters from the five month dataset: Raw turbidity, 17.3 h; Settlement Tank B *E. coli*, 3.9 h and non-coliforms, 6.1 h; Filter Block D turbidity, 10.9 h and Final monitor turbidity, 7.4 h. During the week of the Enterococcus failure, a time lag was observed between Raw spot-sampled pH and Contact Tank HPC37, 23.7 h and over the period of the third 1 L coliform detection, a time lag was observed with GAC Filter coliforms, 0.6 h. The time lags observed from the pH monitor dataset were for: Settlement Tank D turbidity, 16.4 h from the five month dataset; Settlement Tank A *E. coli*, 1.6 h and Tank C *E. coli*, 3.3 h from the week of the Enterococcus failure; and during the week of the third 1 L coliform detection time lags were identified for GAC Filter coliforms, 0.3 h, *E. coli*, 15.0 h and non-coliforms, 17.9 h. With the exception of these time lags, the two pH datasets show similar results. The presence of GAC Filter coliforms from both sets of cross-correlations is interesting; however, the time lags are shorter than would be required for water to be treated to this stage.

6.3.1.8. Raw water temperature cross-correlations

There were 299 applicable raw water temperature results from 342 cross-correlations (Table 15). The majority of cross-correlations showed agreement across the five failure weeks (Appendix 2). This included bacterial and chemical parameters. Most of the results were 0 h, but several time lags were observed (Table 18b). From the five month dataset, there was a lag between a change in the Raw water temperature and Filter Block D turbidity of 17.2 h; Contact Tank turbidity, 11.6 h and Balance Tank turbidity, 4.0 h. During the week of the coliform failure, Settlement Tank B had time lags of 9.5 h and 10.3 h for *E. coli* and non-coliforms, respectively; 9.0 h for Tank D *E. coli*; and 6.2 h for Filter Block D turbidity.

6.3.1.9. Settlement Tank coliform cross-correlations

There were 222 cross-correlations conducted on coliform data from each Settlement Tank. From Tank A, 147 produced results that were both positive and between 0 and 24 h (Table 15). The bacteriological parameters that consistently met the selection criteria in cross-correlations with Tank A coliforms were: Tank A *E. coli* and non-coliforms; and Filter Block ABC coliforms and *E. coli* (Appendix 2). Several of the results also had viable time lags: during the week of the coliform failure, there was a lag of 23.4 h between changes in the settled coliform count and Final coliforms (Table 19). In the dataset for the first 1 L coliform detection, there were lags with GAC Filter coliforms, 4.6 h, *E. coli*, 11.4 h and non-coliforms, 2.4 h; and Final 1 L coliforms, 23.8 h. The trend data show that Settlement Tank A coliforms peak and decline approximately one day before their detection in the Final water. During the week of the second 1 L coliform failure, time lags were observed for Balance Tank turbidity, 9.4 h and Final 1 L non-coliforms, 23.7 h. These results suggest a relationship between Settlement Tank A coliforms and coliforms in the Final water; however, the time lags are approximately three times the time required to treat water to this stage.

There were 131 Settlement Tank B coliform cross-correlations that met the selection criteria (Table 15). Consistently applicable bacteriological results were observed with Filter Block ABC coliforms (Appendix 2) and 10 cross-correlations had viable time lags (Table 20). In the full five month and the first 1 L coliform datasets, Final 1 L coliforms were affected by Tank B coliforms with a time lag of 23.4 h. The trend for the week of the first 1 L coliform detection shows that Settlement Tank B coliforms peak and decline approximately one day before their detection in the Final water. In this dataset,

there were also time lags for GAC Filter coliforms, 7.4 h, *E. coli*, 7.0 h, and non-coliforms, 5.2 h, and for Final flow, 22.4 h, and Final free and total chlorine, 10.2 h and 10.6 h, respectively. This set of results indicates a link between Settlement Tank B coliforms and coliforms in the Final water. As with Settlement Tank A, the time lags were longer than the time required to fully treat water.

Settlement Tank C coliforms produced 145 results between 0 and 24 h (Table 15). The bacteriological parameters that correlated with Tank C coliforms across all five failure weeks were Tank C non-coliforms and Filter Block ABC coliforms and *E. coli* (Appendix 2). Several of the correlation results had viable time lags (Table 21). In the five month dataset, changes in Tank C coliforms occurred before those in the following parameters: Tank C *E. coli*, 7.0 h and turbidity, 9.3 h; Filter Block ABC *E. coli*, 5.6 h; and Balance Tank turbidity, 6.7 h. During the week of the coliform failure there was a time lag between Settlement Tank C coliforms and coliforms in the Final water of 20.2 h. Likewise, Final 1 L coliforms were also correlated with Tank C coliforms, with a lag of 23.6 h in the week of the first 1 L coliform failure. In the same dataset, Tank C coliforms correlated with GAC Filter coliforms, 7.7 h, *E. coli*, 8.6 h, and non-coliforms, 5.3 h; Final flow, 8.1 h and free and total chlorine, 11.1 h and 11.0 h, respectively. During the week of the second 1 L coliform failure, Settlement Tank C coliforms had viable time lags with: Balance Tank turbidity, 11.5 h and Final 1 L non-coliforms, 23.7 h and turbidity, 2.9 h. It can be seen that coliforms in the water leaving Settlement Tank C were correlated with coliforms in the Final water. In both instances, Tank C coliforms peak and decline ahead of the detection in the Final water; but the time lags are longer than those required for full treatment of water.

Settlement Tank D coliform cross-correlations resulted in 137 analyses that met the selection criteria (Table 15). Consistent correlations were observed across the failure weeks for Tank D coliforms with Tank D non-coliforms and Filter Block D coliforms and *E. coli* (Appendix 2). Eight of the cross-correlations had time lags greater than 0 h (Table 22). From the five month dataset, changes in Tank D coliforms occurred 2.8 h before those in Tank D *E. coli*, for Contact Tank turbidity there was a lag of 12.6 h and for Balance Tank turbidity, 12.3 h. During the week of the coliform failure, there was a time lag of 21.8 h with Final coliforms. The first 1 L coliform dataset showed time lags with Final free and total chlorine, 11.2 h and 10.6 h, respectively. During the week of the second 1 L coliform detection, there were time lags with Balance Tank turbidity,

3.6 h and Final 1 L non-coliforms, 23.7 h. Once more, Final coliforms feature in the outputs from Settlement Tank coliform cross-correlations, and again show a peak and decline approximately one day before their detection in the Final water.

6.3.1.10. Settlement Tank *E. coli* cross-correlations

There were 222 cross-correlations conducted on *E. coli* data from each Settlement Tank. From Tank A, 131 generated applicable results that were both positive and between 0 and 24 h; of which three were greater than 0 h (Table 19). The majority of cross-correlations for Settlement Tank B *E. coli* were for 0 h, but 14 produced viable time lags (Table 20). The cross-correlations conducted with Settlement Tank C *E. coli* yielded 132 results that were both positive and between 0 and 24 h. Viable time lags were identified for data from the three 1 L coliform detections (Table 21). The cross-correlations based on Settlement Tank D *E. coli* yielded 127 results meeting the selection criteria, of which 13 had viable time lags (Table 22).

Settlement Tank A *E. coli* achieved consistent correlations with the following bacteriological parameters: Tank A coliforms and non-coliforms; and Filter Block ABC coliforms, *E. coli* and non-coliforms (Appendix 2). Settlement Tank A *E. coli* correlated with Final coliforms during the week of the coliform failure, 23.4 h (Table 19). The trends showed that approximately a day before the regulatory coliform failure, *E. coli* numbers peaked and declined. This finding echoes those of coliforms from this treatment stage.

The following parameters had time lags that met the selection criteria across all failure weeks from cross-correlations with Settlement Tank B *E. coli*: Tank B coliforms and non-coliforms; and Filter Block ABC coliforms and *E. coli* (Appendix 2). In the five month dataset, viable time lags were observed for Settlement Tank B *E. coli* x Tank B coliforms, 1.3 h and Filter Block ABC *E. coli*, 0.1 h (Table 20). During the week of the first 1 L coliform detection, time lags were observed with Tank B coliforms, 5.3 h; GAC Filter coliforms, 16.7 h and non-coliforms, 9.8 h; and Contact Tank HPC37, 10.2 h. A time lag was also observed for the second 1 L coliform failure between Tank B *E. coli* and Final 1 L non-coliforms, 23.7 h. These data show a link between settled *E. coli* and coliforms and other microbiological parameters both at this treatment stage and from downstream processes. The trends show that numbers of *E. coli* and coliforms increased during the week of the coliform failure; and they both decreased during the

week of the first 1 L coliform detection. The numbers of *E. coli* were 1.5 – 3 orders of magnitude smaller than those for coliforms. It is therefore questionable as to whether *E. coli* impacted coliforms instead of the reverse. However, Final coliforms were not impacted by changes in *E. coli* from Settlement Tank B.

Table 19: Settlement Tank A cross-correlations where at least one of the results had a time lag >0 h. Shaded results highlight applicable cross-correlations with Final coliforms or Final 1 L coliforms.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
ASettCO	GACCO	-	-	0.0	4.6	0.0	-
ASettCO	GACEC	-	-	-	11.4	-	-
ASettCO	GACNC	-	-	0.0	2.4	-	-
ASettCO	BALTurb	-	0.0	0.0	0.0	9.4	0.0
ASettCO	FINCO	-	23.4	-	-	-	-
ASettCO	FINCO1L	-	-	-	23.8	-	-
ASettCO	FINNC1L	-	-	-	-	23.7	-
ASettEC	FINCO	-	23.4	-	-	-	-
ASettEC	FINFreeCL	-	0.0	0.0	21.4	0.0	0.0
ASettEC	FINTotalCL	-	0.0	0.0	20.0	0.0	0.0
ASettNC	ASettCO	13.0	0.0	0.0	0.0	0.0	0.0
ASettNC	ASettEC	5.7	0.0	0.0	0.0	0.0	0.0
ASettNC	ASettpH	4.5	0.0	0.0	0.0	0.0	0.0
ASettNC	ABCFiltCO	2.0	0.0	0.0	0.0	0.0	0.0
ASettNC	ABCFiltEC	19.9	0.0	0.0	0.0	0.0	0.0
ASettNC	ABCFiltTurb	13.5	0.0	0.0	0.0	0.0	-
ASettNC	ABCFiltpH	4.2	0.0	0.0	0.0	0.0	0.0
ASettNC	GACpH	4.8	0.0	0.0	0.0	0.0	0.0
ASettNC	CONFreeCL	11.5	0.0	0.0	0.0	0.0	0.0
ASettNC	CONTurb	9.1	0.0	0.0	0.0	0.0	0.0
ASettNC	CONpH	4.9	0.0	0.0	0.0	0.0	0.0
ASettNC	CONTotalCL	11.5	0.0	0.0	0.0	0.0	0.0
ASettNC	BALFreeCL	2.1	0.0	0.0	0.0	0.0	0.0
ASettNC	BALTurb	7.7	0.0	0.0	0.0	0.0	0.0
ASettNC	BALpH	3.7	0.0	0.0	0.0	0.0	0.0
ASettNC	BALTotalCL	3.8	0.0	0.0	0.0	0.0	0.0
ASettNC	FINCLMon	4.5	0.0	0.0	0.0	0.0	0.0
ASettNC	FINFreeCL	0.5	0.0	0.0	0.0	0.0	0.0
ASettNC	FINpH	4.7	0.0	0.0	0.0	0.0	0.0
ASettNC	FINTotalCL	1.5	0.0	0.0	0.0	0.0	0.0
ASettTurb	ASettEC	0.0	0.0	7.5	-	0.0	0.0
ASettTurb	GACCO	-	0.0	0.0	-	0.0	5.7
ASettTurb	GACEC	-	-	-	-	-	13.7
ASettTurb	GACNC	-	0.0	0.0	-	-	9.9
ASettTurb	FINNC1L	-	-	-	-	23.7	-
ASettpH	ASettEC	0.0	0.0	0.6	0.0	0.0	0.0
ASettpH	GACCO	0.0	-	0.0	0.0	0.0	0.2
ASettpH	GACEC	-	-	-	-	-	4.2
ASettpH	GACNC	-	-	0.0	0.0	16.6	4.5

Table 20: Settlement Tank B cross-correlations where at least one of the results had a time lag >0 h. Shaded results highlight applicable cross-correlations with Final coliforms or Final 1 L coliforms.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
BSettCO	GACCO	-	-	0.0	7.4	0.0	-
BSettCO	GACEC	-	-	-	7.0	-	-
BSettCO	GACNC	-	-	0.0	5.2	-	-
BSettCO	BALTurb	0.0	0.0	0.0	0.0	7.7	0.0
BSettCO	FINFlow	-	-	-	22.4	0.0	0.0
BSettCO	FINCO1L	23.4	-	-	23.4	-	-
BSettCO	FINNC1L	-	-	-	-	23.7	-
BSettCO	FINFreeCL	-	0.0	0.0	10.2	0.0	0.0
BSettCO	FINTotalCL	-	0.0	0.0	10.6	0.0	0.0
BSettEC	BSettCO	1.3	0.0	0.0	5.3	0.0	0.0
BSettEC	BSettTurb	9.5	0.0	0.0	11.1	0.0	0.0
BSettEC	ABCFiltEC	0.1	0.0	0.0	0.0	0.0	0.0
BSettEC	GACCO	-	-	0.0	16.7	-	-
BSettEC	GACNC	-	-	0.0	9.8	-	-
BSettEC	CONHPC37	-	-	-	10.2	-	-
BSettEC	BALTurb	-	0.0	-	0.0	11.6	0.0
BSettEC	FINFlow	-	-	-	10.3	0.0	0.0
BSettEC	FINNC1L	-	-	-	-	23.7	-
BSettEC	FINFreeCL	-	0.0	0.0	20.5	0.0	0.0
BSettEC	FINTurb	-	0.0	0.0	0.0	3.0	0.0
BSettEC	FINTotalCL	-	0.0	0.0	19.0	0.0	0.0
BSettNC	BSettCO	5.6	0.0	0.0	0.5	0.0	0.0
BSettNC	BSettEC	10.6	0.0	0.0	0.0	0.0	0.0
BSettNC	BSettTurb	15.7	0.0	0.0	0.6	0.0	-
BSettNC	ABCFiltCO	7.5	0.0	0.0	0.0	0.0	0.0
BSettNC	ABCFiltEC	6.0	0.0	0.0	0.0	0.0	0.0
BSettNC	GACCO	-	-	0.0	11.1	-	-
BSettNC	GACEC	-	-	-	15.0	-	-
BSettNC	GACNC	-	-	0.0	6.8	-	-
BSettNC	GACpH	1.8	0.0	0.0	0.0	0.0	0.0
BSettNC	CONFreeCL	9.0	0.0	0.0	0.0	0.0	0.0
BSettNC	CONTotalCL	9.5	0.0	0.0	0.0	0.0	0.0
BSettNC	BALTurb	12.6	0.0	0.0	0.0	7.1	0.0
BSettNC	BALTotalCL	2.4	0.0	0.0	0.0	0.0	0.0
BSettNC	FINFlow	-	-	0.0	1.0	0.0	0.0
BSettNC	FINCO1L	-	-	-	23.4	-	-
BSettNC	FINNC1L	-	-	-	-	23.7	-
BSettNC	FINFreeCL	3.4	0.0	0.0	12.0	0.0	0.0
BSettNC	FINpH	0.1	0.0	0.0	0.0	0.0	0.0
BSettNC	FINTotalCL	3.7	0.0	0.0	11.2	0.0	0.0
BSettTurb	BSettCO	0.0	0.0	0.0	0.0	0.0	10.2
BSettTurb	ABCFiltEC	-	0.0	0.0	0.0	0.0	9.8
BSettTurb	GACCO	-	-	0.0	0.0	-	4.3
BSettTurb	GACEC	-	-	-	6.2	-	1.5
BSettTurb	GACNC	-	0.0	0.0	0.0	-	6.8
BSettTurb	CONTurb	3.4	0.0	0.0	0.0	0.0	0.0
BSettTurb	BALCO	0.4	-	-	-	-	-
BSettTurb	BALTurb	0.4	0.0	0.0	0.0	0.0	0.0
BSettTurb	FINCO1L	-	-	-	23.4	-	-
BSettTurb	FINNC1L	-	-	-	-	23.7	-
BSettpH	GACCO	0.0	0.0	0.0	0.0	0.0	0.4
BSettpH	GACEC	-	-	-	-	-	3.6
BSettpH	GACNC	-	0.0	0.0	0.0	0.0	5.5

Table 21: Settlement Tank C cross-correlations where at least one of the results had a time lag >0 h. Shaded results highlight applicable cross-correlations with Final coliforms or Final 1 L coliforms.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
CSettCO	CSettEC	7.0	0.0	0.0	0.0	0.0	-
CSettCO	CSettTurb	9.3	0.0	0.0	0.0	0.0	0.0
CSettCO	ABCFiltEC	5.6	0.0	0.0	0.0	0.0	0.0
CSettCO	GACCO	-	0.0	0.0	7.7	-	-
CSettCO	GACEC	-	-	-	8.6	-	-
CSettCO	GACNC	-	-	0.0	5.3	-	-
CSettCO	BALTurb	6.7	0.0	-	0.0	11.5	0.0
CSettCO	FINFlow	-	-	0.0	8.1	0.0	0.0
CSettCO	FINCO	-	20.2	-	-	-	-
CSettCO	FINCO1L	-	-	-	23.6	-	-
CSettCO	FINNC1L	-	-	-	-	23.7	-
CSettCO	FINFreeCL	-	0.0	0.0	11.1	0.0	0.0
CSettCO	FINTurb	-	0.0	0.0	0.0	2.9	0.0
CSettCO	FINTotalCL	-	0.0	0.0	11.0	0.0	0.0
CSettEC	CSettCO	-	0.0	0.0	0.0	0.0	18.9
CSettEC	CSettNC	-	0.0	0.0	0.0	0.0	16.4
CSettEC	ABCFiltEC	0.0	0.0	0.0	0.0	0.0	20.6
CSettEC	ABCFiltNC	-	0.0	-	0.0	0.0	2.9
CSettEC	BALTurb	0.0	0.0	-	0.0	8.1	0.0
CSettEC	FINFlow	-	-	-	9.0	0.0	0.0
CSettEC	FINNC1L	-	-	-	-	23.7	-
CSettEC	FINFreeCL	-	0.0	0.0	20.7	0.0	0.0
CSettEC	FINTotalCL	-	0.0	0.0	19.4	0.0	0.0
CSettNC	BALTurb	4.9	0.0	0.0	0.0	11.4	0.0
CSettNC	FINNC1L	-	-	-	-	23.7	-
CSettNC	FINFreeCL	0.0	0.0	0.0	14.9	0.0	0.0
CSettNC	FINTurb	0.0	0.0	0.0	0.0	1.5	0.0
CSettNC	FINTotalCL	0.0	0.0	0.0	13.9	0.0	0.0
CSettTurb	CSettEC	0.0	0.0	12.3	0.0	0.0	0.0
CSettTurb	CONHPC37	-	-	23.5	-	-	-
CSettTurb	FINNC1L	-	-	-	-	23.7	-
CSettpH	CSettEC	0.0	0.0	2.4	0.0	0.0	0.0
CSettpH	GACCO	0.0	0.0	0.0	0.0	0.0	0.3
CSettpH	GACEC	-	-	-	-	-	12.7
CSettpH	GACNC	-	0.0	0.0	0.0	0.0	10.4

Table 22: Settlement Tank D cross-correlations where at least one of the results had a time lag >0 h. Shaded results highlight applicable cross-correlations with Final coliforms or Final 1 L coliforms.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
DSettCO	DFiltEC	2.8	0.0	0.0	0.0	0.0	0.0
DSettCO	CONTurb	12.6	0.0	0.0	0.0	0.0	0.0
DSettCO	BALTurb	12.3	0.0	0.0	0.0	3.6	0.0
DSettCO	FINCO	-	21.8	-	-	-	-
DSettCO	FINNC1L	-	-	-	-	23.7	-
DSettCO	FINFreeCL	-	0.0	0.0	11.2	0.0	0.0
DSettCO	FINTotalCL	-	0.0	0.0	10.6	0.0	0.0
DSettEC	DSettCO	7.3	10.6	0.0	0.0	0.0	0.0
DSettEC	DFiltCO	3.9	0.0	0.0	0.0	0.0	0.0
DSettEC	DFiltEC	12.8	0.0	0.0	0.0	0.0	0.0
DSettEC	GACNC	-	-	0.0	4.3	-	-
DSettEC	CONFreeCL	4.5	0.0	0.0	0.0	0.0	0.0
DSettEC	CONTurb	-	0.0	0.0	0.0	8.1	0.0
DSettEC	CONTotalCL	3.7	0.0	0.0	0.0	0.0	0.0
DSettEC	BALTurb	-	0.0	-	0.0	16.0	0.0
DSettEC	BALpH	1.7	0.0	0.0	0.0	0.0	0.0
DSettEC	FINCO	-	21.8	-	-	-	-
DSettEC	FINNC1L	-	-	-	-	23.7	-
DSettEC	FINTurb	-	0.0	0.0	0.0	12.8	0.0
DSettNC	DSettCO	4.2	0.0	0.0	0.0	0.0	0.0
DSettNC	DSettEC	4.5	0.0	0.0	0.0	0.0	0.0
DSettNC	CONHPC37	-	-	-	22.8	-	-
DSettNC	CONTurb	18.4	0.0	0.0	0.0	0.0	0.0
DSettNC	BALTurb	8.9	0.0	0.0	0.0	4.0	0.0
DSettNC	FINNC1L	-	-	-	-	23.7	-
DSettNC	FINFreeCL	0.0	0.0	0.0	11.2	0.0	0.0
DSettNC	FINTotalCL	0.0	0.0	0.0	10.2	0.0	0.0
DSettTurb	DSettCO	2.9	0.0	0.0	0.0	0.0	0.0
DSettTurb	DFiltCO	0.0	0.0	3.1	0.0	0.0	0.0
DSettTurb	DFiltTurb	7.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	CONTurb	13.5	0.0	0.0	0.0	0.0	0.0
DSettTurb	BALTurb	14.1	0.0	0.0	0.0	0.0	0.0
DSettTurb	FINCO	-	21.8	-	-	-	-
DSettTurb	FINCO1L	-	-	-	22.2	-	-
DSettTurb	FINNC1L	-	-	-	-	23.7	-
DSettpH	DFiltTurb	11.6	0.0	0.0	0.0	0.0	0.0
DSettpH	GACCO	0.0	0.0	0.0	0.0	0.0	0.1
DSettpH	GACEC	-	-	-	-	-	5.6
DSettpH	GACNC	-	0.0	0.0	0.0	21.6	4.9
DSettpH	FINCO1L	-	-	-	-	-	23.0

Settlement Tank C *E. coli* achieved consistent results across the failure weeks for the following bacteriological parameters: Tank C coliforms and non-coliforms; Filter Block ABC coliforms and *E. coli* (Appendix 2). Tank C *E. coli* achieved a viable time lag with Final 1 L non-coliforms, 23.7 h during the week of the second 1 L coliform failure (Table 21). The third 1 L coliform detection resulted in the following time lags: Tank C coliforms, 18.9 h and non-coliforms, 16.4 h; and Filter Block ABC *E. coli*, 20.6 h and non-coliforms, 2.9 h. *E. coli* counts were again noted to impact settled coliforms and other bacteriological results, but not Final coliforms. The trend showed that coliform numbers increased more rapidly after *E. coli* numbers peaked and entered a decline.

Cross-correlations for Settlement Tank D *E. coli* achieved consistent results for the five failure weeks for the following bacteriological parameters: Tank D coliforms and non-coliforms and Filter Block D coliforms and *E. coli* (Appendix 2). Several of the correlations resulted in viable time lags: Tank D coliforms, 7.3 h and Filter Block D coliforms, 3.9 h and *E. coli*, 12.8 h from the five month dataset (Table 22). These time lags do not tally with the time it would take for water to be treated to these various stages, but they indicate a relationship between settled *E. coli* and the other bacteriological parameters. During the week of the coliform failure, there were correlations with Settlement Tank D coliforms, 10.6 h and Final coliforms, 21.8 h. As with Settlement Tank A, Tank D *E. coli* and coliforms peaked and entered a decline approximately a day before the regulatory coliform detection. Settled *E. coli* results were an order of magnitude smaller than settled coliform counts, again calling into question whether *E. coli* did affect coliforms or whether the reverse was the case. Tank D *E. coli* impacted GAC Filter non-coliforms with a time lag of 4.3 h during the week of the first 1 L coliform failure. In the week of the second 1 L coliform detection there were correlations with Final 1 L non-coliforms, 23.7 h.

6.3.1.11. Settlement Tank non-coliform cross-correlations

There were 222 cross-correlations conducted on non-coliform results from each Settlement Tank. From Settlement Tank A, 147 were both positive and between 0 and 24 h and 20 of these had viable time lags (Table 19). From Settlement Tank B, 143 non-coliform cross-correlations met the selection criteria (Table 20). The majority of the 222 cross-correlations conducted on Settlement Tank C non-coliforms met the selection criteria and six resulted in viable time lags (Table 21). Of the 222 cross-correlations with Settlement Tank D non-coliforms, 143 met the selection criteria (Table 22).

The bacteriological parameters with cross-correlation results for Settlement Tank A non-coliforms that consistently met the selection criteria were: Tank A coliforms and *E. coli* and Filter Block ABC coliforms, *E. coli* and non-coliforms (Appendix 2). Viable time lags for Tank A non-coliforms were all derived from the full five month dataset; of especial interest are the time lags for: Tank A coliforms, 13.0 h and *E. coli*, 5.7 h; ABC Filter Block coliforms, 2.0 h and *E. coli*, 19.9 h (Table 19). Whilst these results suggest an impact between Tank A non-coliforms and other bacteriological parameters, the time lags for all of these are longer than required for water treatment to their respective stages. There were no correlations with Final water coliforms.

Bacteriological parameters that consistently achieved results that met the selection criteria for cross-correlations with Settlement Tank B non-coliforms were: Tank B coliforms and *E. coli* and Filter Block ABC coliforms, *E. coli* and non-coliforms (Appendix 2). There were a number of viable time lags from Settlement Tank B non-coliforms. Of note from the full five month dataset are the time lags for: Settlement Tank B coliforms, 5.6 h and *E. coli*, 10.6 h; and Filter Block ABC coliforms, 7.5 h, and *E. coli*, 6.0 h (Table 20). During the week of the first 1 L coliform failure, Settlement Tank B non-coliforms changed ahead of the following parameters: Tank B coliforms, 0.5 h; GAC Filter coliforms, 11.1 h, *E. coli* 15.0 h and non-coliforms, 6.8 h; and Final 1 L coliforms, 23.4 h. The time lag between Settlement Tank B non-coliforms and Final 1 L coliforms is, as with settled coliforms and *E. coli*, longer than is required for water to be treated to this stage, but it does indicate a relationship between these parameters. A viable time lag resulted from the cross-correlation between Settlement Tank B non-coliforms and Final 1 L non-coliforms, 23.7 h for the week of the third 1 L coliform failure.

The five failure weeks yielded applicable bacteriological cross-correlation results for Settlement Tank C non-coliforms with: Tank C coliforms and Filter Block ABC coliforms, *E. coli* and non-coliforms (Appendix 2). Settlement Tank C non-coliforms correlated with Final non-coliforms, 23.7 h, during the week of the second 1 L coliform failure (Table 21).

Settlement Tank D had results that met the selection criteria across the five failure weeks for cross-correlations with the following bacteriological parameters: Tank D coliforms and *E. coli* and Filter Block D coliforms, *E. coli* and non-coliforms

(Appendix 2). Of interest from the results of Settlement Tank D non-coliforms are the time lags with Tank D coliforms, 4.2 h and *E. coli*, 4.5 h from the five month dataset; Contact Tank HPC37, 22.8 h from the first 1 L coliform failure; and Final 1 L non-coliforms, 23.7 h from the week of the second 1 L coliform detection (Table 22). These results corroborate the inter-connectedness of the bacteriological parameters at the Settlement Tank stage of treatment. Only the results from Tank B non-coliforms were linked with Final coliforms.

6.3.1.12. Settlement Tank turbidity cross-correlations

There were 222 cross-correlations conducted on results for Settlement Tank turbidity (Table 15). From Tank A, 153 had results that were both positive and between 0 and 24 h (Table 19); 154 qualified from Tank B (Table 20); 146 from Tank C (Table 21); and 160 from Tank D (Table 22).

Of the results that consistently met the selection criteria across the failure weeks for cross-correlations with Settlement Tank A turbidity, the following are highlighted: Tank A coliforms, non-coliforms and pH; Filter Block ABC coliforms, non-coliforms, turbidity and pH; and Final monitor and spot-sampled turbidities (Appendix 2). During the week of the Enterococcus failure, changes in Settlement Tank A turbidity occurred 7.5 h ahead of changes to Tank A *E. coli* (Table 19). The week of the second 1 L coliform failure resulted in a time lag of 23.7 h for Tank A turbidity x Final non-coliforms. The week of the third 1 L coliform failure showed time lags with the three GAC Filter bacteriological parameters as follows: coliforms, 5.7 h; *E. coli*, 13.7 h; and non-coliforms, 9.9 h. Settled turbidity impacted bacteriological quality at this treatment stage and in the RGF Filters.

Selected results that showed consistent time lags between 0 and 24 h with Settlement Tank B turbidity were: Tank B coliforms and pH; Filter Block ABC coliforms, *E. coli*, non-coliforms, turbidity and pH; Contact Tank and Balance Tank turbidity; and Final monitor and spot-sampled turbidity (Appendix 2). The five month dataset showed that Settlement Tank B turbidity resulted in viable time lags with Contact Tank turbidity, 3.4 h and Balance Tank coliforms, 0.4 h (Table 20). The Contact Tank time lag is shorter than the 4.0 – 4.5 h required between Settlement and Contact Tanks. In the week of the first 1 L coliform failure, the resulting lags were for GAC Filter *E. coli*, 6.2 h and Final 1 L coliforms, 10.2 h. The trend data show that turbidity was in decline at the time

lag with 1 L coliforms. Final 1 L non-coliforms produced a viable time lag of 23.7 h in the dataset for the second 1 L coliform failure. During the week of the third 1 L coliform detection, the time lags were for: Tank B coliforms, 10.2 h; Filter Block ABC *E. coli*, 9.8 h; and GAC Filter coliforms, 4.3 h, *E. coli*, 1.5 h and non-coliforms, 6.8 h.

Of note from the parameters that exhibited consistent relationships with Settlement Tank C turbidity across the five failure weeks were: Settlement Tank C and Filter Block ABC coliforms, *E. coli*, non-coliforms and pH; Filter Block ABC turbidity; Contact Tank and Balance Tank turbidities; and Final monitor and spot-sampled turbidities (Appendix 2). Only three of the qualifying results for Settlement Tank C turbidity were greater than 0 h (Table 21). In the dataset for the Enterococcus failure, Tank C turbidity correlated with Tank C *E. coli*, 12.3 h and Contact Tank HPC37, 23.5 h and during the week of the second 1 L coliform failure, there was a viable time lag with Final 1 L coliforms, 23.7 h. As mentioned previously, the time lag with Final 1 L coliforms is longer than the time required to treat water between Settlement and Final stages, but it indicates that there is a relationship between settled turbidity and Final bacteriological quality.

The majority of Settlement Tank D turbidity cross-correlations showed agreement across the five failure weeks. Of note were those with: Tank D coliforms, non-coliforms and pH; Filter Block D coliforms, *E. coli*, non-coliforms, turbidity and pH; GAC Filter coliforms and pH; Contact Tank and Balance Tank turbidity; and Final monitor and spot-sampled turbidities (Appendix 2). Final coliforms were found to have viable time lags with Settlement Tank D turbidity (Table 22). These were from the weeks of the coliform failure, 21.8 h and the first 1 L coliform detection, 22.2 h. Several other time lags were observed. From the full five month dataset, there were viable time lags with Tank D coliforms, 2.9 h; Filter Block D turbidity, 7.0 h; Contact Tank turbidity, 13.5 h and Balance Tank turbidity, 14.1 h. During the week of the Enterococcus failure there was a time lag with Filter Block D coliforms, 3.1 h. The dataset for the second 1 L coliform detection yielded a time lag of 23.7 h between Settlement Tank D turbidity and Final 1 L non-coliforms.

6.3.1.13. Settlement Tank pH cross-correlations

A total of 222 cross-correlations were conducted on pH data from each of the Settlement Tanks (Table 15). Most of the results from Tank A were positive and

between 0 and 24 h (Table 19). Settlement Tank B yielded 159 results that met the selection criteria and almost all of these had 0 h time lags (Table 20). Settlement Tanks C and D showed similar propensities (Table 21 and Table 22).

Four of the pH results from Settlement Tank A produced viable time lags (Table 19). These all related to GAC Filter bacteriological parameters. Non-coliforms during the second 1 L coliform failure were affected 23.7 h after changes in Tank A pH. During the week of the third 1 L coliform detection, all three bacteriological parameters resulted in viable time lags: coliforms, 0.2 h; *E. coli*, 4.2 h and non-coliforms, 4.5 h. Whilst most results from these cross-correlations were in agreement across the five failure weeks, the GAC Filter bacteriological parameters were notably inconsistent (Appendix 2). These results show that Settlement Tank A pH had variable impacts upon the waterborne bacteria.

Settlement Tank B pH affected the three bacteriological parameters from the GAC Filters during the week of the third 1 L coliform detection: coliforms, 0.4 h, *E. coli*, 3.6 h and non-coliforms, 5.5 h (Table 20). As with Settlement Tank A, Tank B pH had differing effects upon the GAC Filter bacteriological parameters across the five failure weeks: inconsistent results for GAC Filter *E. coli*, but full agreement for coliforms and non-coliforms (Appendix 2).

During the week of the Enterococcus failure, changes in Settlement Tank C pH occurred 2.4 h before those for Tank C *E. coli* (Table 21). In the dataset for the third 1 L coliform detection, there were time lags with the three bacteriological parameters from the GAC Filters: coliforms, 0.3 h; *E. coli*, 12.7 h; non-coliforms, 10.4 h. Appendix 2 shows that GAC Filter *E. coli* performed similarly in Tank C and Tank B.

The majority of results for Settlement Tank D pH were in agreement across the five failure weeks. As for Tanks B and C, *E. coli* results differed in being impacted inconsistently by pH; similarly, 1 L coliforms were not affected across all failure weeks (Appendix 2). Settlement Tank D pH resulted in six viable time lags (Table 22). From the five month dataset, Filter Block D turbidity responded to changes in Tank D pH, with a lag of 11.6 h. The second 1 L coliform detection identified a time lag with GAC Filter non-coliforms, 21.6 h. During the week of the third 1 L coliform failure, there

were time lags with: GAC Filter coliforms, 0.1 h, *E. coli*, 5.6 h and non-coliforms, 4.9 h; and Final 1 L coliforms, 23.0 h.

6.3.1.14. Filter Block coliform cross-correlations

There were 192 cross-correlations conducted on coliform data from Filter Blocks ABC and D (Table 15). From Block ABC, 125 yielded results that were both positive and between 0 and 24 h (Table 23). Block D yielded 124 applicable results (Table 24).

Bacteriological results for Filter Block ABC coliforms showed agreement across the five failure weeks for Block ABC parameters but not for processes beyond this treatment stage (Appendix 2). Filter Block ABC coliforms resulted in two viable time lags (Table 23). These were for Block ABC *E. coli* from the five month dataset, 2.0 h and GAC Filter *E. coli* from the week of the first 1 L coliform detection, 21.1 h.

Consistent cross-correlation results were observed for Filter Block D coliforms and Block D *E. coli* and GAC Filter coliforms, but not for any other bacteriological parameters (Appendix 2). Filter Block D had three viable time lags (Table 24). These were for: Block D *E. coli* from the five month dataset, 0.5 h; Contact Tank HPC37 during the week of the first 1 L coliform detection, 18.0 h; and Final non-coliforms during the week of the second 1 L coliform failure, 23.7 h. These results show that coliforms impact most of the other bacteriological parameters; although the time lags for all except Filter Block D *E. coli* were greater than the time required to treat water to that stage.

6.3.1.15. Filter Block *E. coli* cross-correlations

There were 192 cross-correlations conducted on *E. coli* results from Filter Blocks ABC and D. The majority of results in both cases were positive and between 0 and 24 h (Table 23 and Table 24).

Filter Block ABC *E. coli* showed consistent cross-correlations with Block ABC coliforms, but with no other bacteriological parameters (Appendix 2). The viable time lags of interest from Filter Block ABC were for: Final coliforms from the five month dataset and the week of the coliform failure, 13.9 h and 6.2 h, respectively (Table 23). It takes approximately 3.0 h for water to pass from post-Filter Block to post-Contact Tank. The time water spends in the Balance Tank and travelling to the sampling location is

unknown. The time for the week of the coliform failure could be realistic. Furthermore, the week of the first 1 L coliform failure returned lags for: GAC Filter coliforms, 13.3 h and non-coliforms, 6.8 h, whilst the second 1 L coliform detection recorded a time lag with Final 1 L non-coliforms, 23.7 h.

The five failure weeks achieved consistent results for bacteriological cross-correlations with Filter Block D *E. coli* for the following parameters: Block D coliforms and non-coliforms (Appendix 2). Time lags were identified between Filter Block D *E. coli* and Final coliforms: five month dataset, 16.9 h and the week of the coliform failure, 18.2 h (Table 24). Other results of interest were for: GAC Filter coliforms, 10.1 h and non-coliforms, 4.2 h and Contact Tank HPC37, 21.9 h, during the week of the first 1 L coliform detection; and Final 1 L non-coliforms, 23.7 h from the week of the second 1 L coliform detection. As with the Settlement Tank results, the filtered *E. coli* data suggest a link with downstream and Final bacteriological quality.

6.3.1.16. Filter Block non-coliform cross-correlations

The majority of the 192 cross-correlations conducted on non-coliform data from Filter Blocks ABC and D were both positive and between 0 and 24 h (Table 23 and Table 24). Consistent bacteriological results were identified for Blocks ABC and D with coliforms and *E. coli*; Block D non-coliforms also showed agreement across the failure weeks for GAC Filter coliforms (Appendix 2). No consistent relationships with bacteriological data were identified beyond the GAC Filters.

Final 1 L coliforms feature twice in the time lags derived from cross-correlations with Filter Block ABC non-coliforms (Table 23). These were found in the weeks of the first and third 1 L coliform failures: 22.0 h and 0.1 h, respectively. There were time lags derived for other bacteriological parameters. From the five month dataset, Block ABC coliforms lagged behind non-coliforms by 0.9 h. It takes approximately an hour for water to be treated by the Filters, so this time lag is possible. During the week of the coliform detection, Filter Block ABC non-coliforms impacted Final HPC37, 21.0 h. The week of the Enterococcus failure saw a time lag with Block ABC *E. coli* of 10.1 h. During the week of the second 1 L coliform detection, Final non-coliforms were impacted 23.7 h after a change in Filter Block ABC non-coliforms. Neither Final coliforms nor Final 1 L coliforms were impacted by Filter Block D non-coliforms (Table 24). There were several viable time lags with other bacteriological parameters,

including coliforms from Block D. These results suggest that Filter Block D behaved differently to Block ABC.

Table 23: Filter Block ABC cross-correlations where at least one of the results had a time lag >0 h. Shaded results highlight applicable cross-correlations with Final coliforms or Final 1 L coliforms.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
ABCFiltCO	ABCFiltEC	2.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	GACEC	-	-	-	21.1	-	-
ABCFiltEC	GACCO	-	-	0.0	13.3	-	-
ABCFiltEC	GACNC	-	-	0.0	6.8	-	-
ABCFiltEC	BALTurb	0.0	0.0	0.0	0.0	10.2	0.0
ABCFiltEC	FINCO	13.9	6.2	-	-	-	-
ABCFiltEC	FINNC1L	-	-	-	-	23.7	-
ABCFiltEC	FINFreeCL	-	0.0	0.0	9.8	0.0	0.0
ABCFiltEC	FINTotalCL	-	0.0	0.0	9.3	0.0	0.0
ABCFiltNC	ABCFiltCO	0.9	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	ABCFiltEC	-	0.0	10.1	0.0	0.0	0.0
ABCFiltNC	BALTurb	19.7	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	FINHPC22	-	21.0	-	-	-	-
ABCFiltNC	FINHPC37	21.6	-	-	-	-	-
ABCFiltNC	FINCO1L	-	-	-	22.0	-	0.1
ABCFiltNC	FINNC1L	-	-	-	-	23.7	
ABCFiltNC	FINTurb	22.3	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	ABCFiltCO	4.4	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	ABCFiltEC	-	0.0	0.0	0.0	0.0	9.7
ABCFiltTurb	ABCFiltNC	1.7	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	GACCO	-	-	0.0	-	-	4.2
ABCFiltTurb	FINTurbMon	0.2	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	GACCO	0.0	0.0	0.0	0.0	0.0	0.2
ABCFiltpH	GACEC	-	-	-	-	-	3.4
ABCFiltpH	GACNC	-	0.0	0.0	0.0	22.4	3.9

6.3.1.17. Filter Block turbidity cross-correlations

There were 192 cross-correlations conducted on turbidity from the two Filter Blocks. From Filter Block ABC, 121 results were both positive and between 0 and 24 h (Table 23); Filter Block D yielded 112 results (Table 24). There was broad agreement between the failure weeks for both Filter Blocks (Appendix 2).

Results from the five month dataset showed that turbidity from Filter Block ABC impacted Block ABC coliforms, 4.4 h and non-coliforms, 1.7 h; and Final monitor turbidity, 0.2 h (Table 23). During the week of the third 1 L coliform detection, Filter Block ABC affected Block ABC *E. coli*, 9.7 h and GAC Filter coliforms, 4.2 h.

Final 1 L coliforms featured twice in the results from Filter Block D turbidity: during the weeks of the first and third 1 L coliform failures: 22.0 h and 23.2 h, correspondingly (Table 24). In both cases, turbidity peaks and enters a decline at these time lags before the detection of the 1 L coliforms. Whilst these time lags are longer than the time

required to treat water between the Filters and Final monitoring point, they suggest not only that turbidity impacts coliform compliance, but also that Blocks ABC and D behave differently. The other parameters impacted by Filter Block D turbidity were: Block D coliforms, 4.3 h and Contact Tank turbidity, 0.5 h from the full five month dataset; and Final 1 L non-coliforms, 23.7 h during the week of the second 1 L coliform detection. GAC Filter bacteriological parameters all featured viable time lags during the week of the third 1 L coliform failure: coliforms, 6.7 h; *E. coli*, 7.3 h; and non-coliforms, 11.2 h. These results show that turbidity from the Filters affects downstream turbidity and bacteriological quality.

Table 24: Filter Block D cross-correlations where at least one of the results had a time lag >0 h. Shaded results highlight applicable cross-correlations with Final coliforms and Final 1 L coliforms.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
DFiltCO	DFiltEC	0.5	0.0	0.0	0.0	0.0	0.0
DFiltCO	CONHPC37	-	-	-	18.0	-	-
DFiltCO	FINNC1L	-	-	-	-	23.7	-
DFiltEC	GACCO	-	-	0.0	10.1	0.0	0.0
DFiltEC	GACNC	-	-	0.0	4.2	-	-
DFiltEC	CONHPC37	-	-	-	21.9	-	-
DFiltEC	BALTurb	-	0.0	0.0	0.0	6.8	0.0
DFiltEC	FINCO	16.9	18.2	-	-	-	-
DFiltEC	FINNC1L	-	-	-	-	23.7	-
DFiltNC	DFiltCO	3.2	0.0	9.0	0.0	0.0	0.0
DFiltNC	DFiltTurb	7.3	0.0	0.0	0.0	0.0	0.0
DFiltNC	DFiltpH	6.0	0.0	0.0	0.0	0.0	0.0
DFiltNC	CONHPC22	-	-	-	-	-	14.7
DFiltNC	CONHPC37	-	-	-	5.7	-	-
DFiltNC	CONpH	16.9	0.0	0.0	0.0	0.0	0.0
DFiltNC	BALTurb	8.1	0.0	0.0	0.0	0.0	0.0
DFiltNC	FINHPC37	19.8	-	-	-	-	-
DFiltNC	FINNC1L	-	-	-	-	23.7	-
DFiltNC	FINTurb	6.5	0.0	0.0	0.0	0.0	0.0
DFiltTurb	DFiltCO	4.3	0.0	0.0	0.0	0.0	0.0
DFiltTurb	GACCO	-	-	0.0	0.0	-	6.7
DFiltTurb	GACEC	-	-	-	0.0	-	7.3
DFiltTurb	GACNC	-	-	0.0	0.0	-	11.2
DFiltTurb	CONTurb	0.5	0.0	0.0	0.0	0.0	0.0
DFiltTurb	FINFlow	7.5	-	0.0	0.0	0.0	0.0
DFiltTurb	FINCO1L	-	-	-	22.0	-	23.2
DFiltTurb	FINNC1L	-	-	-	-	23.7	-
DFiltpH	DFiltTurb	10.2	0.0	0.0	0.0	0.0	0.0
DFiltpH	GACCO	0.0	0.0	0.0	0.0	0.0	0.2
DFiltpH	GACEC	-	-	-	-	-	0.3
DFiltpH	GACNC	-	0.0	0.0	0.0	-	1.0
DFiltpH	CONHPC37	-	-	-	22.6	-	-
DFiltpH	FINCO1L	-	-	-	-	-	23.2

6.3.1.18. Filter Block pH cross-correlations

The 192 cross-correlations conducted on pH data resulted in 132 results that were positive and between 0 and 24 h from both Filter Block ABC and Block D (Table 23 and Table 24). There was broad agreement between the failure weeks for both Filter Blocks (Appendix 2).

During the week of the third 1 L coliform detection, there was a viable time lag between Filter Block D pH and Final 1 L coliforms, 23.2 h (Table 24). At this time lag, the pH of the water peaked and entered a gentle decline ahead of the failure. Other results of interest from the cross-correlations for Filter Block pH include the GAC Filter bacteriological parameters, which were impacted by Blocks ABC and D pH values (Table 23 and Table 24). The results indicate that changes in Filter Block pH impact downstream bacteriological quality and from Block D affects coliform compliance.

6.3.1.19. GAC Filter cross-correlations

There were 162 cross-correlations conducted on each of the GAC Filter parameters. The majority of results were both positive and between 0 and 24 h (Table 15).

GAC Filter coliforms yielded 87 results that met the selection criteria, and 21 of these had viable time lags (Table 25). Final coliforms and Final 1 L coliforms feature in the results for these correlations. During the week of the coliform failure, coliforms were recorded 21.0 h after a change in GAC Filter coliforms; during the first 1 L coliform failure, Final 1 L coliforms occurred 21.8 h later. In both cases, the trend data show that GAC Filter coliforms peaked and entered a decline at these time lags. GAC Filter coliform cross-correlations with GAC Filter non-coliforms returned results during the weeks of the coliform failure and the third 1 L coliform detection: 2.4 h and 22.8 h, respectively. GAC Filter coliforms did not result in consistent correlations across the five failure weeks with any downstream bacteriological parameters (Appendix 2).

GAC Filter *E. coli* impacted Final 1 L coliforms during the weeks of the first and third 1 L coliform detections: 21.8 h and 22.8 h, respectively. In both cases, Final 1 L coliforms were detected after a peak in GAC Filter *E. coli*; although the counts never exceeded 3 CFU 100 ml^{-1}. GAC Filter coliforms were also impacted by the *E. coli* results: from the five month dataset, 2.7 h; during the week of the first 1 L coliform failure, 0.7 h; and during the week of the third 1 L coliform detection, 4.8 h.

Table 25: GAC Filter cross-correlations where at least one of the results had a time lag >0 h. Shaded results highlight applicable cross-correlations with Final coliforms and Final 1 L coliforms.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
GACCO	GACNC	0.6	2.4	0.0	-	0.0	-
GACCO	CONFreeCL	-	0.7	0.0	0.0	0.8	0.0
GACCO	CONTurb	-	5.3	0.0	0.0	8.7	-
GACCO	CONpH	1.2	0.0	0.0	0.0	0.0	0.0
GACCO	CONTotalCL	-	1.0	0.0	0.0	1.3	0.0
GACCO	BALTurb	-	3.3	0.0	0.0	-	0.0
GACCO	FINCLMon	-	0.1	0.0	0.0	0.5	-
GACCO	FINFlow	-	4.0	0.0	17.3	0.0	0.0
GACCO	FINTurbMon	-	14.5	0.0	0.0	2.1	-
GACCO	FINCO	-	21.0	-	-	-	-
GACCO	FINCO1L	-	-	-	21.8	-	22.8
GACCO	FINTurb	-	1.3	0.0	0.0	-	0.0
GACCO	FINpH	2.7	0.0	0.0	0.0	0.0	-
GACEC	GACCO	-	-	-	0.7	-	4.8
GACEC	GACNC	2.7	-	-	-	-	0.0
GACEC	CONFreeCL	-	-	-	-	-	12.9
GACEC	CONTurb	-	-	-	-	-	1.1
GACEC	CONTotalCL	-	-	-	-	-	14.9
GACEC	BALTurb	-	-	-	-	-	0.5
GACEC	FINCO1L	-	-	-	21.8	-	22.8
GACEC	FINTurb	-	-	-	-	-	8.4
GACNC	GACCO	-	-	0.0	0.4	0.0	3.1
GACNC	GACEC	-	-	-	0.2	-	0.0
GACNC	CONHPC37	-	-	21.5	-	-	-
GACNC	CONTurb	-	5.2	0.0	0.0	-	0.0
GACNC	CONpH	-	0.1	0.0	0.0	0.0	0.0
GACNC	BALTurb	-	0.5	0.0	0.0	-	0.0
GACNC	BALpH	10.9	0.0	0.0	0.0	-	-
GACNC	FINCLMon	-	1.3	0.0	0.0	-	-
GACNC	FINFlow	-	0.3	0.0	17.2	3.4	-
GACNC	FINCO1L	-	-	-	21.8	-	22.8
GACNC	FINTurb	-	0.1	0.0	0.0	-	0.0
GACpH	FINHPC22	-	4.8	-	-	-	-
GACpH	FINNC1L	-	13.7	-	-	-	-

GAC Filter non-coliforms achieved viable time lags with Final 1 L coliforms during the first and third 1 L coliform failures: 21.8 h and 22.8 h, respectively (Table 25). In both cases, GAC Filter non-coliforms peaked and entered a decline at the identified time lags. Other results of interest include: a time lag of 21.5 h between GAC Filter non-coliforms and Contact Tank HPC37 during the week of the Enterococcus failure; GAC Filter coliforms, 0.4 h and *E. coli*, 0.2 h during the week of the first 1 L coliform detection; and GAC Filter coliforms, 3.1 h during the week of the third 1 L coliform failure.

There were only two viable time lags from the 162 cross-correlations of GAC Filter pH (Table 25). These were both found in the dataset for the coliform failure and were for Final HPC22, 4.8 h and non-coliforms, 13.7 h. GAC Filter pH consistently impacted

GAC Filter coliforms, but not any other bacteriological parameters at this stage or downstream locations (Appendix 2).

6.3.1.20. Contact Tank, Balance Tank and Final cross-correlations

Results from the Contact Tank, Balance Tank and Final stage exhibited variable proportions of results that were both positive and between 0 and 24 h (Table 15). Cross-correlations conducted on Contact Tank data yielded 14 viable time lags (Table 28); there were five from the Balance Tank stage (Table 27) and 15 from the Final water (Table 26).

During the week of the coliform failure, the following parameters impacted Final coliforms: Contact Tank turbidity, 20.9 h; Final monitor turbidity, 4.5 h; and Final 1 L non-coliforms, 23.0 h. All of these parameters peaked and entered a decline at the identified time lags. During the week of the first 1 L coliform failure, the following parameters impacted Final 1 L coliforms: Balance Tank turbidity, 22.4 h and Final monitor turbidity, 1.5 h. Both of these parameters peaked in the lead up to the 1 L coliform detection. The second 1 L coliform failure occurred 20.2 h after changes to the Contact Tank total chlorine concentration, but the trends are unclear for total chlorine at this time lag. During the week of the third 1 L coliform detection, the following parameters impacted Final 1 L coliforms: Contact Tank turbidity, 22.8 h, free and total chlorine, both 22.8 h; and Balance Tank turbidity, 23.4 h. All four parameters peak and enter a decline at their respective time lags. These results show that peaks in turbidity at these latter stages in the treatment process impact coliform compliance at Strensham. The range for the turbidity results was 0.16 – 0.27 NTU during the 1 L coliform failures; the recorded peak during the coliform failure was 2.00 NTU, but this is believed to be spurious.

Contact Tank turbidity consistently impacted Balance Tank turbidity and Final monitor turbidity (Table 28). Final monitor turbidity and Final spot-sampled turbidity correlated with one another across all five failure weeks and vice versa (Table 26). Final monitor turbidity was also related to monitor free chlorine and spot-sampled total chlorine. Interestingly, neither monitor free chlorine, nor spot-sampled total chlorine correlated with spot-sampled free chlorine.

Table 28: Contact Tank cross-correlations where at least one of the results had a time lag >0 h. Shaded results highlight applicable cross-correlations with Final coliforms or Final 1 L coliforms.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
CONHPC22	BALpH	-	-	-	-	-	0.5
CONHPC37	BALTotalCL	-	-	22.3	-	-	-
CONHPC37	FINFlow	-	-	-	11.6	-	-
CONHPC37	FINpH	20.5	-	-	-	-	-
CONFreeCL	FINCO1L	-	-	-	-	-	22.8
CONTurb	BALTurb	3.5	0.0	0.0	0.0	0.0	0.0
CONTurb	FINFlow	5.4	0.0	0.0	0.0	0.0	0.0
CONTurb	FINTurbMon	16.6	0.0	0.0	0.0	-	0.0
CONTurb	FINCO	-	20.9	-	-	-	-
CONTurb	FINCO1L	-	-	-	-	-	22.8
CONpH	CONHPC37	-	-	-	22.1		-
CONpH	FINTurbMon	4.5	0.0	0.0	0.0	0.0	0.0
CONTotalCL	FINCO1L	-	-	-	-	20.2	22.8

Table 27: Balance Tank cross-correlations where at least one of the results had a time lag >0 h. Shaded results highlight applicable cross-correlations with Final coliforms and Final 1 L coliforms.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
BALCO	FINFreeCL	1.7	-	-	-	-	-
BALCO	FINTotalCL	1.7	-	-	-	-	-
BALTurb	FINCO1L	-	-	-	22.4	-	23.4
BALpH	FINTurbMon	9.1	0.0	0.0	0.0	0.0	0.0

Table 26: Final water cross-correlations where at least one of the results had a time lag >0 h. Shaded results highlight applicable cross-correlations with Final coliforms and Final 1 L coliforms.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
FINCLMon	FINHPC22	-	14.8	-	-	-	-
FINFlow	FINTurbMon	-	3.3	0.0	0.0	0.0	-
FINTurbMon	FINCLMon	-	0.3	0.0	0.0	0.6	0.0
FINTurbMon	FINFlow	-	-	0.0	0.0	0.0	0.4
FINTurbMon	FINCO	-	4.5	-	-	-	-
FINTurbMon	FINCO1L	-	-	-	1.5	-	-
FINTurbMon	FINNC1L	-	-	-	-	20.2	-
FINTurbMon	FINTurb	-	0.0	0.0	0.0	17.6	0.0
FINTurbMon	FINTotalCL	5.2	0.0	0.0	0.0	0.0	0.0
FINHPC22	FINNC1L	-	20.1	-	-	-	-
FINCO1L	FINCLMon	-	-	-	-	-	12.9
FINNC1L	FINCO	23.0	23.0	-	-	-	-
FINTurb	FINTurbMon	-	0.0	0.0	0.0	23.4	0.0

6.3.1.21. Individual Filter Block and GAC Filter turbidity cross-correlations

The spot-sampling from the RGF Filters collects water from a combined stream from Blocks A, B and C and does not consider them individually. There is no spot-sampling for turbidity from the GAC Filters. These monitor data were acquired later to help determine whether the Filter Blocks behaved in the same way and whether the GAC Filter turbidity had an impact downstream.

Table 29: RGF and GAC Filter cross-correlations where at least one of the results had a time lag >0 h. Shaded results highlight applicable cross-correlations for all five failure weeks and, where applicable, the five month dataset. Results in boxes show applicable cross-correlations with Final 1 L coliforms.

Parameter 1	Parameter 2	5 month	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
Rainfall	FiltATurb	-	-	-	0.0	0.0	0.0
Rainfall	FiltBTurb	12.5	0.0	-	-	-	0.0
Rainfall	FiltCTurb	-	-	-	-	-	16.1
Rainfall	FiltDTurb	-	0.0	-	0.0	-	0.0
Rainfall	GACTurbNew	-	0.0	0.0	-	-	0.0
RawTurb	FiltATurb	6.8	0.0	0.0	0.0	0.0	0.0
RawTurb	FiltBTurb	-	0.0	0.0	-	0.0	0.0
RawTurb	FiltCTurb	-	0.0	0.0	-	0.0	-
RawTurb	FiltDTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawTurb	GACTurbNew	-	0.0	0.0	0.0	0.0	0.0
ASettTurb	FiltATurb	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	FiltBTurb	-	0.0	0.0	-	0.0	0.0
CSettTurb	FiltCTurb	-	0.0	0.0	-	0.0	1.9
DSettTurb	FiltDTurb	0.0	0.0	0.0	0.0	0.0	0.0
FiltATurb	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
FiltATurb	ABCFiltEC	-	0.0	-	0.0	0.0	0.0
FiltATurb	ABCFiltNC	0.0	0.0	0.0	0.0	0.0	0.0
FiltATurb	ABCFiltTurb	-	0.0	0.0	0.0	0.0	0.0
FiltATurb	GACTurbNew	3.5	0.0	0.0	0.0	0.0	3.5
FiltATurb	GACCO	-	0.0	0.0	-	-	2.8
FiltATurb	GACNC	-	0.0	0.0	-	-	-
FiltATurb	CONTurb	-	0.0	0.0	0.0	0.0	0.0
FiltATurb	BALTurb	-	0.0	-	-	0.0	0.0
FiltATurb	FINNC1L	-	-	-	-	21.1	-
FiltATurb	FINTurbMon	-	-	-	0.0	0.6	1.4
FiltBTurb	ABCFiltCO	-	0.0	0.0	0.0	0.0	0.0
FiltBTurb	ABCFiltEC	-	0.0	-	-	0.0	7.1
FiltBTurb	ABCFiltNC	-	0.0	0.0	-	0.0	6.9
FiltBTurb	ABCFiltTurb	-	0.0	0.0	-	0.0	0.0
FiltBTurb	GACTurbNew	-	0.0	0.0	-	0.0	3.5
FiltBTurb	GACCO	-	0.0	0.0	-	-	18.4
FiltBTurb	GACEC	-	-	-	-	-	23.7
FiltBTurb	GACNC	-	0.0	0.0	-	-	23.7
FiltBTurb	BALTurb	-	0.0	0.0	-	0.0	7.0
FiltBTurb	FINNC1L	-	-	-	-	21.3	-
FiltBTurb	CONTurb	-	0.0	0.0	-	0.0	0.0
FiltCTurb	ABCFiltCO	-	0.0	0.0	0.0	0.0	0.0
FiltCTurb	ABCFiltEC	-	0.0	-	-	0.0	0.0
FiltCTurb	ABCFiltNC	-	0.0	0.0	0.0	0.0	0.0
FiltCTurb	ABCFiltTurb	-	0.0	0.0	-	0.0	-
FiltCTurb	GACTurbNew	-	2.6	0.0	-	0.0	3.8
FiltCTurb	GACCO	-	-	0.0	-	-	-
FiltCTurb	GACNC	-	0.0	0.0	-	-	-
FiltCTurb	CONTurb	-	0.0	0.0	-	0.0	-
FiltCTurb	BALTurb	-	0.0	0.0	-	0.0	-
FiltCTurb	FINHPC22	-	3.0	-	-	-	-
FiltCTurb	FINCO1L	-	-	-	19.1	21.7	-
FiltCTurb	FINNC1L	-	23.1	-	-	1.2	-
FiltDTurb	DFiltCO	0.0	0.0	13.3	0.0	0.0	0.0
FiltDTurb	DFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
FiltDTurb	DFiltNC	-	0.0	0.0	0.0	0.0	0.0
FiltDTurb	DFiltTurb	0.0	0.0	0.0	0.0	0.0	0.0
FiltDTurb	GACTurbNew	-	0.0	0.0	0.0	0.0	0.0
FiltDTurb	GACCO	0.0	0.0	0.0	0.0	-	7.9
FiltDTurb	GACEC	0.0	-	-	6.7	-	-
FiltDTurb	GACNC	9.0	0.0	0.0	0.0	-	14.5
FiltDTurb	CONTurb	0.0	0.0	0.0	0.0	0.0	0.0
FiltDTurb	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
FiltDTurb	FINCO1L	-	-	-	-	-	18.0
FiltDTurb	FINTurbMon	-	-	-	-	-	15.3
GACTurbNew	GACCO	-	-	0.0	6.0	0.0	0.0
GACTurbNew	GACEC	-	-	-	17.8	-	-
GACTurbNew	GACNC	-	-	0.0	1.7	-	0.0
GACTurbNew	CONTurb	0.0	0.0	0.0	0.0	0.0	0.0
GACTurbNew	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
GACTurbNew	FINTurbMon	-	-	0.0	0.0	0.6	-

Of the 684 cross-correlations conducted on this reduced dataset, 248 were both positive and between 0 and 24 h (Table 29). Thirty-six of these results had viable time lags. There were three cross-correlations with Final 1 L coliforms: with Filter Block C monitor turbidity during the first and second 1 L coliform failures, 19.1 h and 21.7 h, respectively; and Filter Block D monitor turbidity during the week of the third 1 L coliform detection, 18.0 h. The turbidity reading that correlated from the first 1 L coliform failure appears to be spurious, having a value of 159.9 NTU; a reading which occurs sporadically throughout the dataset. The result for the second 1 L coliform detection peaked at 0.93 NTU and dropped off over the identified time lag; there were, however, higher readings recorded before and after this point. The correlation of Filter Block D turbidity with Final 1 L coliforms occurred when turbidity peaked at 4.99 FTU.

The cross-correlations show that rainfall did not consistently correlate with monitored turbidity from the Filter Blocks or GAC Filters (Table 29). However, consistent 0 h time lags were observed between Raw turbidity and turbidity from Filter Blocks A and D and the GAC Filters. Likewise, Settlement Tank A and Filter Block A results changed one with another as did Settlement Tank D and Filter Block D results.

Filter Block turbidity consistently correlated with Filter Block coliforms, but this was not the case for GAC Filter coliforms (Table 29). Filter Blocks A and D and GAC Filter turbidities showed consistent correlations with Contact Tank turbidity. Turbidity readings for Block D and GAC Filters also correlated with Balance Tank turbidity.

6.3.2. Self-Organising Maps

The self-organising maps (SOMs) will be explored working through the WTW and then looking at the climate SOM. Throughout the results the SOM from the five month dataset will be shown and those for the week of each failure can be found in Appendices 3 to 7. For each SOM, the actual range of input data and the range that corresponds to the indicator bacteria will be highlighted in tables for the full five month dataset and for each week of failure.

6.3.2.1. Raw water SOMs

The five month dataset for Strensham raw water shows that high coliform numbers (14,021 – 21,000 CFU 100 ml^{-1}) were found under conditions of low-medium *E. coli* (0 – 6,667 CFU 100 ml^{-1}) relative to the range of counts identified in this dataset (0 –

10,000 CFU 100 ml^{-1}), high non-coliforms (14,685 – 22,000 CFU ml^{-1}), low-medium *C. perfringens* (260 – 787 CFU ml^{-1}) and medium Enterococci (317 – 633 CFU ml^{-1}) (Figure 26 and Table 30). Furthermore, turbidity was low (0.00 – 75.00 NTU), spot-sampled pH was low (6.91 – 7.43 pH units), monitor pH was low-medium (7.00 – 8.20 pH units) and water temperature was low (4.5 – 9.0 °C). High numbers of Enterococci (633 – 950 CFU 100 ml^{-1}) were found with low-medium coliforms (63 – 14,021 CFU 100 ml^{-1}), low *E. coli* (0 – 3,333 CFU 100 ml^{-1}), low non-coliforms (54 – 7,369 CFU 100 ml^{-1}) and medium *C. perfringens* (523 – 787 CFU 100 ml^{-1}); turbidity was low (0.00 – 75.00 NTU), spot-sampled pH was high (7.96 – 8.48 pH units), monitor pH was medium (7.60 – 8.20 pH units), and water temperature was high (13.5 – 18.0 °C).

During the week of the coliform failure, high numbers of coliforms (8,357 – 10,044 CFU 100 ml^{-1}) correlated with low *E. coli* (800 – 1,567 CFU 100 ml^{-1}) relative to the range of counts identified for this failure week (800 – 3,100 CFU 100 ml^{-1}), high non-coliforms (8,033 – 10,000 CFU 100 ml^{-1}), low *C. perfringens* (661 – 677 CFU 100 ml^{-1}), and low Enterococci (789 – 798 CFU 100 ml^{-1}) (Table 30). High coliforms also corresponded to low turbidity (7.06 – 8.00 NTU), low spot-sampled pH (7.90 – 7.95 pH units), low-medium monitor pH (7.69 – 7.83 pH units) and high water temperature (11.7 – 14.6 °C).

The week of the Enterococcus failure saw no Enterococci in the Raw water; for this reason the ranges have been quoted in Table 30. Comparing these ranges with the full five month ranges it is notable that the counts for coliforms, *E. coli* and non-coliforms were low during this week, unlike *C. perfringens*. Turbidity was low, spot-sampled and monitor pH were low-medium and water temperature was high.

During the week of the first 1 L coliform failure high coliforms (10,324 – 11,486 CFU 100 ml^{-1}) corresponded to low *E. coli* (600 – 1,314 CFU 100 ml^{-1}), low non-coliforms (8,664 – 11,465 CFU 100 ml^{-1}), high *C. perfringens* (656 – 686 CFU 100 ml^{-1}) and high Enterococci (723 – 766 CFU 100 ml^{-1}) (Table 30). They also correlated with high turbidity (20.99 – 27.52 NTU), high spot-sampled pH (7.76 – 7.96 pH units), low-high monitor pH (7.79 – 7.93 pH units) and low-high water temperature (5.5 – 8.3 °C).

The week of the second 1 L coliform detection showed that high coliform counts (5,476 – 6,714 CFU 100 ml^{-1}) correlated with low non-coliforms (2,472 – 2,910 CFU

100 ml^{-1}), high *C. perfringens* (424 – 454 CFU 100 ml^{-1}) and high Enterococci (388 – 431 CFU 100 ml^{-1}) (Table 30). High 1 L coliforms corresponded with high turbidity (10.76 – 11.75 NTU), low spot-sampled pH (7.16 – 7.40 pH units), low-high monitor pH (7.67 – 7.83 pH units) and low-high water temperature (5.1 – 6.9 °C). The component plane for *E. coli* did not show a range as identified in the input data and therefore could not be interpreted (see Appendix 6).

The week of the third 1 L coliform failure saw high coliform counts (3,500 – 4,100 CFU 100 ml^{-1}) correlated with high *E. coli* (533 – 700 CFU 100 ml^{-1}), low non-coliforms (2,600 – 2,991 CFU 100 ml^{-1}), low *C. perfringens* (260 – 278 CFU 100 ml^{-1}), and low Enterococci (138 – 167 CFU 100 ml^{-1}) (Table 30). They also corresponded to high turbidity (7.21 – 8.38 NTU), low spot-sampled pH (7.76 – 7.82 pH units), low-medium monitor pH (7.77 – 7.86 pH units) and high water temperature (11.1 – 12.9 °C).

Overall, the results show that high coliforms in the Raw water (3,500 – 11,486 CFU 100 ml^{-1}) occurred when *E. coli* counts were low (533 – 1,567 CFU 100 ml^{-1}) with regard to the ranges identified in the five month dataset, non-coliforms were low-medium (2,472 – 10,000 CFU 100 ml^{-1}), *C. perfringens* were low-medium (260 – 686 CFU 100 ml^{-1}) and Enterococci were low-high (138 – 798 CFU 100 ml^{-1}). Raw water turbidity was low (7.06 – 27.52 NTU), spot-sampled pH was low-medium (7.16 – 7.96 pH units), monitor pH was medium (7.67 – 7.93 pH units) and water temperature was low-medium (5.1 – 14.6 °C).

Correlations with Enterococci results cannot be studied until Strensham Final as they were not monitored through-plant, but the ranges for the other parameters are recorded in the results tables.

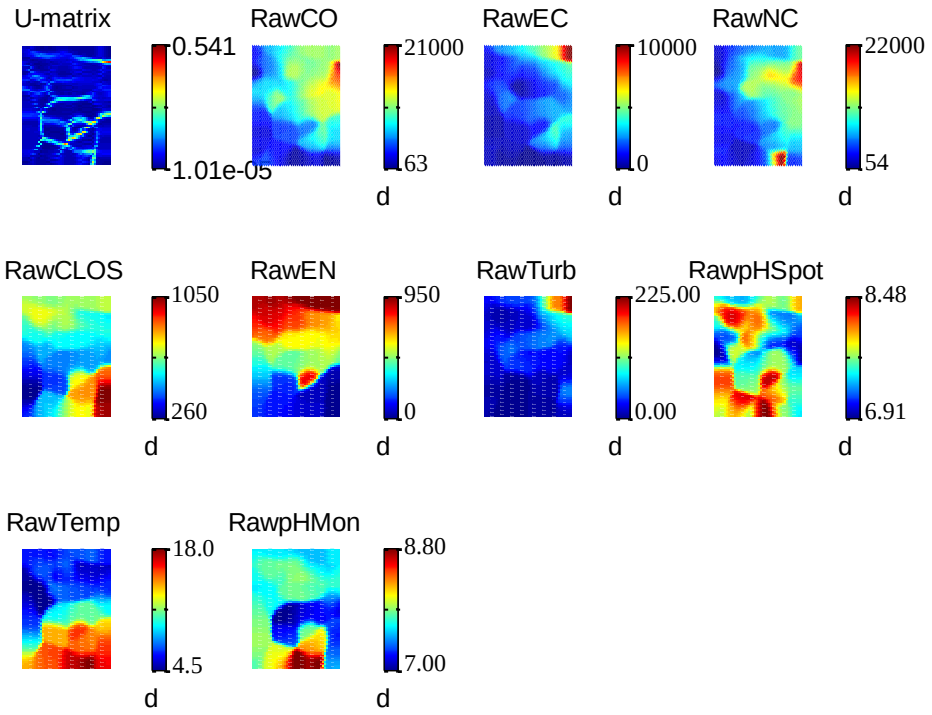

Figure 26: Raw water self-organising map for Strensham five month dataset.

Table 30: Strensham raw water SOM results from the five month dataset and each of the failure weeks. Showing the range represented by the component plane and that corresponding to the indicator organisms. Coliforms, E. coli, non-coliforms, C. perfringens and Enterococci = No. 100 ml^{-1}; turbidity = NTU; pH = pH units; temperature = °C.

RAW	5 month			CO		EN
	Range	CO	EN	Range	CO	Range
Coliforms	63 - 21000	-	63 - 14021	4982 - 10044	-	1500 - 5410
E. coli	0 - 10000	0 - 6667	0 - 3333	800 - 3100	800 - 1567	100 - 1830
Non-coliforms	54 - 22000	14685 - 22000	54 - 7369	4100 - 10000	8033 - 10000	3000 - 5093
C. perfringens	260 - 1050	260 - 787	523 - 787	661 - 710	661 - 677	896 - 1008
Enterococci	0 - 950	317 - 633	-	789 - 815	789 - 798	0
Turbidity	0.00 - 225.00	0.00 - 75.00	0.00 - 75.00	7.06 - 9.87	7.06 - 8.00	5.22 - 16.39
pH (Spot-sampled)	6.91 - 8.48	6.91 - 7.43	7.96 - 8.48	7.90 - 8.05	7.90 - 7.95	7.41 - 7.78
pH (Monitor)	7.00 - 8.80	7.00 - 8.20	7.60 - 8.20	7.69 - 7.90	7.69 - 7.83	7.28 - 7.70
Temperature	4.5 - 18.0	4.5 - 9.0	13.5 - 18.0	5.9 - 14.6	11.7 - 14.6	13.9 - 16.2

	CO 1L (1)		CO 1L (2)		CO 1L (3)	
	Range	CO	Range	CO	Range	CO
Coliforms	8000 - 11486	-	3000 - 6714	-	2300 - 4100	-
E. coli	600 - 2743	600 - 1314	403 - 500	?	200 - 700	533 - 700
Non-coliforms	8664 - 17067	8664 - 11465	2472 - 3787	2472 - 2910	2600 - 3772	2600 - 2991
C. perfringens	596 - 686	656 - 686	364 - 454	424 - 454	260 - 313	260 - 278
Enterococci	636 - 766	723 - 766	301 - 431	388 - 431	138 - 226	138 - 167
Turbidity	7.94 - 27.52	20.99 - 27.52	8.79 - 11.75	10.76 - 11.75	4.88 - 8.38	7.21 - 8.38
pH (Spot-sampled)	7.37 - 7.96	7.76 - 7.96	7.16 - 7.89	7.16 - 7.40	7.76 - 7.94	7.76 - 7.82
pH (Monitor)	7.79 - 7.93	7.79 - 7.93	7.67 - 7.83	7.67 - 7.83	7.77 - 7.90	7.77 - 7.86
Temperature	5.5 - 8.3	5.5 - 8.3	5.1 - 6.9	5.1 - 6.9	7.5 - 12.9	11.1 - 12.9

6.3.2.2. Settlement Tank A SOMs

For Settlement Tank A, the five month dataset showed that high coliform counts (513 – 760 CFU 100 ml^{-1}) correlated with medium-high *E. coli* (40 – 120 CFU 100 ml^{-1}), medium-high non-coliforms (183 – 550 CFU 100 ml^{-1}), low-medium turbidity (0.35 – 1.42 NTU) and high pH (7.27 – 7.67 pH units) (Figure 27 and Table 31).

During the week of the coliform failure, high coliforms (493 – 650 CFU 100 ml^{-1}) corresponded to high *E. coli* (67 – 90 CFU 100 ml^{-1}), low non-coliforms (280 – 379 CFU 100 ml^{-1}), high turbidity (1.16 – 1.34 NTU) and low pH (7.39 – 7.48 pH units). The week of the first 1 L coliform failure showed high coliforms (488 – 620 CFU 100 ml^{-1}) correlated with high *E. coli* (48 – 70 CFU 100 ml^{-1}), low non-coliforms (189 – 309 CFU 100 ml^{-1}), low turbidity (0.79 – 1.08 NTU) and low pH (7.20 – 7.35 pH units). During the week of the second 1 L coliform failure, high coliforms (105 – 133 CFU 100 ml^{-1}) corresponded to high *E. coli* (17 – 20 CFU 100 ml^{-1}), high non-coliforms (71 – 76 CFU 100 ml^{-1}), high turbidity (0.86 – 0.92 NTU) and low pH (7.27 – 7.30 pH units). The third 1 L coliform failure showed high coliforms (139 – 170 CFU 100 ml^{-1}) correlated with low *E. coli* (4 – 8 CFU 100 ml^{-1}), high non-coliforms (191 – 268 CFU 100 ml^{-1}), low turbidity (0.35 – 0.52 NTU) and low pH (7.39 – 7.52 pH units).

In summary, high coliforms from Settlement Tank A (105 – 650 CFU 100 ml^{-1}) correlated with low-medium *E. coli* (4 – 90 CFU 100 ml^{-1}) relative to the range identified in the five month dataset (0 – 120 CFU 100 ml^{-1}), low-medium non-coliforms (71 – 370 CFU 100 ml^{-1}), low-high turbidity (0.35 – 1.34 NTU) and low-high pH (7.20 – 7.52 pH units).

6.3.2.3. Settlement Tank B SOMs

For Settlement Tank B, the five month dataset showed that high coliform counts (867 – 1,300 CFU 100 ml^{-1}) correlated with medium-high *E. coli* (87 – 260 CFU 100 ml^{-1}), low-high non-coliforms (7 – 950 CFU 100 ml^{-1}), medium-high turbidity (0.69 – 1.79 NTU) and low-medium pH (6.75 – 7.37 pH units) (Figure 28 and Table 32).

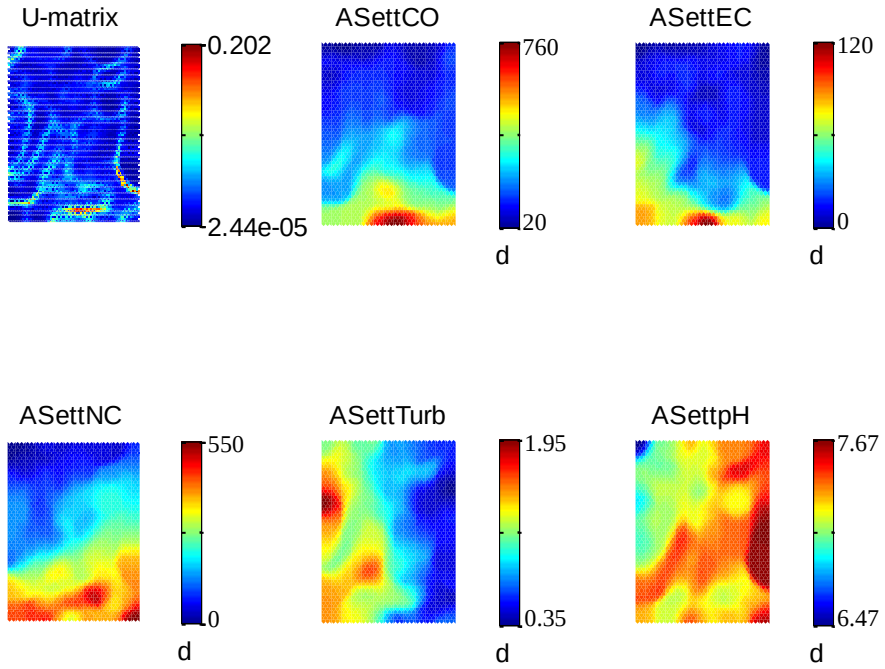

Figure 27: Settlement Tank A self-organising map for Strensham five month dataset.

Table 31: Strensham Settlement Tank A SOM results from the five month dataset and each of the failure weeks. Showing the range represented by the component plane and that corresponding to the indicator organisms. Coliforms, *E. coli* and non-coliforms = CFU 100 ml^{-1}; turbidity = NTU; pH = pH units.

ASETT	5 month		CO		EN	
	Range	CO	Range	CO	Range	-
Coliforms	20 - 760	-	180 - 650	-	70 - 427	-
E. coli	0 - 120	40 - 120	20 - 90	67 - 90	0 -61	-
Non-coliforms	0 - 550	183 - 550	280 - 550	280 - 370	199 - 292	-
Turbidity	0.35 - 1.95	0.35 - 1.42	0.79 - 1.34	1.16 - 1.34	0.56 - 0.85	-
pH	6.47 - 7.67	7.27 - 7.67	7.39 - 7.65	7.39 - 7.48	7.23 - 7.29	-
	CO 1L (1)		CO 1L (2)		CO 1L (3)	
	Range	CO	Range	CO	Range	CO
Coliforms	223 - 620	-	50 - 133	-	78 - 170	-
E. coli	4 - 70	48 - 70	10 - 20	17 - 20	4 - 16	4 - 8
Non-coliforms	189 - 550	189 - 309	60 - 76	71 - 76	36 - 268	191 - 268
Turbidity	0.79 - 1.65	0.79 - 1.08	0.74 - 0.92	0.86 - 0.92	0.35 - 0.85	0.35 - 0.52
pH	7.20 - 7.65	7.20 - 7.35	7.27 - 7.39	7.27 - 7.30	7.39 - 7.52	7.39 - 7.52

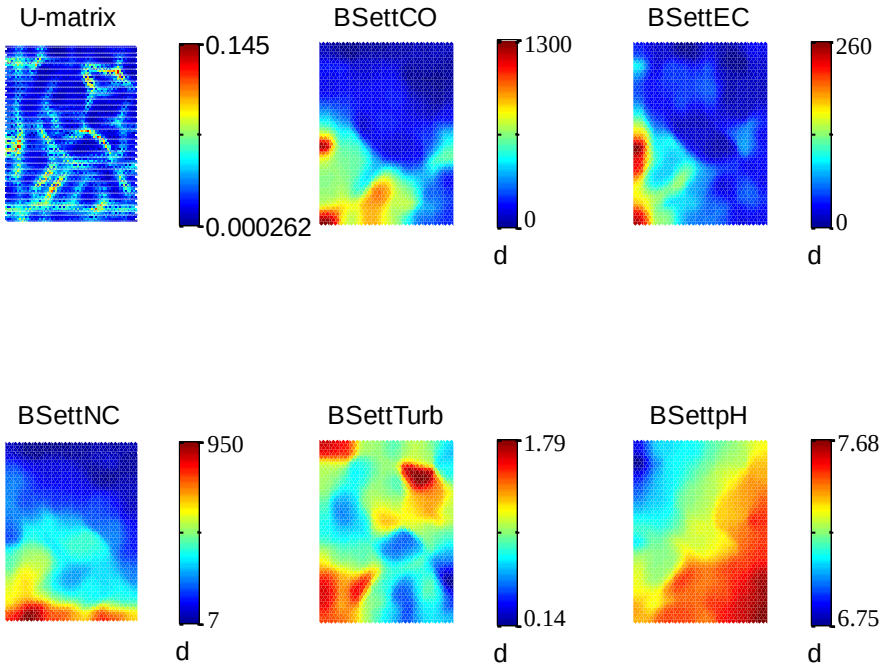

Figure 28: Settlement Tank B self-organising map for Strensham five month dataset.

Table 32: Strensham Settlement Tank B SOM results from the five month dataset and each of the failure weeks. Showing the range represented by the component plane and that corresponding to the indicator organisms. Coliforms, *E. coli* and non-coliforms = CFU 100 ml^{-1}; turbidity = NTU; pH = pH units.

BSETT	5 month		CO		EN	
	Range	CO	Range	CO	Range	-
Coliforms	0 - 1300	-	99 - 817	-	79 - 486	-
E. coli	0 - 260	87 - 260	10 - 70	10 - 30	0 - 117	-
Non-coliforms	7 - 950	7 - 950	169 - 873	169 - 404	299 - 427	-
Turbidity	0.14 - 1.79	0.69 - 1.79	0.75 - 1.29	0.75 - 0.93	0.56 - 0.65	-
pH	6.75 - 7.68	6.75 - 7.37	7.38 - 7.52	7.38 - 7.43	7.27 - 7.37	-
	CO 1L (1)		CO 1L (2)		CO 1L (3)	
	Range	CO	Range	CO	Range	CO
Coliforms	112 - 1300	-	50 - 117	-	108 - 600	-
E. coli	4 - 70	48 - 70	6 - 27	20 - 27	9 - 30	23 - 30
Non-coliforms	141 - 950	680 - 950	30 - 105	30 - 105	54 - 660	458 - 660
Turbidity	0.98 - 1.49	1.32 - 1.49	0.57 - 0.82	0.74 - 0.82	0.66 - 0.93	0.66 - 0.75
pH	7.24 - 7.52	7.43 - 7.52	7.27 - 7.41	7.27 - 7.32	7.43 - 7.62	7.43 - 7.49

During the week of the coliform failure, high coliform counts (578 – 817 CFU 100 ml^{-1}) correlated with low *E. coli* (10 – 30 CFU 100 ml^{-1}), non-coliforms (169 – 404 CFU 100 ml^{-1}), turbidity (0.75 – 0.93 NTU) and pH (7.38 – 7.43 pH units). The week of the first 1 L coliform detection showed high coliform counts (904 – 1,300 CFU 100 ml^{-1}) correlated with high *E. coli* (48 – 70 CFU 100 ml^{-1}), non-coliforms (680 – 950 CFU

100 ml^{-1}), turbidity (1.32 – 1.49 NTU) and pH (7.43 – 7.52 pH units). The week of the second 1 L coliform failure showed high coliforms (95 – 117 CFU 100 ml^{-1}) corresponded to high *E. coli* (20 – 27 CFU 100 ml^{-1}), non-coliforms (30 – 105 CFU 100 ml^{-1}) and turbidity (0.74 – 0.82 NTU) and low pH (7.27 – 7.32 pH units). During the week of the third 1 L coliform detection, high coliforms (436 – 600 CFU 100 ml^{-1}) correlated with high *E. coli* (23 – 30 CFU 100 ml^{-1}) and non-coliforms (458 – 660 CFU 100 ml^{-1}) and low turbidity (0.66 – 0.75 NTU) and pH (7.43 – 7.49 pH units).

An overview of high coliforms from Settlement Tank B (95 – 1,300 CFU 100 ml^{-1}) shows that their occurrence correlated with low *E. coli* (10 – 70 CFU 100 ml^{-1}), low-high non-coliforms (30 – 950 CFU 100 ml^{-1}), medium-high turbidity (0.66 – 1.49 NTU), and medium-high pH (7.27 – 7.52 pH units).

6.3.2.4. Settlement Tank C SOMs

The five month dataset for Settlement Tank C showed high counts of coliforms (480 – 720 CFU 100 ml^{-1}) correlated with medium-high *E. coli* (41 – 123 CFU 100 ml^{-1}), low non-coliforms (0 – 1,000 CFU 100 ml^{-1}), low-medium turbidity (0.07 – 1.11 NTU) and medium-high pH (7.06 – 7.74 pH units) (Figure 29 and Table 33).

During the week of the coliform failure, high coliforms (420 – 530 CFU 100 ml^{-1}) corresponded to low-high *E. coli* (10 – 60 CFU 100 ml^{-1}) and low non-coliforms (229 – 279 CFU 100 ml^{-1}), turbidity (0.62 – 0.78 NTU) and pH (7.56 – 7.62 pH units). During the week of the first 1 L coliform failure, high coliform counts (353 – 490 CFU 100 ml^{-1}) correlated with high *E. coli* (41 – 60 CFU 100 ml^{-1}) and non-coliforms (275 – 380 CFU 100 ml^{-1}), low turbidity (0.68 – 0.82 NTU) and high pH (7.54 – 7.65 pH units). The second 1 L coliform failure showed high coliforms (81 – 106 CFU 100 ml^{-1}) corresponded to high *E. coli* (14 – 18 CFU 100 ml^{-1}), non-coliforms (45 – 68 CFU 100 ml^{-1}) and turbidity (0.76 – 0.84 NTU) and low pH (7.31 – 7.37 pH units). The week of the third 1 L coliform detection showed that high coliforms (104 – 128 CFU 100 ml^{-1}) correlated with high non-coliforms (132 – 182 CFU 100 ml^{-1}) and turbidity (0.76 – 0.92 NTU) and low pH (7.39 – 7.43 pH units). The component plane for *E. coli* did not show a range as identified in the input data and therefore could not be interpreted (see Appendix 7).

Overall, high coliforms from Settlement Tank C (81 – 530 CFU 100 ml^{-1}) were observed to occur with low-medium *E. coli* (10 – 60 CFU 100 ml^{-1}), low non-coliforms (45 – 380 CFU 100 ml^{-1}), medium turbidity (0.62 – 0.92 NTU) and medium-high pH (7.31 – 7.65 pH units).

6.3.2.5. Settlement Tank D SOMs

For Settlement Tank D, the five month dataset showed that high coliform counts (670 – 1,000 CFU 100 ml^{-1}) correlated with low-high *E. coli* (0 – 310 CFU 100 ml^{-1}) and non-coliforms (0 – 1,000 CFU 100 ml^{-1}) and low-medium turbidity (0.40 – 1.12 NTU) and pH (6.89 – 7.43 pH units) (Figure 30 and Table 34).

During the week of the coliform failure, high coliforms (503 – 670 CFU 100 ml^{-1}) corresponded to high *E. coli* (63 – 90 CFU 100 ml^{-1}), low non-coliforms (180 – 353 CFU 100 ml^{-1}), high turbidity (0.86 – 0.99 NTU) and medium pH (7.55 – 7.60 pH units). The week of the first 1 L coliform detection showed high coliforms (483 – 638 CFU 100 ml^{-1}) correlated with high *E. coli* (54 – 71 CFU 100 ml^{-1}), low non-coliforms (1 – 49 CFU 100 ml^{-1}), high turbidity (0.83 – 0.95 NTU) and low pH (7.26 – 7.36 pH units). During the week of the second 1 L coliform failure high coliforms (89 – 109 CFU 100 ml^{-1}) corresponded to high *E. coli* (22 – 33 CFU 100 ml^{-1}), non-coliforms (93 – 110 CFU 100 ml^{-1}) and turbidity (0.60 – 0.66 NTU) and low pH (7.32 – 7.35 pH units). The third 1 L coliform failure showed high coliform counts (114 – 160 CFU 100 ml^{-1}) correlated with low *E. coli* (4 – 10 CFU 100 ml^{-1}), high non-coliforms (234 – 333 CFU 100 ml^{-1}) and low turbidity (0.46 – 0.53 NTU) and pH (7.40 – 7.42 pH units).

In summary, high coliforms from Settlement Tank D (89 – 670 CFU 100 ml^{-1}) correlated with low *E. coli* (4 – 90 CFU 100 ml^{-1}), low non-coliforms (1 – 353 CFU 100 ml^{-1}), low-medium turbidity (0.46 – 0.99 NTU), and medium-high pH (7.26 – 7.60 pH units).

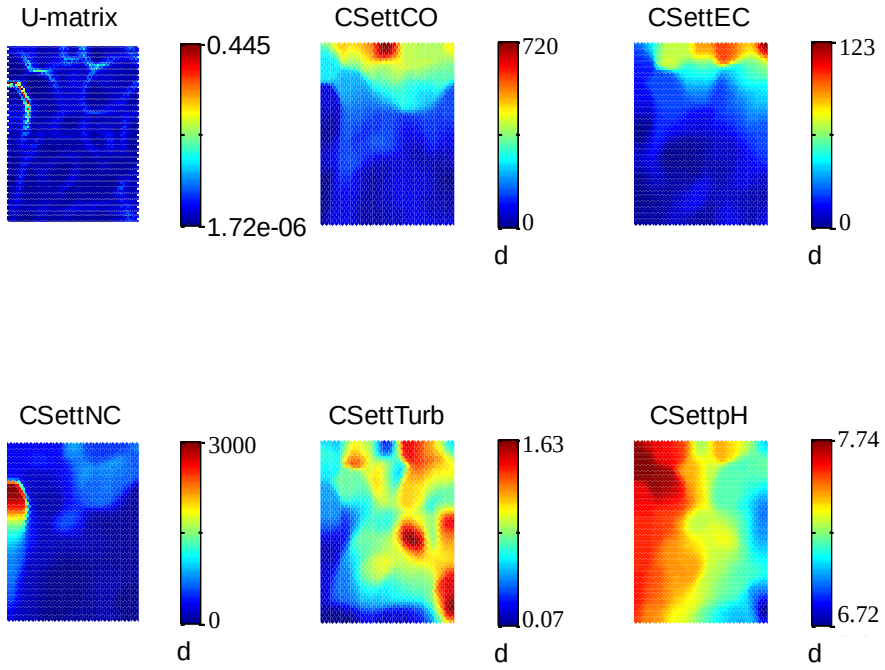

Figure 29: Settlement Tank C self-organising map for Strensham five month dataset.

Table 33: Strensham Settlement Tank C SOM results from the five month dataset and each of the failure weeks. Showing the range represented by the component plane and that corresponding to the indicator organisms. Coliforms, *E. coli* and non-coliforms = CFU 100 ml^{-1}; turbidity = NTU; pH = pH units.

CSETT	5 month		CO		EN	
	Range	CO	Range	CO	Range	-
Coliforms	0 - 720	-	200 - 530	-	79 - 383	-
E. coli	0 - 123	41 - 123	10 - 60	10 - 60	0 - 47	-
Non-coliforms	0 - 3000	0 - 1000	229 - 380	229 - 279	305 - 707	-
Turbidity	0.07 - 1.63	0.07 - 1.11	0.62 - 1.10	0.62 - 0.78	0.60 - 0.91	-
pH	6.72 - 7.74	7.06 - 7.74	7.56 - 7.74	7.56 - 7.62	7.33 - 7.36	-
	CO 1L (1)		CO 1L (2)		CO 1L (3)	
	Range	CO	Range	CO	Range	CO
Coliforms	80 - 490	-	30 - 106	-	55 - 128	-
E. coli	4 - 60	41 - 60	6 - 18	14 - 18	0 - 4	?
Non-coliforms	64 - 380	275 - 380	0 - 68	45 - 68	32 - 182	132 - 182
Turbidity	0.68 - 1.10	0.68 - 0.82	0.59 - 0.84	0.76 - 0.84	0.43 - 0.92	0.76 - 0.92
pH	7.32 - 7.65	7.54 - 7.65	7.31 - 7.50	7.31 - 7.37	7.39 - 7.52	7.39 - 7.43

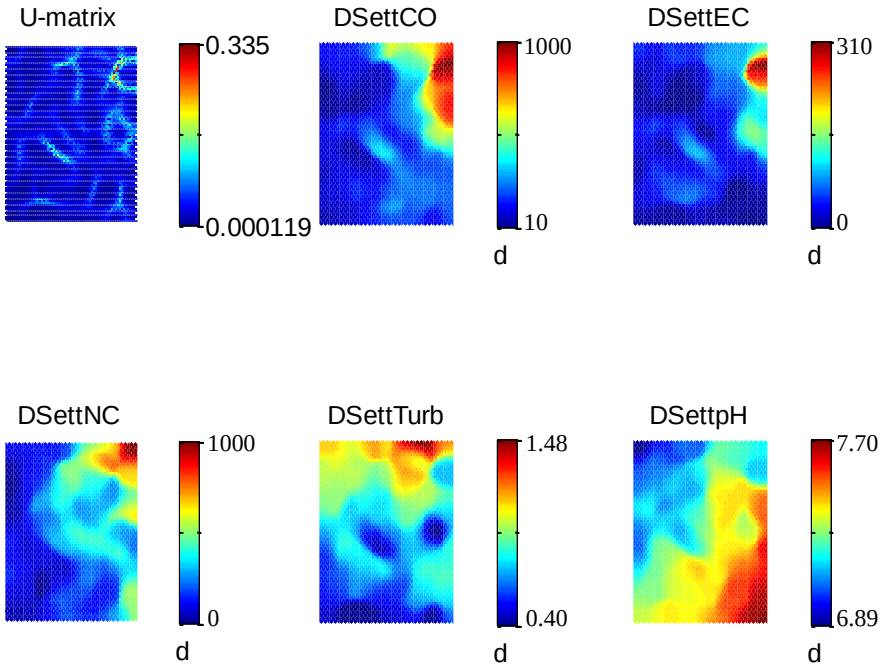

Figure 30: Settlement Tank D self-organising map for Strensham five month dataset.

Table 34: Strensham Settlement Tank D SOM results from the five month dataset and each of the failure weeks. Showing the range represented by the component plane and that corresponding to the indicator organisms. Coliforms, *E. coli* and non-coliforms = CFU 100 ml^{-1}; turbidity = NTU; pH = pH units.

DSETT	5 month		CO		EN	
	Range	CO	Range	CO	Range	-
Coliforms	10 - 1000	-	170 - 670	-	79 - 427	-
E. coli	0 - 310	0 - 310	10 - 90	63 - 90	0 - 134	-
Non-coliforms	0 - 1000	0 - 1000	180 - 700	180 - 353	310 - 509	-
Turbidity	0.40 - 1.48	0.40 - 1.12	0.59 - 0.99	0.86 - 0.99	0.67 - 0.98	-
pH	6.89 - 7.70	6.89 - 7.43	7.50 - 7.65	7.55 - 7.60	7.15 - 7.39	-
	CO 1L (1)		CO 1L (2)		CO 1L (3)	
	Range	CO	Range	CO	Range	CO
Coliforms	172 - 638	-	50 - 109	-	23 - 160	-
E. coli	20 - 71	54 - 71	0 - 33	22 - 33	4 - 23	4 - 10
Non-coliforms	1 - 144	1 - 49	60 - 110	93 - 110	36 - 333	234 - 333
Turbidity	0.59 - 0.95	0.83 - 0.95	0.49 - 0.66	0.60 - 0.66	0.46 - 0.68	0.46 - 0.53
pH	7.26 - 7.56	7.26 - 7.36	7.32 - 7.40	7.32 - 7.35	7.40 - 7.47	7.40 - 7.42

6.3.2.6. Filter Block ABC SOMs

The five month dataset for Filter Block ABC showed that high coliform counts (135 – 183 CFU 100 ml^{-1}) correlated with low *E. coli* (6 – 37 CFU 100 ml^{-1}), high non-coliforms (95 – 143 CFU 100 ml^{-1}) and medium turbidity (0.47 – 0.87 NTU) and pH (7.00 – 7.33 pH units) (Figure 31 and Table 35).

During the weeks of the coliform and first 1 L coliform failures, there were no peaks in coliform numbers, both having counts of 100 CFU 100 ml^{-1} (see Appendices 3 and 5). During the week of the second 1 L coliform failure, high coliform counts (90 – 100 CFU 100 ml^{-1}) correlated with high *E. coli* (17 – 22 CFU 100 ml^{-1}), non-coliforms (62 – 63 CFU 100 ml^{-1}) and turbidity (0.20 – 0.24 NTU) and low pH (7.26 – 7.28 pH units). The week of the third 1 L coliform detection showed high coliform counts (98 – 100 CFU 100 ml^{-1}) corresponded to low *E. coli* (7 – 15 CFU 100 ml^{-1}), high non-coliforms (78 – 100 CFU 100 ml^{-1}), low turbidity (0.17 – 0.20 NTU) and high pH (7.51 – 7.57 pH units).

During the weeks of the second and third 1 L coliform failures, high coliform counts (90 – 100 CFU 100 ml^{-1}) corresponded to low *E. coli* (7 – 22 CFU 100 ml^{-1}), low-medium non-coliforms (62 – 100 CFU 100 ml^{-1}), low turbidity (0.17 – 0.24 NTU), and high pH (7.26 – 7.57 pH units).

6.3.2.7. Filter Block D SOMs

The five month dataset for Filter Block D showed that high coliform counts (204 – 300 CFU 100 ml^{-1}) correlated with low *E. coli* (1 – 34 CFU 100 ml^{-1}), high non-coliforms (115 – 172 CFU 100 ml^{-1}), medium turbidity (0.33 – 0.67 NTU) and low pH (6.88 – 7.14 pH units) (Figure 32 and Table 36).

There was no peak in coliform counts during the weeks of both the coliform and the first 1 L coliform failures, both weeks having counts of 100 CFU 100 ml^{-1} (see Appendices 3 and 5). During the week of the second 1 L coliform failure high coliform counts (87 – 97 CFU 100 ml^{-1}) correlated with high *E. coli* (17 – 23 CFU 100 ml^{-1}), non-coliforms (70 – 81 CFU 100 ml^{-1}) and turbidity (0.10 – 0.13 NTU), and low pH (7.24 – 7.25 pH units). The third 1 L coliform detection showed high coliform counts (91 – 100 CFU 100 ml^{-1}) corresponded to low-high *E. coli* (7 – 19 CFU 100 ml^{-1}), high non-coliforms (81 – 100 CFU 100 ml^{-1}), and low-high turbidity (0.11 – 0.18 NTU) and pH (7.26 – 7.50 pH units).

To summarise the findings from Filter Block D for the second and third 1 L coliform detections: high coliforms (87 – 100 CFU 100 ml^{-1}) were observed to occur with low *E. coli* (7 – 23 CFU 100 ml^{-1}), medium non-coliforms (70 – 100 CFU 100 ml^{-1}), low turbidity (0.10 – 0.18 NTU), and medium-high pH (7.24 – 7.50 pH units).

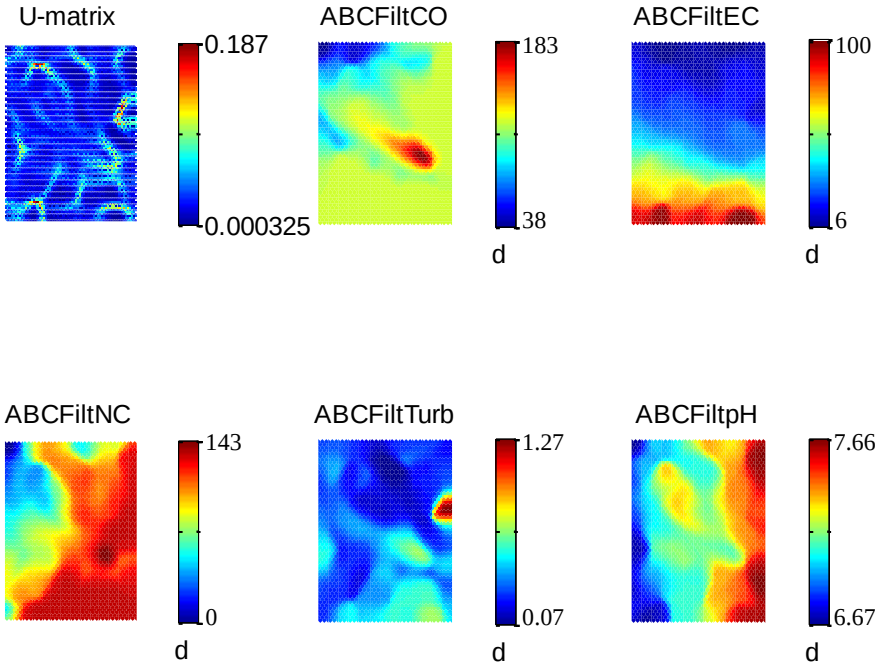

Figure 31: Filter Block ABC self-organising map for Strensham five month dataset.

Table 35: Strensham Filter Block ABC SOM results from the five month dataset and each of the failure weeks. Showing the range represented by the component plane and that corresponding to the indicator organisms. Coliforms, *E. coli* and non-coliforms = CFU 100 ml^{-1}; turbidity = NTU; pH = pH units.

ABCFilt	5 month		CO		EN	
	Range	CO	Range	CO	Range	-
Coliforms	38 - 183	-	100	-	92 - 100	-
E. coli	6 - 100	6 - 37	43 - 100	-	9 - 55	-
Non-coliforms	0 - 143	95 - 143	99 - 100	-	55 - 100	-
Turbidity	0.07 - 1.27	0.47 - 0.87	0.30 - 0.57	-	0.07 - 0.19	-
pH	6.67 - 7.66	7.00 - 7.33	7.51 - 7.62	-	7.17 - 7.31	-
	CO 1L (1)		CO 1L (2)		CO 1L (3)	
	Range	CO	Range	CO	Range	CO
Coliforms	100	-	70 - 100	-	95 - 100	-
E. coli	29 - 100	-	6 - 22	17 - 22	7 - 30	7 - 15
Non-coliforms	61 - 100	-	59 - 63	62 - 63	34 - 100	78 - 100
Turbidity	0.28 - 0.57	-	0.12 - 0.24	0.20 - 0.24	0.17 - 0.25	0.17 - 0.20
pH	7.25 - 7.59	-	7.26 - 7.33	7.26 - 7.28	7.40 - 7.57	7.51 - 7.57

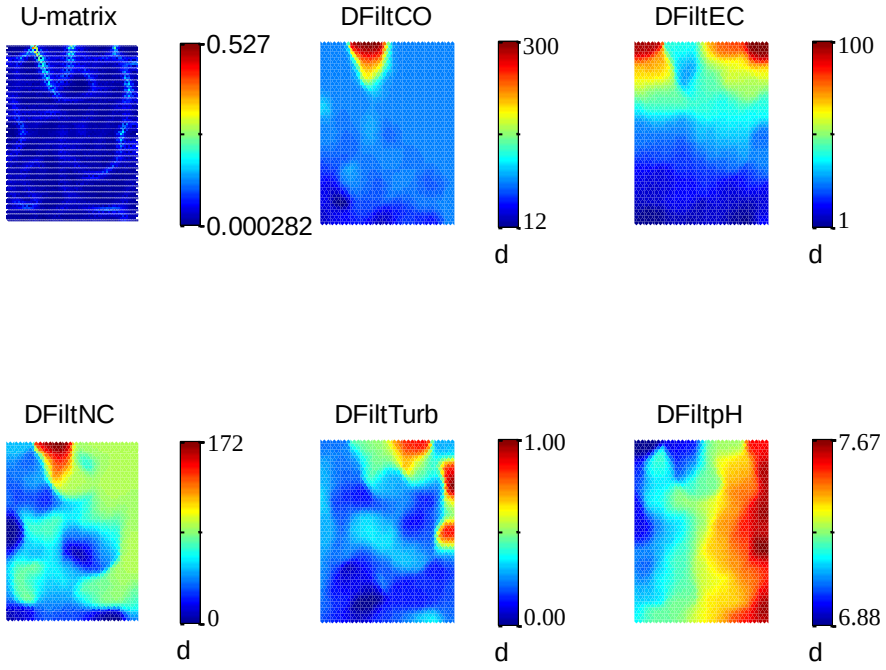

Figure 32: Filter Block D self-organising map for Strensham five month dataset.

Table 36: Strensham Filter Block D SOM results from the five month dataset and each of the failure weeks. Showing the range represented by the component plane and that corresponding to the indicator organisms. Coliforms, *E. coli* and non-coliforms = CFU 100 ml^{-1}; turbidity = NTU; pH = pH units.

DFilt	5 month		CO		EN	
	Range	CO	Range	CO	Range	-
Coliforms	12 - 300	-	100	-	19 - 100	-
E. coli	1 - 100	1 - 34	44 - 100	-	14 - 52	-
Non-coliforms	0 - 172	115 - 172	99 - 100	-	43 - 100	-
Turbidity	0.00 - 1.00	0.33 - 0.67	0.15 - 0.82	-	0.14 - 0.20	-
pH	6.88 - 7.67	6.88 - 7.14	7.46 - 7.55	-	7.19 - 7.24	-
	CO 1L (1)		CO 1L (2)		CO 1L (3)	
	Range	CO	Range	CO	Range	CO
Coliforms	100	-	68 - 97	-	74 - 100	-
E. coli	40 - 100	-	6 - 23	17 - 23	7 - 19	7 - 19
Non-coliforms	64 - 100	-	49 - 81	70 - 81	43 - 100	81 - 100
Turbidity	0.16 - 0.30	-	0.05 - 0.13	0.10 - 0.13	0.11 - 0.18	0.11 - 0.18
pH	7.30 - 7.54	-	7.24 - 7.27	7.24 - 7.25	7.26 - 7.50	7.26 - 7.50

6.3.2.8. GAC Filter SOMs

At the GAC Filter stage of treatment, the five month dataset showed high coliforms (67 – 100 CFU 100 ml^{-1}) correlated with low-high *E. coli* (0 – 120 CFU 100 ml^{-1}), medium-high non-coliforms (33 – 100 CFU 100 ml^{-1}) and low-high pH (2.00 – 7.38 pH units) (Figure 33 and Table 37). There is no pH adjustment until after the Contact Tank and this is with sodium hydroxide. The lowest pH recorded pre-GAC Filter was 6.47 pH

units, from Settlement Tank A. The low pH values recorded by the GAC Filter monitor (2.00 pH units) during several periods in January 2013 are therefore presumed erroneous.

During the week of the coliform failure high coliform counts (1 – 2 CFU 100 ml^{-1}) corresponded to medium-high non-coliforms (1 – 3 CFU 100 ml^{-1}) and pH (7.23 – 7.29 pH units); there were no *E. coli* enumerated over this time period. High coliforms during the weeks of the first (5 – 8 CFU 100 ml^{-1}) and third (1 – 2 CFU 100 ml^{-1}) 1 L coliform detections correlated with high *E. coli* (2 – 3 CFU 100 ml^{-1} and 1 CFU 100 ml^{-1}, respectively) and non-coliforms (3 – 5 CFU 100 ml^{-1}; 1 – 2 CFU 100 ml^{-1}) and low-high pH (7.13 – 7.26 pH units; 7.06 – 7.29 pH units). The SOM for the second 1 L coliform detection was inconclusive (see Appendix 6).

Overall, the results from the GAC Filters show that high coliforms (1 – 8 CFU 100 ml^{-1}) corresponded to low *E. coli* (0 – 3 CFU 100 ml^{-1}), low non-coliforms (1 – 5 CFU 100 ml^{-1}) and high pH (7.06 – 7.29 pH units).

6.3.2.9. Contact Tank SOMs

Results from the Contact Tank only showed coliforms in the five month dataset. This showed that a count of 1 CFU 100 ml^{-1} correlated with high HPC22 (3 – 5 CFU m^{-1}) and low HPC37 (0 – 6 CFU ml^{-1}), as well as high free and total chlorine (1.67 – 2.27 mg l^{-1} and 2.00 – 2.27 mg l^{-1}, respectively), medium turbidity (0.19 – 0.32 NTU) and medium-high pH (6.79 – 7.64 pH units) (Figure 34 and Table 38). No coliforms were enumerated from this treatment stage during any of the weeks of failure. The ranges for the parameters are in Table 38. The following points are notable: HPCs at 22 and 37 °C were low for all weeks of failure (≤ 2 CFU ml^{-1}); free and total chlorines were consistently toward the upper end of the range identified in the five month dataset; turbidity was low-medium across all failure weeks; and pH was always ≥ 7.00 pH units.

6.3.2.10. Balance Tank SOMs

Coliforms at the Balance Tank stage were also only recorded in the five month dataset. This showed that a count of 1 CFU 100 ml^{-1} correlated with low-medium free chlorine (0.54 – 0.83 mg l^{-1}), low total chlorine (0.66 – 0.79 mg l^{-1}), low turbidity (0.05 – 0.17 NTU) and low-medium pH (6.95 – 7.55 pH units) (Figure 35 and Table 39). No coliforms were enumerated from this treatment stage during any of the weeks of failure.

The ranges for the parameters are in Table 39. The ranges for the failure weeks have the following details in common: free and total chlorines were always medium-high based on the ranges identified in the five month dataset; turbidity was consistently low-medium across the failure weeks; and pH was always ≥ 7.26, rising to the maximum for the five month period (7.84 pH units) during the weeks of the coliform and first 1 L coliform failures.

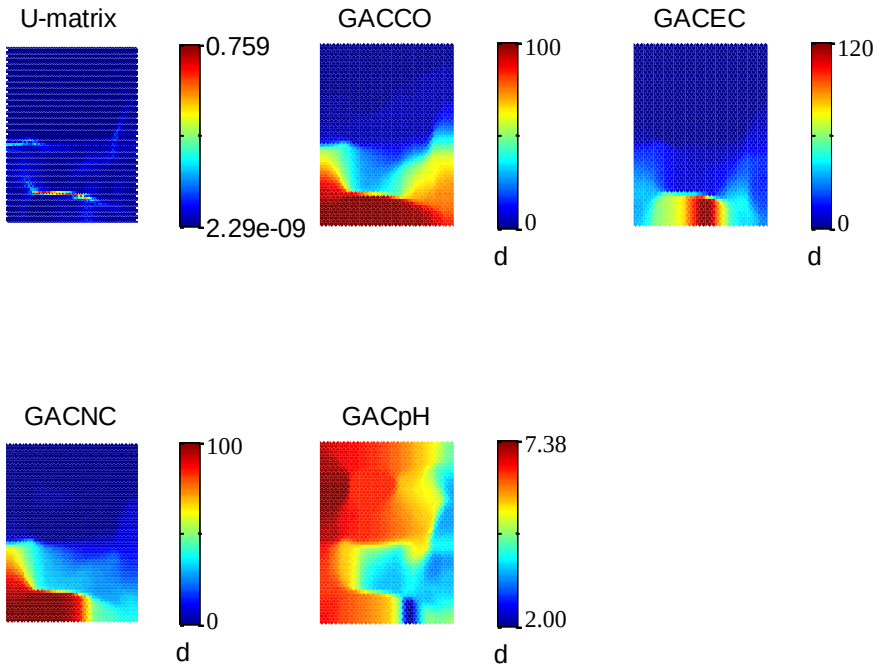

Figure 33: GAC Filter self-organising map for Strensham five month dataset.

Table 37: Strensham GAC Filter SOM results from the five month dataset and each of the failure weeks. Showing the range represented by the component plane and that corresponding to the indicator organisms. Coliforms, *E. coli* and non-coliforms = CFU 100 ml^{-1}; pH = pH units.

GAC	5 month		CO		EN	
	Range	CO	Range	CO	Range	-
Coliforms	0 - 100	-	0 - 2	-	4 - 5	-
E. coli	0 - 120	0 - 120	0	0	0	-
Non-coliforms	0 - 100	33 - 100	0 - 3	1 - 3	1	-
pH	2.00 - 7.38	2.00 - 7.38	7.20 - 7.29	7.23 - 7.29	6.66 - 7.08	-
	CO 1L (1)		CO 1L (2)		CO 1L (3)	
	Range	CO	Range	CO	Range	CO
Coliforms	0 - 8	-	0 - 1	-	0 - 1	-
E. coli	0 - 3	2 - 3	0	0	0 - 1	1
Non-coliforms	0 - 5	3 - 5	0 - 2	?	0 - 2	1 - 2
pH	7.13 - 7.26	7.13 - 7.26	6.96 - 7.13	?	7.06 - 7.29	7.06 - 7.29

6.3.2.11. Final SOMs

The five month dataset showed that the coliform detection correlated with: high monitor free chlorine (1.37 – 2.06 mg l^{-1}) and low spot-sampled free and total chlorines (0.48 – 0.70 mg l^{-1} and 0.52 – 0.77 mg l^{-1}, respectively); medium flow (26.3 – 52.7 ML d^{-1}); medium monitor turbidity (0.67 – 1.33 NTU) and high spot-sampled turbidity (0.18 – 0.24 NTU); and medium pH (7.33 – 7.60 pH units) (Figure 36 and Table 40). The 1 L coliform failures correlated with: medium-high monitor free chlorine (0.69 – 2.06 mg l^{-1}) and low-medium spot-sampled free and total chlorines (0.70 – 0.93 mg l^{-1} and 0.77 – 1.02 mg l^{-1}, respectively), medium-high flow (26.3 – 52.7 ML d^{-1}); low monitor turbidity (0.00 – 0.67 NTU) and medium-high spot-sampled turbidity (0.12 – 0.18 NTU) and medium-high pH (7.60 – 7.88 pH units). The Enterococcus failure corresponded to conditions of medium-high monitor chlorine (0.69 – 2.06 mg l^{-1}); medium spot-sampled free and total chlorine (0.48 – 0.93 mg l^{-1} and 0.52 – 1.02 mg l^{-1}, respectively); medium flow (26.3 – 79.0 ML d^{-1}); low monitor turbidity (0.00 – 0.67 NTU) and medium spot-sampled turbidity (0.12 – 0.24 NTU); and high pH (7.33 – 7.88 pH units). The majority of bacteriological parameters were 0 CFU ml^{-1}/100 ml^{-1}; but low-high HPCs at 22 °C (0 – 173 CFU ml^{-1}) correlated with the coliform failure and medium HPCs at 37 °C (1 CFU ml^{-1}) corresponded to the Enterococcus detection. These results show that no failures were identified under the following conditions: low flow; high monitor turbidity; low spot-sampled turbidity; high free and/or total chlorines; and low pH.

During the week of the coliform failure the following conditions correlated with the coliform detection in the Final water: low-medium monitor free chlorine (0.73 – 0.86 mg l^{-1}); low spot-sampled free chlorine (0.48 – 0.61 mg l^{-1}) and high spot-sampled total chlorine (0.80 – 0.94 mg l^{-1}); medium flow (42.8 – 60.7 ML d^{-1}); low monitor turbidity (0.00 – 0.67 NTU) and high spot-sampled turbidity (0.22 – 0.24 NTU); and low-medium pH (7.38 – 7.48 pH units). No other bacteria were enumerated that week (Table 40).

The detection of the Enterococcus coincided with: medium monitor free chlorine (0.77 – 0.83 mg l^{-1}); low-medium spot-sampled free chlorine (0.63 – 0.71 mg l^{-1}); medium-high spot-sampled total chlorine (0.87 – 0.94 mg l^{-1}); high flow (48.8 – 64.2 ML d^{-1}); low monitor turbidity (0.03 – 0.10 NTU) and medium-high spot-sampled turbidity (0.16

– 0.19 NTU); and high pH (7.68 – 7.75 pH units). No other bacteria were enumerated that week (Table 40).

During the week of the first 1 L coliform failure, the coliform detection occurred under the following conditions: low monitor free chlorine (0.69 – 0.80 mg l^{-1}); low spot-sampled free chlorine (0.48 – 0.58 mg l^{-1}) and high spot-sampled total chlorine (0.73 – 0.84 mg l^{-1}); high flow (59.8 – 77.5 ML d^{-1}); low monitor turbidity (0.03 – 0.08 NTU) and spot-sampled turbidity (0.14 – 0.17 NTU); and low pH (7.36 – 7.45 pH units) (Table 40).

The second 1 L coliform failure showed that the coliform detection correlated with: low monitor free chlorine (0.79 – 0.85 mg l^{-1}); low spot-sampled free chlorine (0.65 – 0.72 mg l^{-1}) and high spot-sampled total chlorine (0.87 – 0.91 mg l^{-1}); high flow (54.8 – 69.6 mg l^{-1}); low monitor turbidity (0.00 – 0.67 NTU) and high spot-sampled turbidity (0.15 – 0.19 NTU); and high pH (7.50 – 7.56 pH units) (Table 40).

Data for the week of the third 1 L coliform failure demonstrate that the detection occurred with: low monitor free chlorine (0.27 – 0.51 mg l^{-1}); high spot-sampled free and total chlorines (0.78 – 0.84 mg l^{-1} and 0.87 – 0.90 mg l^{-1}, respectively); low flow (0.0 – 26.1 ML d^{-1}); medium monitor turbidity (0.67 – 1.33 NTU) and low spot-sampled turbidity (0.08 – 0.13 NTU); and low pH (7.44 – 7.49 pH units) (Table 40). The low chlorines and high turbidity were checked against the Works Management Master Log (WIMS) to identify whether they were caused by an incident or WTW maintenance. The period of low monitor free chlorine was limited on the trend to two hours on the day of the failure, due to a power cut at the WTW. This event was observed after the collection of the failing sample. Strensham WTW was shut down for the duration of the power cut. The turbidity spike was due to the monitor being cleaned.

In summary, the SOM results for the 1 L coliform failures show that the detections correlated with: low-medium monitor free chlorine (0.27 – 0.85 mg l^{-1}); low-medium free and total spot-sampled chlorines (0.48 – 0.84 mg l^{-1} and 0.73 – 0.91 mg l^{-1}, respectively); low-medium monitor turbidity (0.00 – 1.33 NTU) and low-high spot-sampled turbidity (0.08 – 0.19 NTU); low-high flow (0.0 – 77.5 ML d^{-1}); and medium pH (7.36 – 7.56 pH units).

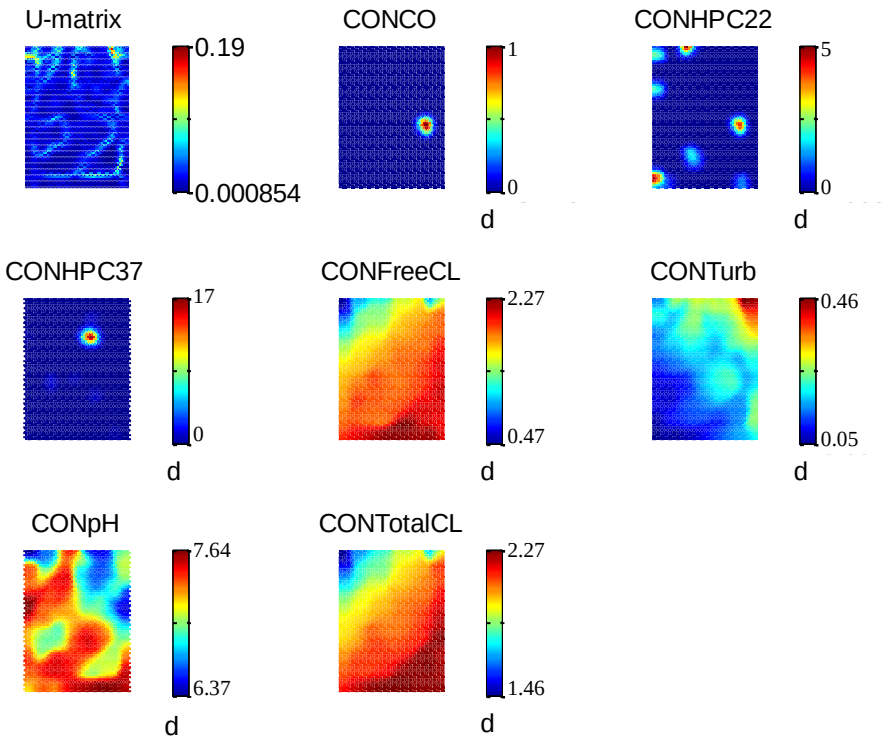

Figure 34: Contact Tank self-organising map for Strensham five month dataset.

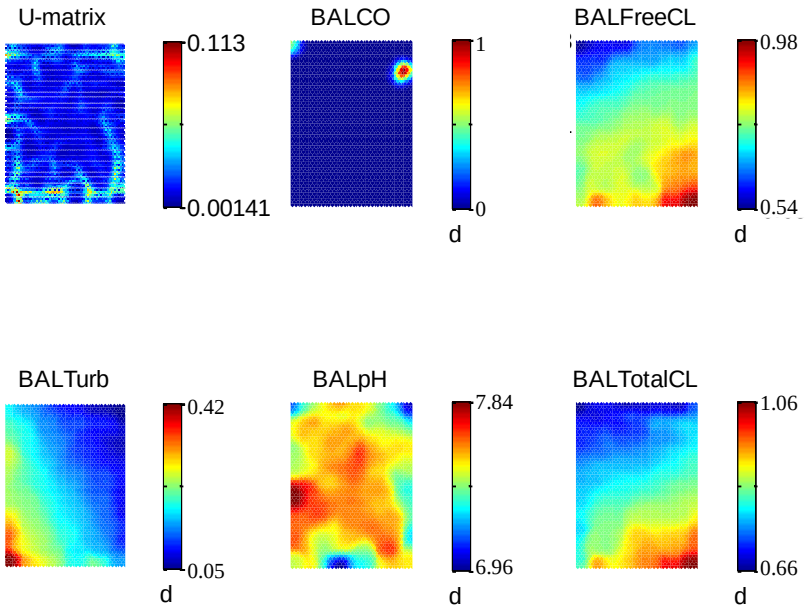

Figure 35: Balance Tank self-organising map for Strensham five month dataset.

Table 38: Strensham Contact Tank SOM results from the five month dataset and each of the failure weeks. Showing the range represented by the component plane and that corresponding to the indicator organisms. Coliforms = CFU 100 ml^{-1}; HPC22 and HPC37 = CFU ml^{-1}; free and total chlorine = mg l^{-1}; turbidity = NTU; pH = pH units.

CON	5 month				
	Range	CO	CO	EN	CO 1L (1)
Coliforms	0 - 1	-	0	0	0
HPC22	0 - 5	3 - 5	0	0	0
HPC37	0 - 17	0 - 6	0	0	0 - 1
FreeCL	0.47 - 2.27	1.67 - 2.27	1.76 - 2.01	1.98 - 2.10	1.90 - 2.12
TotalCL	1.46 - 2.27	2.00 - 2.27	1.84 - 2.11	1.99 - 2.21	1.99 - 2.18
Turbidity	0.05 - 0.46	0.19 - 0.32	0.12 - 0.29	0.11 - 0.19	0.08 - 0.25
pH	6.37 - 7.64	6.79 - 7.64	7.36 - 7.64	7.00 - 7.63	7.32 - 7.51

	CO 1L (2)	CO 1L (3)
Coliforms	0	0
HPC22	0	1 - 2
HPC37	0	0
FreeCL	1.85 - 2.08	1.83 - 2.01
TotalCL	1.93 - 2.20	1.93 - 2.11
Turbidity	0.07 - 0.17	0.10 - 0.19
pH	7.06 - 7.36	7.20 - 7.46

Table 39: Strensham Balance Tank SOM results from the five month dataset and each of the failure weeks. Showing the range represented by the component plane and that corresponding to the indicator organisms. Coliforms = CFU 100 ml^{-1}; free and total chlorine = mg l^{-1}; turbidity = NTU; pH = pH units.

BAL	5 month				
	Range	CO	CO	EN	CO 1L (1)
Coliforms	0 - 1	-	0	0	0
FreeCL	0.54 - 0.98	0.54 - 0.83	0.65 - 0.87	0.72 - 0.81	0.74 - 0.82
TotalCL	0.66 - 1.06	0.66 - 0.79	0.76 - 0.94	0.79 - 0.89	0.81 - 0.86
Turbidity	0.05 - 0.42	0.05 - 0.17	0.16 - 0.24	0.11 - 0.26	0.08 - 0.31
pH	6.96 - 7.84	6.96 - 7.55	7.44 - 7.84	7.42 - 7.67	7.56 - 7.84

	CO 1L (2)	CO 1L (3)
Coliforms	0	0
FreeCL	0.73 - 0.87	0.66 - 0.82
TotalCL	0.86 - 0.95	0.74 - 0.89
Turbidity	0.05 - 0.19	0.08 - 0.20
pH	7.26 - 7.52	7.43 - 7.63

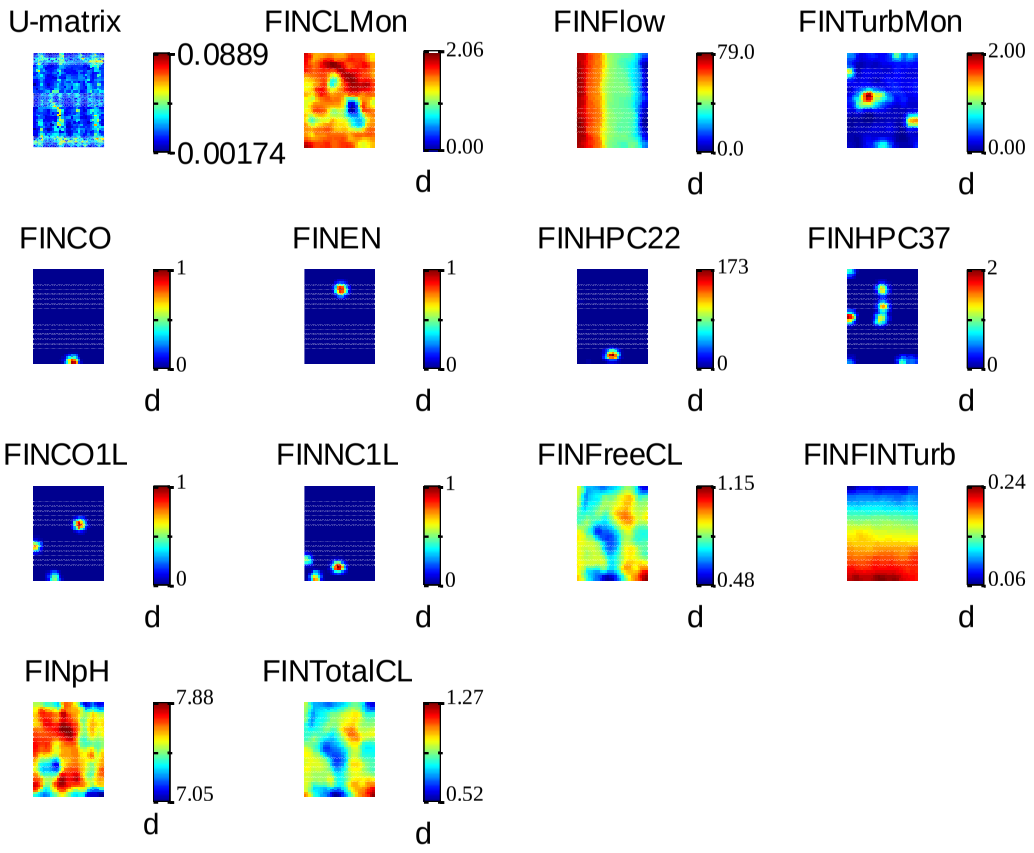

Figure 36: Final water self-organising map for Strensham five month dataset.

Table 40: Strensham Final water SOM results from the five month dataset and each of the failure weeks. Showing the range represented by the component plane and that corresponding to the indicator organisms. Monitor free chlorine = mg l^{-1}; monitor turbidity = NTU; flow = ML d^{-1}; coliforms and Enterococci = CFU 100 ml^{-1}; HPC22 and HPC37 = CFU ml^{-1}; coliforms 1 L and non-coliforms 1 L = CFU L^{-1}; free and total chlorine = mg l^{-1}; turbidity = NTU; pH = pH units.

Final	5 month				CO		EN	
	Range	CO	EN	CO 1L	Range	CO	Range	EN
FreeCL (Monitor)	0.00 - 2.06	1.37 - 2.06	0.69 - 2.06	0.69 - 2.06	0.73 - 1.11	0.73 - 0.86	0.72 - 0.88	0.77 - 0.83
Flow	0.0 - 79.0	26.3 - 52.7	26.3 - 52.7	26.3 - 79.0	24.8 - 78.7	42.8 - 60.7	18.1 - 64.2	48.8 - 64.2
Turbidity (Monitor)	0.00 - 2.00	0.67 - 1.33	0.00 - 0.67	0.00 - 0.67	0.00 - 2.00	0.00 - 0.67	0.03 - 0.24	0.03 - 0.10
Coliforms	0 - 1	-	0	0	0 - 1	-	0	0
Enterococci	0 - 1	0	-	0	0	0	0 - 1	-
HPC22	0 - 173	0 - 173	-	0	0 - 5	0	0	0
HPC37	0 - 2	0	1	0	0	0	0	0
Coliforms 1L	0 - 1	0	0	-	0	0	0	0
Non-coliforms 1L	0 - 1	0	0	0	0 - 1	0	0	0
FreeCL	0.48 - 1.15	0.48 - 0.70	0.70 - 0.93	0.48 - 0.93	0.48 - 0.87	0.48 - 0.61	0.63 - 0.87	0.63 - 0.71
TotalCL	0.52 - 1.27	0.52 - 0.77	0.77 - 1.02	0.52 - 1.02	0.52 - 0.94	0.80 - 0.94	0.74 - 0.94	0.87 - 0.94
Turbidity	0.06 - 0.24	0.18 - 0.24	0.12 - 0.18	0.12 - 0.24	0.18 - 0.24	0.22 - 0.24	0.11 - 0.19	0.16 - 0.19
pH	7.05 - 7.88	7.33 - 7.60	7.60 - 7.88	7.33 - 7.88	7.38 - 7.67	7.38 - 7.48	7.54 - 7.75	7.68 - 7.75

	CO 1L (1)		CO 1L (2)		CO 1L (3)	
	Range	CO 1L	Range	CO 1L	Range	CO 1L
FreeCL (Monitor)	0.69 - 1.03	0.69 - 0.80	0.79 - 0.96	0.79 - 0.85	0.27 - 1.00	0.27 - 0.51
Flow	24.3 - 77.5	59.8 - 77.5	25.3 - 69.6	54.8 - 69.6	0.0 - 78.4	0.0 - 26.1
Turbidity (Monitor)	0.03 - 0.19	0.03 - 0.08	0.00 - 2.00	0.00 - 0.67	0.00 - 2.00	0.67 - 1.33
Coliforms	0	0	0	0	0	0
Enterococci	0	0	0	0	0	0
HPC22	0	0	0	0	0	0
HPC37	0	0	0	0	0	0
Coliforms 1L	0 - 1	-	0 - 1	-	0 - 1	-
Non-coliforms 1L	0	0	0 - 1	0	0	0
FreeCL	0.48 - 0.78	0.48 - 0.58	0.65 - 0.85	0.65 - 0.72	0.66 - 0.84	0.78 - 0.84
TotalCL	0.52 - 0.84	0.73 - 0.84	0.78 - 0.91	0.87 - 0.91	0.80 - 0.90	0.87 - 0.90
Turbidity	0.14 - 0.24	0.14 - 0.17	0.07 - 0.19	0.15 - 0.19	0.08 - 0.22	0.08 - 0.13
pH	7.36 - 7.64	7.36 - 7.45	7.38 - 7.56	7.50 - 7.56	7.44 - 7.59	7.44 - 7.49

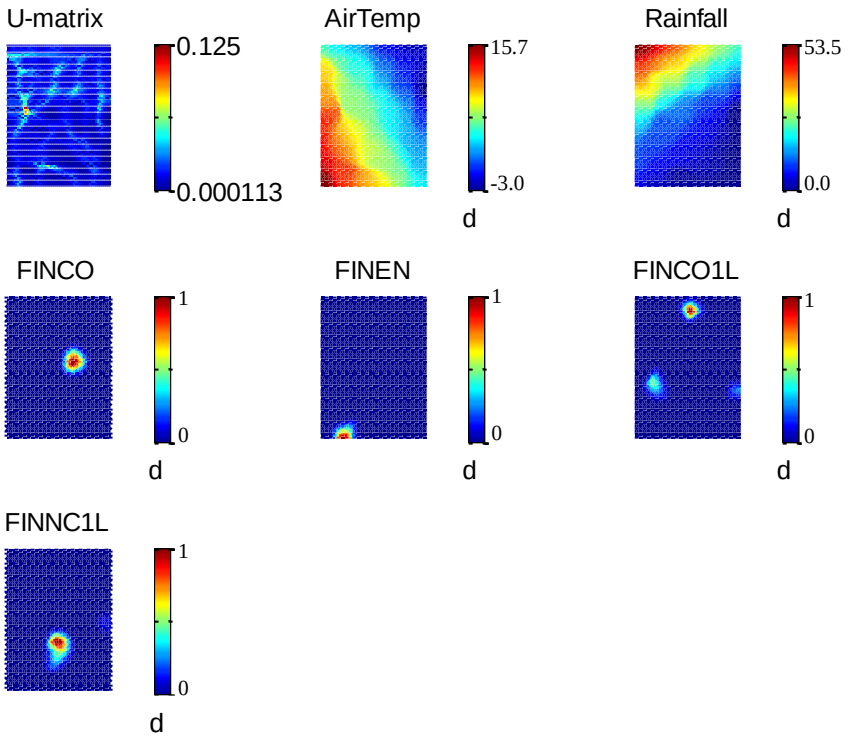

Figure 37: Rainfall and air temperature self-organising map for Strensham five month dataset.

Table 41: Strensham local rainfall and air temperature SOM results from the five month dataset and each of the failure weeks. Showing the range represented by the component plane and that corresponding to the indicator organisms. Rainfall = mm week^{-1}; air temperature = °C; coliforms and Enterococci = CFU 100 ml^{-1}; 1 L coliforms = CFU L^{-1}.

Climate	5 month				CO	
	Range	CO	EN	CO 1L	Range	CO
AirTemp	-3.0 - 15.7	3.2 - 9.5	9.5 - 15.7	-3.0 - 15.7	-0.6 - 6.8	-0.6 - 1.9
Rainfall	0.0 - 53.5	0.0 - 17.8	0.0 - 17.8	0.0 - 53.5	0.6 - 13.9	9.5 - 13.9
	EN		CO 1L (1)		CO 1L (2)	
	Range	EN	Range	CO 1L	Range	CO 1L
AirTemp	7.4 - 11.2	9.9 - 11.2	-0.6 - 6.2	3.9 - 6.2	1.0 - 3.3	2.5 - 3.3
Rainfall	0.8 - 5.2	3.7 - 5.2	9.1 - 43.6	32.1 - 43.6	0.0 - 3.6	?
	CO 1L (3)					
	Range	CO 1L				
AirTemp	5.4 - 12.6	10.2 - 12.6				
Rainfall	6.6 - 10.5	6.6 - 7.9				

6.3.2.12. Climate and Final bacteria SOMs

In the five month dataset, the coliform failure corresponded to low rainfall (0.0 – 17.8 mm week^{-1}) and medium air temperature (3.2 – 9.5 °C) (Figure 37 and Table 41). The Enterococcus detection also occurred with low rainfall (0.0 – 17.8 mm week^{-1}), but when the air temperature was high (9.5 – 15.7 °C). The three 1 L coliform failures

correlated with the full range of both rainfall (0.0 – 53.5 mm week^{-1}) and air temperature (-3.0 – 15.7 mm week^{-1}).

With the exception of the week of the coliform detection all bacteriological failures occurred when the air temperature was high for that period (ranging from 2.5 to 12.6 °C); during the week of the coliform failure the air temperature range was -0.6 – 1.9 °C (Table 41). The coliform, Enterococcus and first 1 L coliform failures occurred when rainfall was high (between 3.7 and 43.6 mm week^{-1}). The third 1 L coliform correlated with low rainfall for that week (6.6 – 7.9 mm week^{-1}) (Table 41). The component plane for rainfall for the second 1 L coliform detection did not show a range as identified in the input data and therefore could not be interpreted (see Appendix 3). These results suggest that rainfall has an impact on bacteriological compliance, but that there is not a clear relationship with rainfall intensity.

6.3.2.13. Coliforms

Figure 38 shows the change in coliform numbers through Strensham WTW. It demonstrates that coliform numbers upstream of the RGF Filter Blocks differed between the coliform and 1 L coliform detections. The coliform detection correlated with the following coliform counts: medium Raw water (7,042 – 14,021 CFU 100 ml^{-1}), high Settlement Tank A (513 – 760 CFU 100 ml^{-1}), high Tank B (867 – 1,300 CFU 100 ml^{-1}), high Tank C (480 – 720 CFU 100 ml^{-1}) and medium Tank D (340 – 670 CFU 100 ml^{-1}). The 1 L coliform detections were found under the following coliform counts: low Raw water (63 – 7,042 CFU 100 ml^{-1}), medium Settlement Tank A (267 – 513 CFU 100 ml^{-1}), low Tank B (0 – 433 CFU 100 ml^{-1}), low Tank C (0 – 240 CFU 100 ml^{-1}), and low Tank D (10 – 340 CFU 100 ml^{-1}). The downstream counts for the coliform and 1 L coliform failures were: medium Filter Block ABC (86 – 135 CFU 100 ml^{-1}), medium Block D (108 – 240 CFU 100 ml^{-1}), low GAC (33 – 67 CFU 100 ml^{-1}), low Contact Tank (0 – 1 CFU 100 ml^{-1}), and low Balance Tank (0 – 1 CFU 100 ml^{-1}).

These results show that the coliform failures were never associated with high Raw water coliforms, which is contrary to expectation. This is of note because Figure 38 shows that the high Raw water coliforms corresponded to high coliforms from Filter Blocks ABC and D. It is interesting that these regions of high coliform loading were not observed across any of the Settlement Tanks, or beyond the RGFs.

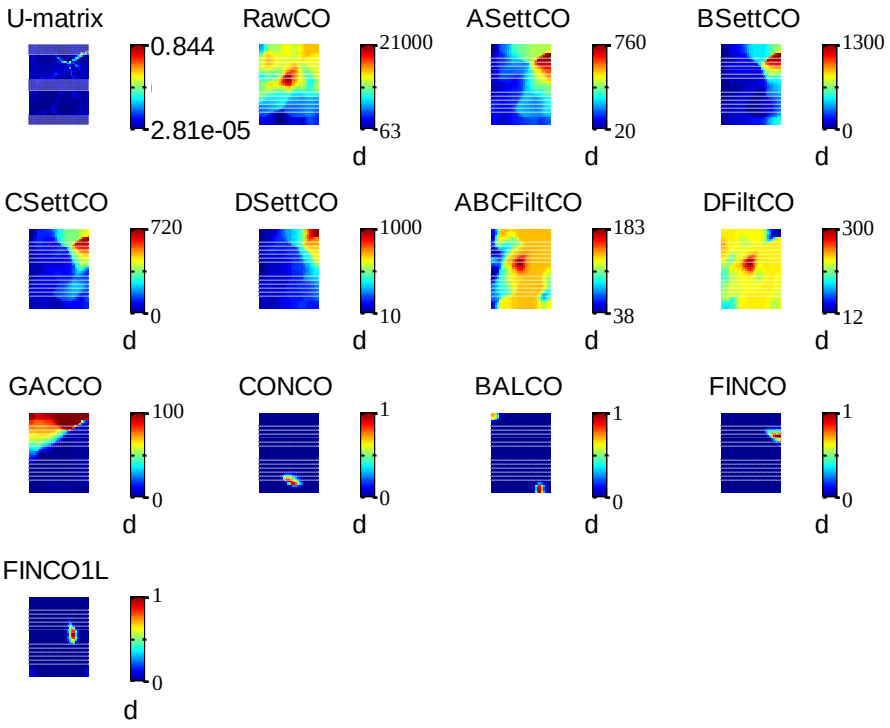

Figure 38: Coliforms self-organising map for Strensham five month dataset.

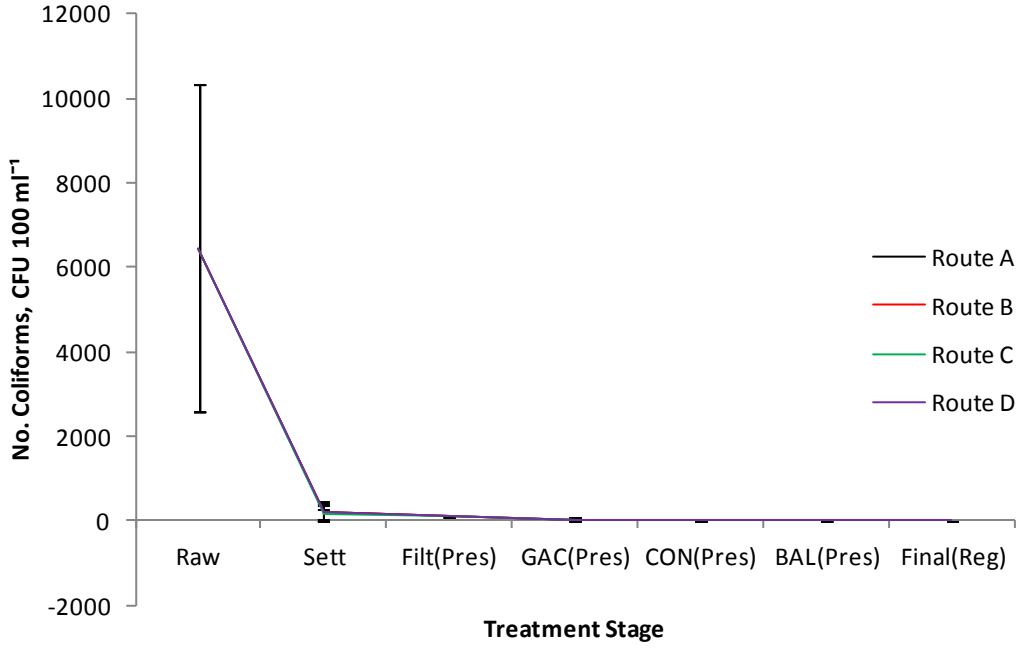

Figure 39: Mean removal of coliforms through Strensham WTW. n = 61 (Raw), 61 (ASett), 60 (BSett, CSett, DSett), 61 (ABCFilt, DFilt), 71 (GAC), 107 (CON), 106 (BAL) and 151 (Final); standard deviation shown. Routes: A = ASett and ABCFilt; B = BSett and ABCFilt; C = CSett and ABCFilt; and, D = DSett and DFilt.

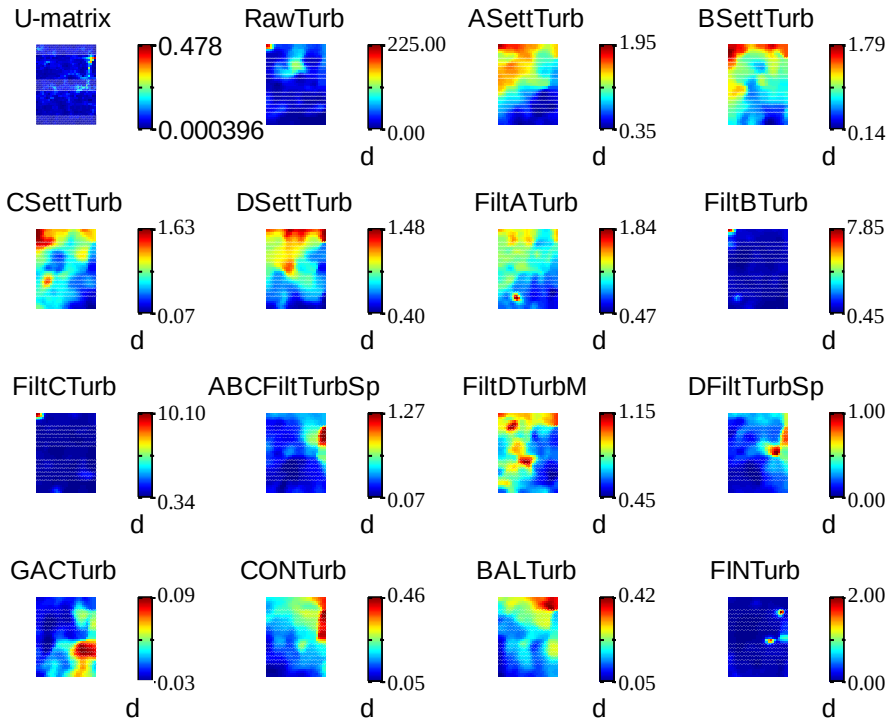

Figure 40: Turbidity self-organising map for Strensham five month dataset.

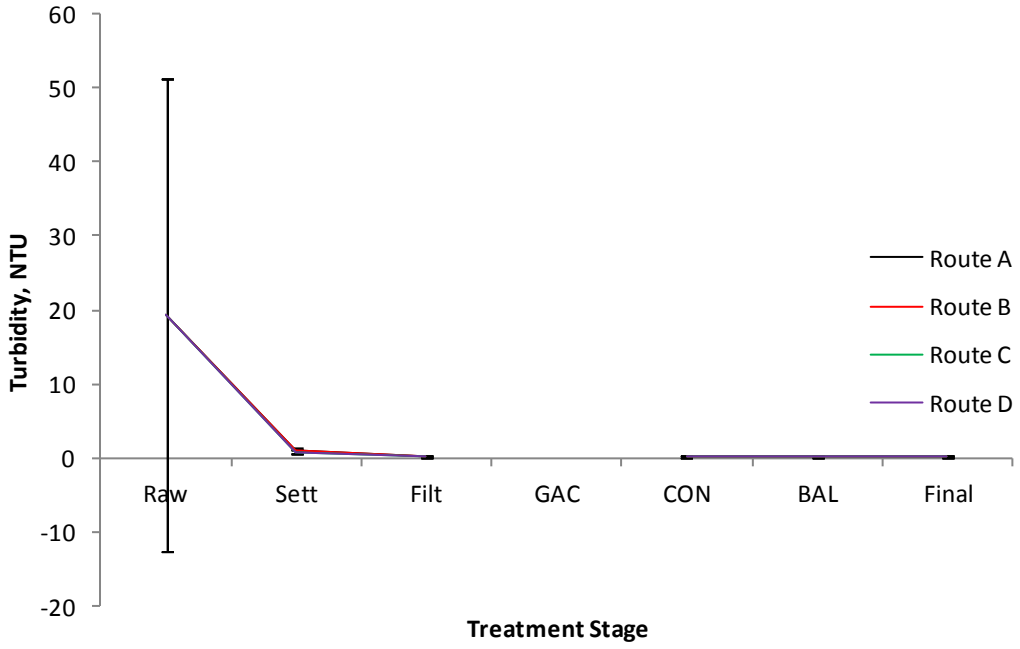

Figure 41: Mean removal of turbidity through Strensham WTW. n = 61 (Raw), 62 (ASett), 61 (BSett, CSett, DSett, ABCFilt, DFilt), 0 (GAC), 107 (CON), 107 (BAL) and 151 (Final); standard deviation shown. Routes: A = ASett and ABCFilt; B = BSett and ABCFilt; C = CSett and ABCFilt; and, D = DSett and DFilt.

To determine the effectiveness of the treatment processes, the mean coliform removal by each was calculated using all the raw data from the five month dataset and is shown graphically in Figure 39. After the Settlement Tanks, 1.46- – 1.68-log of coliforms had been removed[3]; 1.84-log were removed following the RGF Filter Blocks; the GAC Filters increased removal to 2.34-log and the Contact Tank and Final cumulative removal rates were 6.00-log; however, the Balance Tank saw a slight decrease in removal to 5.52-log of Raw water coliforms.

6.3.2.14. Turbidity

Turbidity, *E. coli*, non-coliforms and pH were all monitored throughout Strensham WTW. The cross-correlation results showed that Contact Tank, Balance Tank and Final turbidity correlated with Final coliforms and Final 1 L coliforms. Therefore, a SOM of through-plant turbidity was generated in order to understand the relationship of upstream turbidity to that of the latter treatment stages. Turbidity results frequently featured with bacteriological parameters in the cross-correlations that were both positive and <24 h. This section looks at the relationship among the turbidity values from Raw to Final water. The turbidity SOM (Figure 40) shows that high Raw turbidity (150.00 – 225.00 NTU) correlated with high monitor turbidity from Filter Blocks B and C (5.38 – 7.85 NTU and 6.85 – 10.10 NTU, respectively). It also shows that Filter Blocks A and D have turbidity profiles that are similar in pattern to their preceding Settlement Tanks; unlike Blocks B and C. None of Blocks A, B or C had component planes that agreed with the combined Filter Block ABC pattern and this disagreement was also noted between spot-sampled and monitored Block D turbidities. High Final monitor turbidity (1.33 – 2.00 NTU) correlated with high spot-sampled turbidities from Filter Blocks ABC and D (0.87 – 1.27 NTU and 0.67 – 1.00 NTU, correspondingly), but do not appear to be related to high turbidities from subsequent processes.

Figure 41 shows the removal of turbidity through Strensham WTW. It is based on spot-sampled data from the five month dataset, and thus there are no results for GAC Filters. Between 1.30- and 1.42-log of turbidity was removed by the Settlement Tanks; 1.87-log following RGF Filtration; 2.01-log by the Contact Tank; 2.03-log following the Balance Tank; and 2.10-log had been removed by the Final monitoring point.

[3] Log removal = $\log_{10}(100/(100 - X))$, where X = percent removal out of 100
E.g. 96.53 % removal: $\log_{10}(100/(100 - 96.53))$ = 1.46-log

6.3.3. Results summary

6.3.3.1. Cross-correlation

Rainfall impacted Raw water turbidity and bacteriological quality, including coliform counts. Increasing air temperature led to increasing Raw water temperature; changes in Raw water temperature did not impact coliforms or Enterococci. Rainfall did not consistently affect monitor turbidity across the four Filter Blocks.

Settlement Tank coliforms (and *E. coli* and non-coliforms) increased with rainfall. The impact of rainfall on turbidity was less apparent by the outlet of the Settlement Tanks. Coliform numbers coming off the RGF Filter Blocks increased with rainfall, as did *E. coli* and non-coliforms. GAC Filter coliforms were impacted by rainfall. Monitoring rainfall on-site could provide a warning of coliforms passing through the GAC Filters. There was no impact of rainfall on bacteriological parameters beyond this treatment stage.

Changes in Raw water coliforms impacted settled and filtered coliforms. An increase in Raw water coliforms led to an increase in coliforms from the GAC Filters, but not from treatment processes further downstream; they also impacted downstream *E. coli*. Coliforms and non-coliforms in the Raw water increased after Raw *E. coli* numbers peaked and entered a decline. Raw *E. coli* were also shown to impact downstream *E. coli* counts but it was observed that they were effectively controlled by Strensham's disinfection strategy.

Raw water turbidity consistently affected the bacteriological quality of the Raw water and of Filter Blocks ABC and D. It always affected the turbidity of water leaving Settlement Tanks A, B and C, but this was not the case for Tank D. Raw water turbidity was a factor in the turbidity measured at Filter Blocks ABC and D and Final water, both monitor and spot-sampled.

Coliforms leaving the Settlement Tanks consistently affected coliforms from the Filter Blocks and were observed, on occasion, to impact the Final monitoring point. This was true for Settlement Tank *E. coli* and non-coliforms as well. Settled non-coliforms impacted Final coliforms only from Tank B.

Settlement Tank turbidity consistently impacted settled and Filter Block bacteriological quality and affected RGF Filter, Contact Tank, Balance Tank and Final turbidity.

Settled pH affected bacteriological quality from the GAC Filters.

Turbidity from Settlement Tanks B, C and D affected Final 1 L coliforms.

Filtered coliforms had a consistent impact on the other bacteriological parameters from the Filter Blocks. Filter Block D coliforms and non-coliforms were always correlated with GAC Filter coliforms.

E. coli from Filter Blocks ABC and D impacted Final coliforms and 1 L coliforms. Non-coliforms from Block ABC also affected coliform compliance.

Filter Block D spot-sampled turbidity impacted GAC bacteriological parameters and Final 1 L coliforms. Similar correlations were not observed for Block ABC turbidity. The pH from both Filter Blocks impacted downstream bacteriological quality and pH from Block D affected coliform compliance. Monitor turbidity from all four Filter Blocks correlated with Filter Block coliforms, but not with GAC coliforms. The monitor turbidity from Blocks A and D and the GAC Filters correlated with Contact Tank turbidity; monitor turbidity from Filter Block D and the GAC Filters correlated with Balance Tank turbidity.

GAC Filter coliforms impacted Final coliforms and 1 L coliforms. GAC Filter *E. coli* and non-coliforms affected GAC Filter coliforms. GAC Filter *E. coli* also impacted Final 1 L coliforms.

Contact Tank, Balance Tank and Final (monitor) turbidity all impacted Final coliforms and 1 L coliforms.

The third 1 L coliform failure was impacted by Final free and total chlorine concentrations.

The cross-correlation analyses were unable to provide any insight into the Enterococcus failure.

6.3.3.2. Self-Organising Maps

High coliforms in the Raw water (3,500 – 11,486 CFU 100 ml^{-1}) occurred with low *E. coli* (533 – 1,567 CFU 100 ml^{-1}), low-medium non-coliforms (2,472 – 10,000 CFU 100 ml^{-1}), low-medium *C. perfringens* (260 – 686 CFU 100 ml^{-1}), low-high Enterococci (138 – 798 CFU 100 ml^{-1}), low turbidity (7.06 – 27.52 NTU), low-medium spot-sampled pH (7.16 – 7.96 pH units), medium monitor pH (7.67 – 7.93 pH units) and low-medium water temperature (5.1 – 14.6 °C).

Settlement Tank A high coliforms (105 – 650 CFU 100 ml^{-1}) correlated with low-medium *E. coli* (4 – 90 CFU 100 ml^{-1}), low-medium non-coliforms (71 – 370 CFU 100 ml^{-1}), low-high turbidity (0.35 – 1.34 NTU) and low-high pH (7.20 – 7.52 pH units). The occurrence of high coliforms from Settlement Tank B (95 – 1,300 CFU 100 ml^{-1}) corresponded to low *E. coli* (10 – 70 CFU 100 ml^{-1}), low-high non-coliforms (30 – 950 CFU 100 ml^{-1}), medium-high turbidity (0.66 – 1.49 NTU), and medium-high pH (7.27 – 7.52 pH units). Settlement Tank C high coliforms (81 – 530 CFU 100 ml^{-1}) were observed to correlate with low-medium *E. coli* (10 – 60 CFU 100 ml^{-1}), low non-coliforms (45 – 380 CFU 100 ml^{-1}), medium turbidity (0.62 – 0.92 NTU) and medium-high pH (7.31 – 7.65 pH units). High coliforms from Settlement Tank D (89 – 670 CFU 100 ml^{-1}) occurred with low *E. coli* (4 – 90 CFU 100 ml^{-1}), low non-coliforms (1 – 353 CFU 100 ml^{-1}), low-medium turbidity (0.46 – 0.99 NTU), and medium-high pH (7.26 – 7.60 pH units). Counts of *E. coli* were always less than for coliforms. With the exception of Settlement Tank B, non-coliforms remained below 380 CFU 100 ml^{-1}. Tank B had the greatest range of both coliform and non-coliform counts; the highest count of coliforms was twice that for the other three Settlement Tanks.

The failure weeks for the second and third 1 L coliform detections provided details of the conditions for high coliform counts from both sets of Filter Block data. From Block ABC, high coliform counts (90 – 100 CFU 100 ml^{-1}) corresponded to low *E. coli* (7 – 22 CFU 100 ml^{-1}), low-medium non-coliforms (62 – 100 CFU 100 ml^{-1}), low turbidity (0.17 – 0.24 NTU), and high pH (7.26 – 7.57 pH units). From Filter Block D high coliforms (87 – 100 CFU 100 ml^{-1}) were observed to occur with low *E. coli* (7 – 23 CFU 100 ml^{-1}), medium non-coliforms (70 – 100 CFU 100 ml^{-1}), low turbidity (0.10 – 0.18 NTU), and medium-high pH (7.24 – 7.50 pH units). Overall, high coliforms

occurred when *E. coli* counts were low, non-coliforms were low-medium, turbidity was low, and pH was medium-high.

The GAC Filters showed that high coliforms (1 – 8 CFU 100 ml^{-1}) corresponded to low *E. coli* (0 – 3 CFU 100 ml^{-1}), low non-coliforms (1 – 5 CFU 100 ml^{-1}) and high pH (7.06 – 7.29 pH units).

Results from the Contact Tank only showed coliforms in the five month dataset. This demonstrated that a count of 1 CFU 100 ml^{-1} correlated with high HPC22 (3 – 5 CFU ml^{-1}) and low HPC37 (0 – 6 CFU ml^{-1}), as well as high free and total chlorine (1.67 – 2.27 mg l^{-1} and 2.00 – 2.27 mg l^{-1}, respectively), medium turbidity (0.19 – 0.32 NTU) and medium-high pH (6.79 – 7.64 pH units).
Coliforms at the Balance Tank stage were also only recorded in the five month dataset. This showed that a count of 1 CFU 100 ml^{-1} correlated with low-medium free chlorine (0.54 – 0.83 mg l^{-1}), low total chlorine (0.66 – 0.79 mg l^{-1}), low turbidity (0.05 – 0.17 NTU) and low-medium pH (6.96 – 7.55 pH units).

During the week of the coliform failure the following Final water conditions correlated with the coliform detection in the Final water: low-medium monitor free chlorine (0.73 – 0.86 mg l^{-1}); low spot-sampled free chlorine (0.48 – 0.61 mg l^{-1}) and medium spot-sampled total chlorine (0.80 – 0.94 mg l^{-1}); medium-high flow (42.8 – 60.7 ML d^{-1}); low monitor turbidity (0.00 – 0.67 NTU) and high spot-sampled turbidity (0.22 – 0.24 NTU); and medium pH (7.38 – 7.48 pH units). No other bacteria were enumerated that week.

The detection of the Enterococcus coincided with: low-medium monitor free chlorine (0.77 – 0.83 mg l^{-1}) and spot-sampled free chlorine (0.63 – 0.71 mg l^{-1}); medium-high spot-sampled total chlorine (0.87 – 0.94 mg l^{-1}); medium-high flow (48.8 – 64.2 ML d^{-1}); low monitor turbidity (0.03 – 0.10 NTU) and medium-high spot-sampled turbidity (0.16 – 0.19 NTU); and high pH (7.68 – 7.75 pH units). No other bacteria were enumerated that week.

The SOM results for the weeks of the 1 L coliform detections showed that 1 L coliforms correlated with the following Final water conditions: low-medium monitor free chlorine (0.27 – 0.85 mg l^{-1}); low-medium free and total spot-sampled chlorines (0.48 –

0.84 mg l^{-1} and 0.73 – 0.91 mg l^{-1}, respectively); low-medium monitor turbidity (0.00 – 1.33 NTU) and low-high spot-sampled turbidity (0.08 – 0.19 NTU); low-high flow (0.0 – 77.5 ML d^{-1}); and medium pH (7.36 – 7.56 pH units).

These five bacteriological failures were detected under conditions of low-high air temperatures (-0.6 – 12.6 °C) and low-high rainfall (3.7 – 43.6 mm $week^{-1}$).

Final coliforms corresponded to medium Raw coliforms, high coliforms from Settlement Tanks A, B and C and medium coliforms from Tank D. The 1 L coliforms correlated with low Raw coliforms, medium Tank A coliforms and low coliforms from Tanks B, C and D. Both coliforms and 1 L coliforms were observed to occur with medium coliforms from Filter Blocks ABC and D, and low coliforms from GAC Filters, Contact Tank and Balance Tank.

The treatment process removed 6.00-log of Raw coliforms and 2.10-log of Raw turbidity.

6.4. Discussion

6.4.1. Comparison of the results from cross-correlation and Self-Organising Maps

Cross-correlation aims to provide a time lag between the changes in two selected parameters. The way these results have been assessed in this method means that only the strongest correlations were considered viable. This tool cannot determine whether a rise or a fall in the first parameter affected the second. The data were plotted and the graphs scrutinised to answer this (where possible); this information is necessary to inform operators' responses to changes in water quality. The SOM analysis incorporates all the data and shows how one parameter relates to another; it has no time element. The use of both methods was intended to provide useful information to operators for the management of bacteriological quality of treated water at Strensham WTW.

6.4.1.1. Rainfall

In Chapter 3 it was shown that when comparing the incidence of bacteriological failures across the STW region with average rainfall for the area there was only a weak positive correlation. It seemed unlikely that at a more specific scale a stronger relationship would be observed. The cross-correlation analysis of the Strensham dataset demonstrates that Raw water quality is impacted by rainfall: coliforms, *E. coli* and non-

coliforms increase with increasing rainfall, and pH changes inversely. All the failures (including the Enterococcus detection) occurred during weeks when rainfall was > 0.0 mm week^{-1}.

The SOMs showed that higher Raw water coliforms were associated with low Raw water turbidity and medium monitor pH. The cross-correlation results demonstrate that short-term increases within these ranges corresponded with increased coliform counts. These results concur with the observations made by Schets *et al.* (2005) and Pitkänen *et al.* (2008). Rainfall did not consistently impact the quality of water leaving the Settlement Tanks and RGF Filter Blocks. There was evidence that rainfall impacted the bacteriological quality of water from the GAC Filters. Interestingly, rainfall sporadically impacted the turbidity leaving the GAC Filters: during the weeks of the coliform, Enterococcus and third 1 L coliform failures.

6.4.1.2. Turbidity

The cross-correlation results showed that an increase in Raw turbidity was a factor in the presence of high numbers of Raw water coliforms and the SOMs show that the effective range across the failure weeks was 5.22 – 27.52 NTU. The overall range identified from the five month dataset was 0.00 – 225.00 NTU; thus the failure weeks were affected by turbidities in the lowest 12 % of the range. The Raw water SOM shows that these low values were the norm across the investigation period.

Turbidity removal of 1 – 1.3-log is seen as the target for conventional Settlement Tanks (Parsons and Jefferson, 2006), and the ones at Strensham consistently achieved >1.3-log removal. This shows that the Settlement Tanks were performing effectively across the five failure weeks.

RGF Filter turbidity cross-correlations showed that Settlement Tank A turbidity impacted RGF Filter Block A turbidity, and Tank D impacted Block D too. Turbidity values from Blocks A and D were observed to impact turbidity leaving the GAC Filters. The cross-correlations focusing on spot-sampled data suggested that Blocks A, B and C did not behave in the same way. This analysis of turbidity corroborates that proposition. However, it was RGF Filter Blocks C and D that had monitor turbidities which impacted Final 1 L coliforms. The process stream that includes Settlement Tank D and

Filter Block D is newer than the A, B and C streams. These results suggest that filter performance across all Filter Blocks is currently impaired.

GAC Filter turbidity consistently impacted turbidity from the Contact and Balance Tanks. Contact Tank turbidity always correlated with chlorine concentrations at this treatment stage, and from the Balance Tank and Final. Likewise, Balance Tank turbidity always affected Final turbidity. This suggests that increased GAC Filter turbidity could affect the disinfection efficacy of downstream processes at Strensham WTW, as indicated by LeChevallier *et al.* (1984), Camper *et al.* (1986), LeChevallier *et al.* (1988a), Stewart *et al.* (1990) and Hammes *et al.* (2008).

The cross-correlations showed that Final monitor turbidity affected Final monitor chlorine during all failure weeks, but was not consistently linked to the bacteriological failures. The SOMs show that these turbidities were low during the weeks when coliforms, 1 L coliforms and Enterococci were detected. The Final results broadly concur with those for Mythe WTW (Chapter 5), except for the anomalous turbidity spike of 1.33 NTU during the week of the third 1 L coliform failure. The Strensham (and Mythe) case studies were initiated because the Exception Reports could not identify causes for the failures, which means that the WTW was deemed to be performing within normal operating ranges. High turbidity was not an important factor in the non-compliances at Strensham.

6.4.1.3. Chlorination

The cross-correlation results showed only two connections between chlorine concentration and the presence of coliforms in the Final water: Contact Tank total chlorine and Final monitor free chlorine. The SOM results showed that during the weeks of the coliform, Enterococcus and 1 L coliform failures the Final monitor and spot-sampled free chlorines were always low-medium. The Drinking Water Safety Plan (DWSP) for Strensham shows that chlorine is dosed at the Contact Tank to 1.8 mg l^{-1}; the expected dose before de-chlorination is 1.5 mg l^{-1} and the target Final concentration is 0.7 mg l^{-1}. The monitor free chlorine concentration was above 0.73 mg l^{-1} for the coliform, Enterococcus and second 1 L coliform failures. The lower end of the range for the first 1 L coliform failure was 0.69 mg l^{-1}; the range for the third 1 L coliform failure was impacted by the power cut and WTW shut down (0.27 – 0.51 mg l^{-1}). The trend shows that the chlorine concentration returned to > 0.7 mg l^{-1} after the event. The

DWSP gives the ideal pH for chlorination at Strensham: 7.2 pH units. The range that was apparent across the weeks for the coliform and 1 L coliform detections was 7.06 – 7.29 pH units. Since high pHs encourage the dissociation of HOCl to OCl^- (the latter being a weaker disinfectant), the pH is unlikely to have impacted disinfection efficacy on these occasions. The monitor chlorine results differ from those for spot-sampling and highlight the importance of such tools for the management of drinking water quality: their higher sampling frequency enables them to identify treatment flaws more quickly.

Research by Mahto and Goel (2008), Francisque *et al.* (2009) and Wang *et al.* (2009) suggested that a residual of 0.3 mg l^{-1} is sufficient to protect against re-growth in the distribution system. In the cases of the Strensham failures this finding does not hold, as the indicator bacteria recovered between the Contact Tank and Final sampling points despite 'adequate' chlorine concentrations. The water temperature was consistently below the 15 °C that the World Health Organization (2004) identified as a risk factor. The low water temperature could have reduced the disinfection efficacy at Strensham WTW.

6.4.1.4. Coliforms

The cross-correlation results showed that high numbers of coliforms leaving the Settlement Tanks, Filter Blocks and GAC Filters correlated with the detection of Final coliforms. This indicates that Strensham WTW is not optimised to treat water with a high bacteriological load suspended in relatively low turbidity Raw water.

Turbidity leaving the GAC Filters was observed to be low during the weeks of failure, but the coliform, *E. coli* and non-coliform counts were high. This suggests that when low turbidity water is passing through and released from the GAC Filters bacteria are not effectively captured in the media. On average across the five month period, the coliform removal at this treatment stage was 2.34-log %. Coliform removal increased to 6.00-log by the time water left the Contact Tank. However, the average number of coliforms increased between the Contact Tank and Final. This shows that a) disinfection in the Contact Tank is not consistently killing coliforms and b) conditions in the Balance Tank can enable injured coliforms to recover from the effects of chlorination.

Biofilm growth is a potential reason for the recovery of coliforms after the Contact Tank. Chlorine can be consumed by biofilms (Levi, 2004; Al-Jasser, 2007) and bacteria

that form part of the biofilm are able to resist disinfectants, even at target concentrations (LeChevallier *et al.*, 1988a; Berry *et al.*, 2006; Deborde and von Gunten, 2008). The methods by which this resistance is achieved are not fully known, but Szewzyk *et al.* (2000), Berry *et al.* (2006) and Bichai *et al.* (2008) postulate the following: evolved disinfection resistance as a result of past treatment failures, protection due to the extracellular polymeric substances, ability to exist in a viable, but non-culturable state, and harbouring by amoebae and protozoa. The internal condition of the Contact and Balance Tanks and Final monitoring sample point is unknown, but should be investigated for biofilms.

The Exception Report for this series of failures shows that the coliform and 1 L coliform detections were for *Enterobacter cloacae*. This bacterium demonstrates both thermotolerant (faecal) and non-thermotolerant (environmental) characteristics (Standing Committee of Analysts, 2009). *E. cloacae* has been observed to adsorb to the surfaces of particulates in laboratory tests, including GAC particles and biofilms (Camper *et al.*, 1986; Herson *et al.*, 1987).

6.4.1.5. Enterococci

The paucity of Raw water and through-plant data for Enterococci means it is not possible to determine what caused the failure.

6.4.2. Raw data and data manipulation

The availability of through-plant data and climate data for Strensham WTW has enabled this research to build on the analyses of Mythe WTW data.

The inclusion of more monitor data in this assessment was intended to elucidate the subtle changes in chlorine, turbidity, pH and flow. However, there were several anomalies. The majority of these were recorded in the five month dataset: Final monitor chlorine concentration of 0.0 mg l^{-1}; turbidity range of 0.00 – 2.00 NTU (which recurred in the weeks of the coliform and second and third 1 L coliform failures); a repeated RGF Filter Block turbidity of 159.91 NTU; GAC Filter pH of 2.0 pH units. The values, for example the RGF Filter Block turbidities, did produce cross-correlation results. It also impacted the turbidity SOM: low turbidity became 0.00 – 52.77 NTU. This suggests that a screening process should have been employed to remove obviously erroneous data before interpolation. In this case, the very high RGF Filter turbidities and

very low GAC Filter pHs should have been deleted. Furthermore, it is important to understand maintenance activities that occur at WTWs, to avoid attributing a failure to the consequence of, for example, cleaning a turbidity monitor.

The raw data in this case study were sampled over a variety of time-scales from once per week for the rainfall data to every minute for the monitor chlorine and turbidity. As with the Mythe data analysis, the processes of interpolating or zero-padding means that a large proportion of the analysed dataset is assumed data. This increases the importance of incorporating a screening step in future data analyses.

Rainfall raw data was provided as mm week^{-1}. In this method the rainfall data were extrapolated without any prior amendment. This means that, for example, when the total rainfall for the first week was 10 mm and for the second, 20 mm, the extrapolation assumes that these values are per minute (to fit the template time parameter) and changing on a linear scale between the first and second weeks' measurements. This is inaccurate and the values should have been divided among the time slots available. Whilst this has not affected the loci of peaks and troughs in the resultant dataset, it does mean that the amounts of rainfall recorded against the failures should be used with caution.

The use of cross-correlation was of some value, but it produced a largely false impression of the working of the WTW in suggesting that many upstream processes or water conditions have no impact downstream. It is probable that this is because the selection method focuses only on the tallest XCORR peaks where the correlation is strongest, rather than being able to record more subtle changes in the data. It may be more useful to adjust the data selection algorithm to ignore values that are clearly erroneous. This would avoid the results being dominated by values that are likely to be monitor faults and could thus generate more useful lag times. At present, this tool is not useful to operators and it cannot provide an indication of how Parameter 1 changed with respect to Parameter 2. This information needs to be found by referring to the data trends.

6.4.3. Operational value of the results from the two methods

As with the Mythe datasets, cross-correlation and SOMs were useful for identifying relationships among a variety of water quality parameters. Cross-correlation generates a

time lag based on the strongest correlation coefficient, but the tendency for qualifying results to be 0 h simply highlights the normal variability of water quality parameters. Correlations with coliform data were observed at the five month and weekly time-scales. The SOMs allow the correlation of more than two parameters and expand upon the relationships identified in the cross-correlations. This series of datasets has shown that in order for such tools to be reliably employed by operators there must be a screening process to remove erroneous data points.

The outcomes of this research suggest that raised numbers of bacteria leaving the GAC Filters and the presence of coliforms in the Balance Tank encouraged the failures. These failures were detected despite chlorine in the Contact Tank being between 1.76 mg l^{-1} and 2.12 mg l^{-1} (target 1.8 mg l^{-1}) and in the Balance Tank being 0.65 – 0.87 mg l^{-1} (target 0.7 mg l^{-1}); pH being 7.13 – 7.29 pH units (ideal pH, 7.2 pH units), post-GAC Filters; and Final turbidity ranging from 0.00 – 0.67 NTU. These failures may be due to biofilm growth in the Contact Tank, Balance Tank and/or Final monitoring point. Other indicator bacteria from the Final water were killed: there were no *E. coli* or *C. perfringens* recorded throughout the monitoring period.

This work has shown that the bacteriological failures were observed under conditions of low Raw and Final turbidity (5.22 – 27.52 NTU and 0.00 – 0.67 NTU, respectively) and adequate Contact Tank, Balance Tank and Final chlorine concentrations (>0.7 mg l^{-1}). It is possible to monitor these parameters on-line and to act upon any anomalous readings in a timely fashion. One of the main limitations of this research is the low sampling frequency for bacteriological parameters. This was especially notable for Enterococci where monitoring was conducted only monthly in the Raw water and never through-plant. Using current tools it is not possible to monitor on-line changes in bacteriological loading through the WTW. The low resolution of sampling also impacts the results derived from the analyses. Several of the time lags that were derived from the cross-correlations were for 20.0 – 23.9 h and these times will relate to the sampling intervals. In reality, the impacts of the other parameters may have been felt more strongly or negated if the sampling had been conducted at a different time. The sampling schedules lead to additional uncertainty in developing solutions to prevent indicator bacteria being detected in Final water.

6.5. Conclusions

This work has built on the results from the Mythe datasets. Cross-correlation and SOMs were used to determine whether on-line water quality monitoring data could be used to inform the root cause analysis of bacteriological failures identified during spot-sampling at Strensham WTW. It is the first time that these tools have been applied to bacteriological water quality from the raw water to the final monitoring point at a WTW. One five month dataset (1st January to 31st May 2013) was examined and the five failure weeks within it were extracted and analysed separately. There were detections of coliforms, Enterococci and 1 L coliforms over the five month period. It has been beneficial to observe the changes in water quality through Strensham WTW to help determine a root cause for the bacteriological failures at this site.

The cross-correlation analyses have shown that:

- Increased rainfall and decreased air and water temperatures correlated with raised turbidity and bacteriological counts in Raw water.
- Rainfall affected coliforms from the Settlement Tank, RGF Filter Blocks and GAC Filters.
- Rainfall did not consistently affect RGF Filter turbidity.
- Raw water turbidity consistently affected Raw water bacteriological parameters.
- Increasing numbers of Raw water coliforms resulted in raised numbers of coliforms from the Settlement Tank, RGF Filter Blocks and GAC Filters.
- Changes in the numbers of settled coliforms consistently correlated with the presence of coliforms in the RGF Filters; Settlement Tank coliforms sometimes affected coliforms in the Final water.
- Turbidity from Settlement Tanks B, C and D affected Final 1 L coliforms.
- Spot-sampled turbidity from RGF Filter Block D affected GAC bacteriological parameters and Final coliforms.
- RGF Filter Block and GAC monitor turbidity impacted turbidity from the Contact and Balance Tanks.
- GAC Filter coliforms impacted Final 1 L coliforms.
- Contact Tank, Balance Tank and Final (monitor) turbidity affected Final coliforms and Final 1 L coliforms.

The SOM results have provided the following fingerprints from the weeks of failure, focusing on numbers of coliforms through-plant (high coliform counts in parentheses, unless stated otherwise):

- Raw water (3,500 – 11,486 CFU 100 ml^{-1}): turbidity, 7.06 – 27.52 NTU; pH, spot-sampled and monitor, 7.16 – 7.96 pH units; water temperature 5.1 – 14.6 °C.
- Settlement Tanks (81 – 1,300 CFU 100 ml^{-1}): turbidity, 0.35 – 1.49 NTU; pH, 7.20 – 7.65 pH units.
- RGF Filter Blocks (87 – 100 CFU 100 ml^{-1}): turbidity, 0.10 – 0.24 NTU; pH, 7.24 – 7.50 pH units.
- GAC Filters (1 – 8 CFU 100 ml^{-1}): pH, 7.06 – 7.29 pH units.
- Contact Tank (1 CFU 100 ml^{-1}): turbidity, 0.19 – 0.32 NTU; pH, 6.79 – 7.64 pH units; free chlorine, 1.67 – 2.27 mg l^{-1}; total chlorine, 2.00 – 2.27 mg l^{-1}.
- Balance Tank (1 CFU 100 ml^{-1}): turbidity, 0.05 – 0.17 NTU; pH, 6.96 – 7.55 pH units; free chlorine, 0.54 – 0.83 mg l^{-1}; total chlorine, 0.66 – 0.79 mg l^{-1}.
- Final (1 CFU coliforms 100 ml^{-1}; 1 CFU Enterococci 100 ml^{-1}; 1 CFU coliforms 1 L^{-1}): monitor turbidity, 0.00 – 0.67 NTU (coliform and Enterococcus) and 0.00 – 1.33 NTU (1 L coliforms); spot-sampled turbidity, 0.08 – 0.24 NTU; pH, 7.36 – 7.75 pH units; monitor free chlorine, 0.73 – 0.86 mg l^{-1} (coliform and Enterococcus) and 0.27 – 0.85 mg l^{-1} (1 L coliforms); spot-sampled free chlorine, 0.48 – 0.84 mg l^{-1}; spot-sampled total chlorine, 0.73 – 0.94 mg l^{-1}; and flow, 42.8 – 64.4 ML d^{-1} (coliform and Enterococcus) and 0.0 – 77.5 ML d^{-1} (1 L coliforms).
- Temperatures of -0.6 – 12.6 °C and rainfall of 3.7 – 43.6 mm $week^{-1}$ were apparent during the failure weeks at Strensham.
- The SOMs also showed that Final coliforms correlated with medium Raw water coliforms, high coliforms from Settlement Tanks A, B and C and medium coliforms from Tank D. Conversely, Final 1 L coliforms corresponded to low Raw water coliforms, medium Settlement Tank A coliforms and low coliforms from Tanks B, C and D. Both Final coliforms and 1 L coliforms correlated with medium RGF Filter coliforms, and low coliforms from the GAC Filters, Contact Tank and Balance Tank.

An analysis of through-plant removal of coliforms and turbidity showed that 6.00-log of Raw water coliforms and 2.10-log of Raw turbidity were removed.

The analyses strongly suggest that the coliform failures were associated with the following findings:

- High numbers of bacteria passing through the GAC Filter;
- And/or, recovery of indicator organisms between the Contact Tank and the Final monitoring point.

It was not possible to find a reason for the Enterococcus failure. This was because Raw water monitoring was monthly, instead of every two to three days as for coliforms, and there was no through-plant monitoring for this parameter.

The research questions asked whether improved analysis of on-line and spot-sample data could be used to inform the root cause analysis of bacteriological failures and if weather phenomena impacted water quality. The analyses have shown that cross-correlation and SOMs enable a better understanding of the water treatment processes during periods of decreased bacteriological quality.

Cross-correlation has shown that rainfall impacts the bacteriological quality of raw water and that this impacts effluent quality from settlement tanks, RGF filters and GAC filters. These findings corroborate the outcomes of research by Schets *et al*. (2005) and Pitkänen *et al*. (2008) in demonstrating that rainfall impacts final water quality. They also confirm the findings outlined in Chapter 3 that there is not a lengthy time lag between rainfall events and their impacts on WTWs (as suggested by Curriero *et al.*, 2001). Rainfall has an indirect impact on the bacteriological compliance of final treated water, principally through affecting the microbiological loading on upstream treatment processes. However, as with the data analysis for Mythe WTW, the majority of cross-correlation results that were both positive and between 0 and 24 h were for 0 h. These values are not useful to operators as they do not allow a time lag in which to act to prevent a future failure. The fact that 0 h lags predominated in the Strensham WTW analyses, despite the presence of through-plant data, suggests that the method is not universally applicable to these WTWs datasets.

The use of SOMs at each stage in the WTW enabled an understanding of which factors correlated with high coliform counts throughout the WTW. These results are an improvement upon the work in Chapter 5. Analysing the water quality from each

treatment process in relation to the parameter of interest (in this case, coliforms) can enable targeted remedial work to develop more robust treatment.

This Chapter builds on the work from Chapter 5. It documents the first use of cross-correlation and SOMs for the analysis of through-plant bacteriological quality using spot-sampled and on-line monitoring data from a WTW. The results show that these tools can extract useful information from a large volume of data. They are also able to assist in the derivation of a failure cause where no obvious fault was identified in the initial root cause investigation.

6.6. Recommendations for the management of bacteriological quality at Strensham WTW

- It is advised that the GAC Filters be inspected and the media cleaned/regenerated, since they appear to harbour indicator bacteria, which are subsequently released.
- The Contact Tank, Balance Tank and Final sampling point should be inspected. Indicator bacteria are recovering between the Contact Tank and Final monitoring stage at the WTW. The inspection should include an assessment of biofilm growth within the Balance Tank, since *E. cloacae* has been found in biofilms.

6.7. Further work

- Rainfall impacts some of the treatment processes in a WTW and therefore has an indirect effect upon Final compliance. On-site monitoring of rainfall would improve the ability of operators to act upon changing water conditions. This work shows that rainfall results in high numbers of bacteria suspended in low turbidity water. Furthermore, there is scope for the development of chlorine doses and contact times that are related to Raw water risks as indicated by rainfall and/or Raw water turbidity.
- Before a similar analysis of compliance at downstream service reservoirs is conducted, it is important to have monitoring tools that more closely reflect bacteriological water quality. The work from Mythe and Strensham has shown that changes in turbidity and chlorine concentrations are not clearly related to the presence of indicator organisms in Final water. Such tools may include the use of on-line flow cytometry (or similar fluorescence methods) (Berney *et al.*, 2008; Hammes *et al.*, 2008) to identify changes in bacterial numbers – especially at through-plant locations, such as post-GAC Filters. This would enable the chlorine

dose or contact time to be increased to ensure a sufficient kill rate. At present, there are no flow cytometric tools that are able to specifically identify indicator bacteria or waterborne pathogens (Chapter 2).

7. Cost effectiveness of the research for Severn Trent Water[4]

7.1. Introduction

This research project has involved collaboration among Severn Trent Water (STW), the University of Sheffield and Imperial College London under the banner of the STREAM Programme. The STREAM Programme is part-financed by the Engineering and Physical Sciences Research Council. The project was commissioned to enable STW to better comply with water quality regulations for bacteriological parameters. To that end, they have made significant investment in the research. This Chapter explores the use of that money and considers whether STW have received a good return on their outlay.

7.2. Severn Trent Water's investment in this STREAM project

STW have invested £43,150 in this research project. The cost breakdown is as follows:

- STREAM Programme fees: £40,000 (paid to the University of Sheffield)
- Training and resources: £3,150

Figure 42: Tap rig designed and commissioned to investigate methods of protecting sample taps from environmental contamination.

A portion of the fees were ring-fenced by the University of Sheffield for purchasing equipment for the project and remunerating expenses. This amounted to £25,000 and approximately £9,000 remained unspent.

£180 was spent on an ESRI ArcGIS training course.

The original research plan for this project focussed on assessing ways of protecting taps from environmental contamination. It involved the design, construction and commissioning of an experimental rig at a service reservoir in Derby (Figure 42). The materials and installation cost £2,910

[4] Parts of this chapter were submitted for the STREAM TSEL assessment, which was awarded a mark of 89 %.

and initial reagent supplies purchased via an STW contract cost £60. These costs were borne by STW. From the ring-fenced share paid to the University of Sheffield, approximately £9,000 was spent on laboratory and sampling equipment. The total expenditure on this part of the project was approximately £11,970. This research plan had to be abandoned due to the author's ill health.

The remaining £7,000 of expenditure from the University of Sheffield share was spent on software (including MATLAB), climate data, technical modules at Newcastle University, Transferable Skills and Engineering Leadership courses, STREAM Challenge Weeks, the 'Faecal Indicators: Problem or Solution?' conference, Edinburgh (2011), the Sensors for the Water Industry Group conference, Edinburgh (2012), the Computing and Control for the Water Industry conference, Perugia (2013), and sundry expenses, including fuel.

7.3. Principal findings and recommendations from the research

The author's work with STW has focussed on three core areas: an assessment of company failure data between 2008 and 2011 (Chapter 3), derivation of the cost of bacteriological failures to STW (Chapter 4), and an analysis of the value of on-line monitoring data in the identification of root causes and the prevention of failures (Chapters 5 and 6).

7.3.1. Company data analysis

Chapter 3 detailed the findings from an analysis of the 218 bacteriological failures across the STW region between 2008 and 2011. This study identified that water quality exhibited high compliance with the regulations. Bacteriological failures were rare, but the majority of detections were for coliforms. It was uncommon for failing samples to contain more than 10 cells per 100 ml.

The most vulnerable sampling point was the customer tap, but one third of failing samples were collected from assets. WTW finals and reservoirs are within the control of STW. Furthermore, failures at assets are indicative of greater risk to human health due to the number of properties served, compared with a failure at an individual customer property. Interrogation of the Exception Reports for all failures showed that the majority of investigations were closed with the failure cause 'Unknown' because the re-samples were compliant. Where a cause was identified, the tap was the most likely source of the

indicator bacteria. It was observed that surface water samples accounted for the highest number of failures (WTW finals, reservoirs and customers' taps), followed by groundwater supplies; blended water samples had a lower incidence of non-compliance. However, it was noted that between 2008 and 2011, groundwater WTW finals accounted for more failures than surface water WTWs.

These findings led to several recommendations:

- Cool-medium water temperatures accounted for the greatest number of failures. Clear disinfection policies are currently in place for warm water conditions. It is suggested that improved residual chlorine management under cool-medium water temperatures could reduce the frequency of failures.
    - Since the initial findings were circulated within STW, they have now increased the availability of water temperature-based automated chlorine dosing rigs to improve chlorine management throughout the year.
- Surface water sources are viewed as being of higher bacteriological risk. The greater number of failures from groundwater WTWs at STW should encourage an analysis of disinfection practices at these sites to ensure their compliance with bacteriological water quality parameters.
    - Since the initial findings were circulated within STW, they have begun to convert marginal chlorination groundwater sites to super- and de-chlorination to enable disinfection.
- STW has a sample line replacement programme. This programme can be interrupted by the need to respond to bacteriological failures traced back to the sample line or tap. This means that 'at risk' sites may not get their sampling equipment replaced in a timely fashion. This therefore perpetuates the problem of false positives. Greater and ring-fenced investment is recommended in this crucial preventive measure.
    - Since the initial findings were circulated within STW, they have increased funding for the sample line replacement programme and have raised the profile of tap and sample line maintenance activities throughout the company.

7.3.2. The use of on-line water quality monitoring to inform the root cause analysis of bacteriological failures

This part of the project used cross-correlation and self-organising maps (SOMs) in MATLAB to determine whether on-line water quality monitoring data could be used to inform the root cause analysis of bacteriological failures.

7.3.2.1. Mythe WTW

Three datasets from Mythe WTW were examined, each dataset included the following parameters: monitored flow rate (ML d^{-1}), monitored turbidity (NTU), monitored free chlorine (mg l^{-1}), spot sampled free chlorine (mg l^{-1}), water temperature (°C), heterotrophic plate counts at 22 and 37 °C (colony forming units [CFU] ml^{-1}), and coliforms (CFU 100 ml^{-1}). They represented six months of monitoring data from January to June in 2011 and 2012 and six months between September 2012 and February 2013. There was a single coliform detection in each six month period.

The small number of non-compliant coliform tests available for this case study means that definitive WTW conditions cannot be asserted for Mythe WTW at this time.

The following work is recommended at Mythe WTW to mitigate future bacteriological non-compliances:

- Mythe's chlorine dosing is related to flow rate, however, this should not affect the resulting concentration but rather the (unmeasured) rate of disinfectant addition. Since the cross-correlations indicated that chlorine concentration was impacted by flow rate, the dosing rig should be examined and repaired/replaced as necessary.
- All three of the coliform detections were observed when both the chlorine concentration and water temperature were low-medium. It is therefore recommended that the dose and/or the contact time be increased when disinfecting water at Mythe under low-medium temperature conditions.

Further work to develop this research should include:

- In order to increase confidence in the conditions leading to a bacteriological failure, more historical data needs to be collected and examined using the same protocols. For Mythe, this should involve collecting the data for the same parameters for historical bacteriological non-compliances. Furthermore, sampling at a higher

frequency for bacteriological parameters (involving the development of on-line monitoring) would greatly aid this.

- A set of tools that can aid operators in their work to maintain water quality should be an aim of future research. One of the key requirements would therefore be to develop an output that recommends timely interventions, for example, 'increase chlorine residual concentration by X mg l^{-1},' or 'reduce flow rate through WTW by X ML d^{-1},' within a suitable time-frame. Such a system could be based on an artificial neural network which uses lagged time-series monitoring signals (with time-lags identified by cross correlation) for predicting operational conditions.
- To increase the time lag available between a change in water quality and the detection of a bacteriological failure, it would be beneficial to test data from earlier in the WTW process train. Collecting data from after the rapid gravity filters or the granular activated carbon filters may provide greater insight into the complex relationships between the different parameters under examination.
- The bacteriological quality of water is known to decline with distance from the WTW (Levi, 2004). Using the cross-correlation and SOM tools to determine whether actions at the WTW could have prevented a failure at a service reservoir would be valuable.

The development of site-specific water quality fingerprints will enhance the ability of STW to proactively manage its bacteriological quality. These fingerprints could be incorporated into the Drinking Water Safety Plans for each asset.

7.3.2.2. Strensham WTW

One dataset from Strensham WTW (outlet RSA 1) was analysed, spanning 1st January to 31st May 2013. This dataset was made up of data for: coliforms (CFU 100 ml^{-1}), 1 L coliforms (CFU 1 L^{-1}), *E. coli* (CFU 100 ml^{-1}), non-coliforms (CFU 100 ml^{-1}), 1 L non-coliforms (CFU 1 L^{-1}), Enterococci (CFU 100 ml^{-1}), HPCs at 22 °C and 37 °C (HPC22 and HPC37) (CFU ml^{-1}), pH (pH units), turbidity (NTU), free and total chlorine (mg l^{-1}) and water temperature (°C). These data were collected from Raw water, Final water and through-plant sampling points. In addition, data for daily air temperature (°C) and weekly rainfall (mm) were received from Met Office Hadley Centre for Climate Change (2013) and STW's Water Resources Strategy team, respectively. Further on-line monitoring data were received from STW's Asset Creation Data Team for monitor turbidity: RGF Filter Blocks A, B and C (NTU), Filter Block D (formazin turbidity

units [FTU]) and GAC Filters (NTU). There was one failure for coliforms, three for 1 L coliforms and one for Enterococci over the five month period.

The paucity of data for Enterococci meant that it was not possible to identify causative factors for that failure.

The analysis of data for the weeks of the coliform and 1 L coliform failures led to the following recommendations for improvements at Strensham WTW:

- It is advised that the GAC Filters be inspected and the media cleaned/regenerated, since they appear to harbour indicator bacteria, which are subsequently released.
- The Contact Tank, Balance Tank and Final sampling point should be inspected. Indicator bacteria are recovering between the Contact Tank and Final monitoring stage at the WTW. The coliform and 1 L coliform failures were due to *Enterobacter cloacae*. The inspection should include an assessment of biofilm growth within the Balance Tank, since *E. cloacae* have been found in biofilms.

Additional research was recommended for the maintenance of bacteriological quality in STW's supplies:

- Rainfall impacts some of the treatment processes in a WTW and therefore has an indirect effect upon Final compliance. On-site monitoring of rainfall would improve the ability of operators to act upon changing water conditions. This work shows that rainfall results in high numbers of bacteria suspended in low turbidity water.
- Before a similar analysis of compliance at downstream service reservoirs is conducted, it is important to have monitor tools that more closely reflect bacteriological water quality. The work from Mythe and Strensham has shown that changes in turbidity and chlorine concentrations are not clearly related to the presence of indicator organisms in Final water. Such tools may include the use of on-line flow cytometry (or similar fluorescence methods) (Berney *et al.*, 2008; Hammes *et al.*, 2008) to identify changes in bacterial numbers – especially at through-plant locations, such as post-GAC Filters. This would enable the chlorine dose or contact time to be increased to ensure a sufficient kill rate. At present, there are no flow cytometric tools that are able to specifically identify indicator bacteria or waterborne pathogens (Chapter 2).

7.3.3. Cost of Bacteriological Failures

Chapter 4 detailed the findings of the costing analysis for investigating and remediating the 218 bacteriological failures recorded between 2008 and 2011. This was the first time such a piece of work had been completed and it was appreciated throughout the company. The total cost for investigation and remediation was £3,235,000. There were 16 failures at WTWs, 69 at service reservoirs and 133 at customers' taps.

A total of £335,000 was spent on investigations: £42,650 on WTW failures, £165,000 on service reservoir failures, and £125,000 on customer tap failures. The average investigation cost from a WTW was £2,700, from a service reservoir it was £2,500 and from a customer tap, £1,000. The similarity in the investigation costs for service reservoirs and WTWs was because some reservoir investigations required a drain down and inspect operation which inflated the total and average costs.

Remediation costs were much greater. The total cost was £2,900,000. The costs of remedial works at customers' properties were assumed to be borne by the customers. The cost to STW of remediating WTWs was £65,550. This value included replacing or enhancing chlorination equipment and improving turbidity removal. Remediation at service reservoirs cost £2,800,000. A large proportion of this cost (£2,270,000) was for the de-commissioning and replacement of North Malvern reservoir. Other remedial options at service reservoirs included draining down and cleaning, and replacing hatch seals or membranes. The average costs of remediation were £4,100 for WTWs and £42,400 for service reservoirs; if North Malvern reservoir was excluded, the average cost of service reservoir remediation was £8,100.

The total investigation and remediation costs were £125,000 for customer tap failures, £2,965,000 for service reservoir failures and £108,000 for WTW failures.

STW had previously estimated the average cost of bacteriological failures at £100. The outcomes of this piece of work have enabled them to significantly up-rate their consideration of such compliance events.

7.4. Further benefits to Severn Trent Water from research

The research has raised the profile of STW, and the Research and Development team, through publishing articles and papers relating to this work.

- K Ellis. (April 2011). 'Increasing knowledge about taps and samples'. IN: *WET News.*
- K Ellis, B Ryan, M R Templeton and C A Biggs. (2012). 'Improving Bacteriological Water Quality Compliance of Drinking Water'. IN: D Kay and C Fricker (eds.). *The Significance of Faecal Indicators in Water: A Global Perspective*. Cambridge: Royal Society of Chemistry.
- K Ellis, B Ryan, M R Templeton and C A Biggs. (2013). 'Bacteriological Water Quality Compliance and Root Cause Analysis: An Industry Case Study'. IN: *Water Science and Technology: Water Supply*. **13** (4), pp 1034-1045.
- K Ellis, S R Mounce, B Ryan, M R Templeton and C A Biggs. (In Press). 'Use of On-line Water Quality Monitoring Data to Predict Bacteriological Failures'. IN: Procedia Engineering – 12th International Conference on Computing and Control for the Water Industry.

An oral presentation was given at an international conference and slides were contributed for a second:

- Computing and Control for the Water Industry Conference, 2nd – 4th September 2013, University of Perugia, Italy (presentation)
- American Water Works Association Water Quality Technical Conference and Exposition, 3rd – 7th November 2013, Long Beach, California (slides)

Poster presentations were given at two international conferences:

- Royal Society of Chemistry Faecal Indicators: Problem or Solution Conference, 6th – 8th June 2011, Heriot-Watt University, Edinburgh
- International Water Association UK 14th National Young Water Professionals Conference, 17th – 19th April 2013, Teesside University, Darlington

The Cost of Failure work was widely disseminated within STW. This has been achieved through a report, a Brown Paper presentation to operational and managerial staff (Figure 43), a 'Communication Cell' slide and a summary to be included in training packages for new and existing Quality Inspectors.

This research project has enabled a continuing working relationship between STW and the University of Sheffield and Imperial College London.

7.4.1. Does the work represent value for money?

The research has shifted the focus of STW's efforts to achieve the business target of zero quality failures in distribution. It has highlighted the amount of money that is spent every time an indicator organism is detected. The project has also demonstrated the potential of using advanced data analysis tools with on-line monitoring data to determine the causes of bacteriological failures.

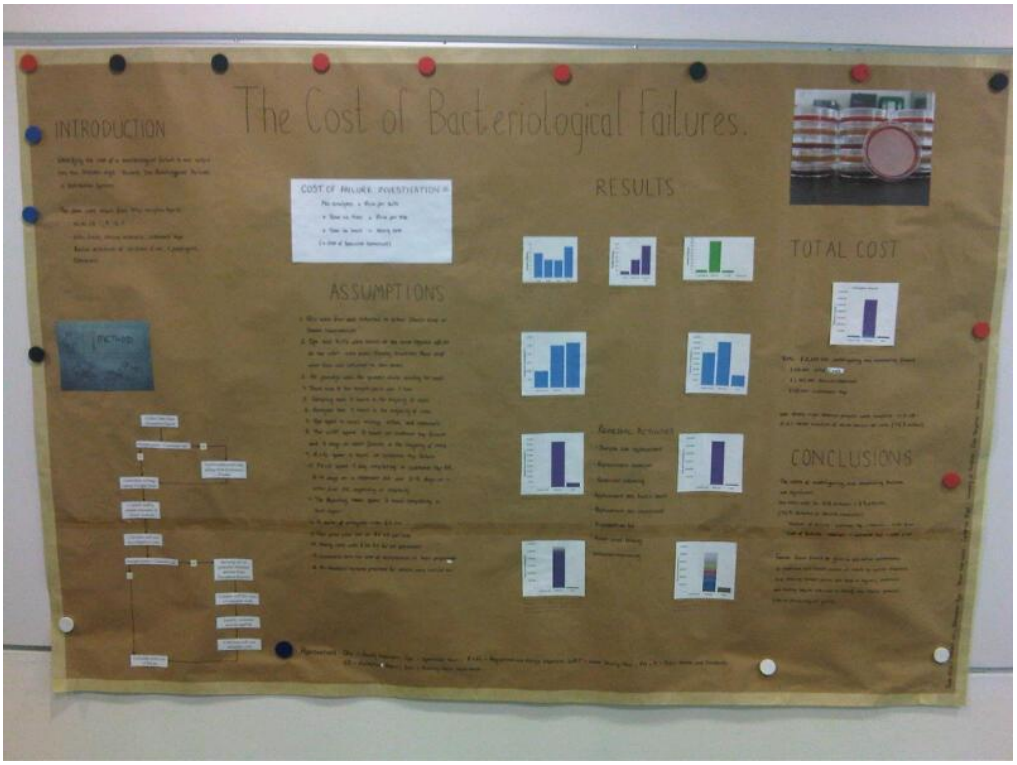

Figure 43: The Cost of Failure Brown Paper presented to operational and managerial staff at Severn Trent Water.

These principal outcomes of this research programme were achieved as part of the total spending of £43,152 by STW. The portion of the research that is simplest to cost is the Cost of Failure investigation. In total, this aspect of the project took one year full-time. If this work had been undertaken by an STW employee working 47 weeks per year, and using STW's hourly rate of £26.50 (which includes salary, training and pension costs), it would have cost the company £46,700. Therefore, if the Cost of Failure were the only output of the four year project, it represents a cost saving to STW. The project has also provided the company with workable recommendations for the improvement of bacteriological compliance, developed more advanced uses for on-line monitoring data, and a variety of further benefits. This work can therefore be considered good value for money.

7.5. How the research has benefited, and will benefit, Severn Trent Water

Several aspects of this project have impacted STW already. Correspondence has been received detailing a variety of changes to practice since the dissemination of research findings.

- Some sites have had temperature triggers introduced to enable automatic increasing/decreasing of chlorine residuals in the distribution system. These units are being reviewed for efficacy. The introduction of these tools enables pro-active changes to chlorine dosing for bacteriological management, rather than relying on manual adjustment based on retrospective trends.
- Having shown that groundwater WTWs were failing more often than surface water sites, they have received greater focus. Performance in 2012 was improved. Furthermore, some groundwater sites with marginal chlorination have been, or are being, up-graded to super- and de-chlorination to enable disinfection at these WTWs.
- More funding has been made available for the sample line and tap programme to ensure that it is maintained even in the face of remedial works. New maintenance guidelines for sample points have also been released.
- The figures from the Cost of Failure work are being incorporated into the Private Cost of Failure calculations for Asset Management Plan 2014. Using these figures instead of the previous estimate of £100 per failure means that STW should be able to break even in terms of required expenditure for investigations.
- The work on recurring bacteriological failures at Mythe and Strensham WTWs has provided insight into the risk factors and causes of (principally) coliform failures. Interventions have been recommended to improve compliance at these sites.

7.6. Conclusions

This research project has provided STW with greater understanding of their compliance data and of the costs associated with bacteriological failures. The use of enhanced data analysis tools can improve the success of root cause investigations, especially where there is through-plant data collection. Cross-correlation and SOMs are powerful tools for the analysis of large datasets.

8. Discussion

8.1. Overview of the findings

To bring Severn Trent Water (STW) closer to their target of zero failures in distribution systems, this research project has sought to inform improved compliance for bacteriological water quality parameters: coliforms, *Escherichia coli*, *Clostridium perfringens* and Enterococci (indicator bacteria). The sampling points of interest were water treatment works (WTW) finals, service reservoirs and customers' taps. The literature review revealed a variety of potential sources of indicator bacteria in water samples: raw water quality, treatment failure, ingress to the distribution system, biofilms in the pipes, contamination of the sample taps and poor hygiene practice by samplers or analysts.

Analyses were conducted on data relating to failures in STW's routine sampling programme. These failures occurred under apparently normal supply and distribution conditions; that is, they were not related to reported pipe bursts, severe weather events or a major disruption of WTW processes. The proportion of bacteriological tests that failed between 2008 and 2011 was 0.08 %. The majority of the failures studied in Chapter 3 were for fewer than 10 CFU 100 ml^{-1} and not one of the 218 failures was associated with reported ill health in the population. The majority of detections were for total coliforms; these organisms can be derived from environmental or faecal sources. A cause was identified for only one-third of failures; the majority of these showed that the cleanliness of the tap was the problem, and most of them were from customers' taps. Two-thirds of failures had no cause identified and this meant that it was not possible to take action to prevent future non-compliances. Customers' taps accounted for the majority of non-compliances; one of which was linked back to water quality from an upstream asset. Non-compliance at a customer tap affects the residents of that property. The one-third of failures from assets had the potential to affect many households. Overall, surface water supplies had the highest number of failures.

The average costs of investigating bacteriological failures were £2,700 for WTWs, £2,500 for reservoirs and £1,000 for customers' taps. Remediation costs were, on average, £4,100 for WTWs and £42,400 for reservoirs (or £8,100 without North Malvern reservoir). The total cost for the 218 failures between 2008 and 2011 was

£3,235,000. Other countries which have comparable regulatory requirements are likely to have failure costs of a similar order of magnitude.

Cross-correlation and self-organising maps (SOMs) were used to determine whether on-line water quality data could be used to inform the root cause analysis of bacteriological failures at WTWs and protect reservoirs and customers' taps downstream. Two case study sites were selected that had experienced multiple non-compliances during the project time-scale: Mythe and Strensham WTWs. Mythe WTW experienced three failures over two years and Strensham WTW experienced five non-compliances from the same sample point in five months. The analysis of the Mythe datasets was the first application of cross-correlation and SOMs in assessing the bacteriological quality of WTW final water; the Strensham dataset saw the extension of their application to through-plant data.

The final water quality analyses for Strensham show broad agreement with those for Mythe: the coliform failures occurred under conditions of low-medium water temperature (Mythe, 4.2 – 14.2 °C; Strensham, 5.1 – 14.6 °C); and low-medium free chlorine (Mythe, 0.42 – 0.84 mg l^{-1} monitor and 0.45 – 0.88 mg l^{-1} spot-sampled; Strensham, 0.27 – 0.86 mg l^{-1} monitor and 0.48 – 0.84 mg l^{-1} spot-sampled). Final turbidity was higher at Strensham (0.00 – 1.33 NTU monitor; 0.08 – 0.24 spot-sampled) than at Mythe (0.03 – 0.08 NTU). The data analyses enabled the determination of risk factors in the maintenance of bacteriological quality in water entering the distribution system.

The analysis of Mythe data resulted in the following recommendations: a) the chlorine dosing rig should be inspected and repaired/replaced to ensure that dosing is truly flow-controlled; and b) chlorine dose or contact time should be increased when water temperature is low-medium, since low-medium free chlorine concentrations correlated with low-medium water temperatures at the time of the non-compliances. At Strensham, the results suggested these interventions: a) the GAC Filters should be inspected and the media cleaned/regenerated as they appear to be harbouring indicator bacteria; and b) the Contact Tank, Balance Tank and Final monitoring sample point should all be inspected for biofilm growth, as indicator bacteria were recovered despite chlorine concentrations being on target; the identified coliforms were *Enterobacter cloacae* which has been

observed to occur in biofilms. Furthermore, the data analysis revealed that rainfall impacts raw water quality and that these impacts persist through the WTW.

Water quality in England and Wales is of a very high quality, but approximately half of all regulatory failures are for bacteriological parameters (UK Water Industry Research, 2006). Preventing bacteriological non-compliances is preferable and more cost-effective than having to investigate and remediate them after the fact. Developing tools that can alert operators to changes in bacteriological water quality would enable treatment parameters to be altered to maintain compliance. This is particularly important for WTWs that are not manned 24 h a day. Reducing the number of bacteriological failures increases consumer confidence in their water company.

8.2. Advantages and disadvantages of some of the analytical techniques

8.2.1. Cost of bacteriological failures

At the start of this project there were no defined methods for the calculation of the cost of bacteriological non-compliances. Since then, the publishing of the Revised Total Coliform Rule (rTCR) will require that all coliform and *E. coli* failures in the USA be investigated to determine their cause (US Environmental Protection Agency, 2012). To that end, the US Environmental Protection Agency has issued costing guidelines to enable water authorities to prepare for the additional expenditure. This method is based upon generalisations (different cost functions apply depending on the size of the supply zone, for example). It is not yet known how accurate this costing method is. The method used in this project, despite the list of assumptions, does not generalise the failures and it is argued that it provides a more exact estimate. However, the work was time-consuming, which explains why it has not been completed within STW before. Furthermore, the feedback by the operational teams who could benefit from better cost estimates is that they would seek to develop a high level version of the method on account of the amount of work involved. The rTCR method, when translated to UK/European water company investigation structures, may enable all water companies to properly account for, and report, the costs of investigating non-compliances.

8.2.2. Cross-correlation and Self-Organising Maps

Cross-correlation has been applied to a range of signal processing purposes, including telecommunications (Beck, 1981); spectroscopy (Wong *et al.*, 2005); meteorology (Leese *et al.*, 1971) and earthquake detection (Shearer, 1997). SOMs have also been used in a variety of disciplines, including economics (Deboeck and Kohonen, 1998),

genetics (Tamayo *et al.*, 1999), climatology (Hewitson and Crane, 2002), engineering (Kohonen *et al.*, 1996) and water quality (Kalteh and Hijorth, 2008). This research has shown that they are valuable tools for water industry applications as well.

The intended use of the cross-correlation results was to determine how far in advance of a failure other water quality parameters change. This knowledge would enable operators to take timely action to prevent a failure. Cross-correlation provided useful outputs for the Mythe WTW analyses, which was primarily due to the small number of parameters involved. When it came to the analysis of the Strensham data, not only were there a lot of results, the majority of those that were both positive and between 0 and 24 h were for 0 h. These results suggested that, broadly speaking, upstream processes did not impact the downstream ones, which does not make intuitive sense. Thus, the recommendation at the end of Chapter 5 that cross-correlation results could be used to inform an artificial neural network-based tool to give operators warning of declining water quality no longer seems appropriate. Assuming that there are further time-based relationships to be elicited from the datasets, alternative methods ought to be sought for this part of a warning system. The Auto-regressive Integrated Moving Average method was not suited to the raw data, some parameters of which had a sparse sampling frequency. Wavelet analysis, which was avoided because it was computationally expensive, may have resulted in more useful time lag results.

The benefits of the SOMs are that they can provide a visual representation of complex datasets, they are not limited to the correlation of two parameters (as cross-correlation is), and they are easy to code and interpret. The disadvantage of SOMs lies in the plotting of the component planes. As an effect of the normalisation of the data the axes on the component planes do not represent the true minimum, maximum and mid-point values of the parameters. This became clearer with the Strensham data analysis and the axes were modified for this case study to reflect the true minima and maxima. If the component planes were read without reference to the raw data they would be mis-leading.

The main limitation of these tools is the need for equal numbers of rows in the analysed dataset, which can mean that a significant portion of the analyses are based upon assumed data. Because it was important to maintain the high resolution of the monitor chlorine, turbidity, pH and flow data these formed the backbones of the datasets for the

spot-sampled values. Therefore the bulk of the completed datasets were formed of extrapolated or zero-padded data. Since the bacteriological data, which were of especial interest, were sampled daily at most, this meant that most of these datasets were formed of assumed data. There is a need for on-line monitoring tools for bacteriological quality to provide real-time data for these parameters.

Since this project was the first application of cross-correlation and SOMs in the root cause analysis of bacteriological failures, it was beneficial to limit the scope of the work to WTW finals or through-plant at a WTW. This meant that the factors that could affect final bacteriological quality were reduced to the raw water quality and efficacy of the treatment processes and disinfection. Before the scope of these tools can be extended to include downstream service reservoirs and customer properties it is important that they are made more user-friendly. In particular, it would be beneficial to develop a better method for deriving time lag data to inform operators.

9. Conclusions

This research project has answered the research questions:

1. What are the main causes of bacteriological non-compliances in UK water supplies?
    - This study has shown that most bacteriological failures at STW have no cause identified. It concurs with the findings of UK Water Industry Research (2009). This makes it difficult for water companies to act upon non-compliances to improve performance. The research has highlighted the need for better investigative tools. Where causes were identified, the failures were most often attributed to the cleanliness of the taps from which the samples were drawn (Chapter 3).
2. Where in the water supply system do most bacteriological failures occur?
    - Most bacteriological failures were detected at customers' taps. Of the sites within the control of STW, the highest risk sample points are service reservoirs (Chapter 3). Nevertheless, a failure at a WTW has the potential to impact a larger number of consumers and non-compliances at these sites should take precedence. Service reservoirs and WTW finals require significant investment in terms of both investigation and remediation. The Office of Water (Ofwat) and the Drinking Water Inspectorate expect the water quality from company assets to be compliant. Financial sanctions are imposed for coliform failures from WTWs and service reservoirs (Chapter 4).
3. Which indicator organism is most frequently detected?
    - Coliforms were the indicator organism that was most commonly detected (Chapter 3). These bacteria can be derived from environmental and faecal sources.
4. Is UK bacteriological compliance impacted by weather phenomena?
    - There was a weak correlation between weather phenomena and bacteriological failures (Chapter 3), which concurs with the findings of Schets *et al.* (2005) and Pitkänen *et al.* (2008). With regard to rainfall, the relationship was further weakened by including a time lag of one or two months, which differed from the observations made by Curriero *et al.* (2001). Furthermore, the research has shown that failures are detected all year round at customers' taps and service reservoirs, but that those at WTW finals were more common under cooler water conditions. Thus it is

necessary for greater efforts to be directed at improving bacteriological compliance at WTWs under cool water temperatures to improve the quality of water in the distribution system. The analysis of the Strensham datasets showed that rainfall led to increased turbidity and numbers of bacteria in the raw water and that this impact persisted through much of the WTW (Chapter 6). The Mythe and Strensham work (Chapters 5 and 6) showed that low-medium water temperatures correlated with low-medium chlorine concentrations at the times of failure.

5. Can improved analysis of on-line monitoring and spot-sample data be used to inform the root cause analysis of bacteriological failures?
    - The cross-correlation and SOM analyses were able to provide insight into the function of both Mythe and Strensham WTWs. SOMs were easier to use and interpret and could readily be employed in the root cause analysis for other asset failures. The weakness of these two tools is that they require equal numbers of rows for every parameter and much of the bacteriological data assessed was either extrapolated or zero-padded. Cross-correlation and SOM analyses cannot at present be used to predict bacteriological failures, but they can provide valuable information for root cause analyses.
6. What financial impact do bacteriological failures have on a UK water company?
    - The average costs to STW of investigating bacteriological failures were £2,700 for WTWs, £2,500 for reservoirs and £1,000 for customers' taps. Remediation costs were, on average, £4,100 for WTWs and £42,400 for reservoirs (or £8,100 without North Malvern reservoir). The total cost for the 218 failures between 2008 and 2011 was £3,235,000. It is important to make the expenditure to find the cause of bacteriological failures. However, at the moment, the significant costs of investigation result in only one third of root causes being identified.

Important outcomes from the research are:

- This research has shown that none of the routinely measured parameters alone (free chlorine, turbidity, water temperature, etc.) is a suitable predictor for bacteriological quality and that even with water quality parameters within normal operating ranges at the time of sampling, non-compliances do still occur (Chapters 3, 5 and 6). This work has demonstrated the need for more effective investigatory tools.

- The project has provided the first detailed calculation of the cost of bacteriological failures for a UK water company (Chapter 4).
- It has also demonstrated the use of cross-correlation and SOMs in the root cause analysis of bacteriological failures (Chapters 5 and 6). Despite the data manipulation and interpretation limitations, the tools provided valuable information on the failures at Mythe and Strensham WTWs. The use of cross-correlation and SOMs enabled the generation of advice for the improvement of compliance at these two sites.

10. Recommendations

10.1. Severn Trent Water

- The cleaning schedule for contact and balance tanks should be revised to enable more frequent servicing. Furthermore, it would be wise to conduct this operation after a WTW failure (where the cause was unknown), as a means of reducing the likelihood of future non-compliances.
- Disinfection equipment, for example chlorinators, should be inspected and tested more regularly to ensure they are performing properly. A daily check is routine, but daily performance tests are recommended.
- Contact times and/or target chlorine concentrations should be re-investigated for low-medium water temperature conditions. For Mythe and Strensham, one or both factors need to be revised upwards.
- Since raw water bacteriological quality was shown to affect downstream water quality, it is recommended that raw water samples are analysed for Enterococci and *C. perfringens* at the same frequency as coliforms and *E. coli* (which was every two to three days at Strensham WTW). This would provide better understanding of the raw water quality in the period preceding a failure and aid the root cause analyses.

10.2. The water industry

- UK water companies should share their experiences of failures and remediation methods more readily. This would ensure that solutions could be shared and that research efforts, within and beyond company Research and Development teams, were focussed on the most challenging problems. Since bacteriological compliance affects most water companies to a similar degree, this is one area where an inter-company collaboration would be beneficial.
- Greater vigilance at WTWs is required when rain falls. This has been shown to impact the bacteriological quality of raw water and that of water through the treatment process. The settlement tanks were shown to absorb much of the change in water quality, thus the focus should be on rapid gravity and GAC filters. Flow rate through the WTW should be reduced to enable the filters to be back-washed with greater frequency to reduce the likelihood of turbidity and bacteriological breakthrough. There is, therefore, scope to enhance disinfection and minimise disinfection by-product formation through the introduction of chlorine dosing and

contact times that are related to raw water challenge as indicated by rainfall and/or raw water turbidity.

10.3. Research organisations

- Artificial neural networks (such as SOMs) 'teach' themselves about the data they are presented with, but fuzzy logic systems are programmed using human input parameters. This means the outputs can be controlled. Water quality fingerprints relating to bacteriological failures developed using cross-correlation and SOMs can be used to form the basis of an alarm system based on fuzzy logic. For example, using the results from Strensham, an alarm could be set to sound if chlorine residual falls below 0.7 mg l^{-1} AND turbidity rises above 1.00 NTU AND/OR pH rises above 7.2 pH units. This would enable operators to act to increase the chlorine dose and contact time to assure the bacteriological quality of the water sent to supply.
- Improved understanding of the financial impact of bacteriological non-compliance would be beneficial to all water companies. It would ensure that their financial forecasting to Ofwat reflected reality. To achieve this, the data for several water companies, covering the same time period (the four years analysed in Chapter 4 provided a range of failure types and interventions; shorter time periods are not recommended), should be collected and the cost results published. On account of company confidentiality, this work would need to be conducted by an impartial research institute, for example, a university, and published with the company data anonymised. Furthermore, it would be beneficial to compare the method employed in this project with that of the rTCR to determine a) if it is an appropriate tool for cost estimates and b) if it would help water companies by providing a reliable higher level method.
- The research has highlighted the need for bacteriological monitoring tools that can respond in real-time to changes in water quality. This is especially important as the analysis of Mythe and Strensham data showed that the indicator bacteria in the final water were often associated with low turbidity. Turbidity has been used as a surrogate for bacteriological quality in the past, but these analyses show that this use is not appropriate under normal operating conditions. On-line tools based on flow cytometry or other fluorescence tools, although not yet capable of identifying indicator bacteria, would, if situated prior to contact tanks enable operators to act quickly to increase chlorine doses or contact times if bacteriological quality declines. These on-line tools could then be connected to the fuzzy logic system

outlined above and provide a more comprehensive method for the management of microbiological water quality.

- Turbidity breakthrough from GAC Filters is a concern. Research into reducing the loss of particulate matter from these filters is recommended to reduce the impact on disinfection. This may involve particulate filters, a settling tank pre-contact tank, recirculation of high turbidity GAC-filtered water, etc.
- Furthermore, it remains important for water companies to strive to prevent false positives at their assets, i.e. those that are due to poor tap cleanliness or faults in the sample line (as planned in Chapter 7). Improved methods for the protection of sample taps and lines should be investigated, so that failures are related to the quality of the water and not of the sampling apparatus. This would involve investigations into whether asset taps should be kept constantly running, the value of using the caps on a Harris tap, whether sample points situated in kiosks are more hygienic than those in large rooms/pump houses, etc.

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Appendix 1. MATLAB code for Mythe: six month datasets

```
%% Import files to be merged

% Identify the files
file_1='Mythe11Cl2B'; %name before .csv
file_2='Mythe11FlowB';
file_3='Mythe11TurbB';
file_4='Mythe11Cl2Spot';
file_5='Mythe11Temp';
file_6='Mythe11HPC22';
file_7='Mythe11HPC37';
file_8='Mythe11CO';
file_9='Mythe12Cl2';
file_10='Mythe12Flow';
file_11='Mythe12Turb';
file_12='Mythe12Cl2Spot';
file_13='Mythe12Temp';
file_14='Mythe12HPC22';
file_15='Mythe12HPC37';
file_16='Mythe12CO';
file_17='Mythe12BCl2';
file_18='Mythe12BFlow';
file_19='Mythe12BTurb';
file_20='Mythe12BCl2Spot2';
file_21='Mythe12BTemp';
file_22='Mythe12BHPC22B';
file_23='Mythe12BHPC37B';
file_24='Mythe12BCOB';

disp('Open and read from files');

% CSV files access
filename1 = strcat(file_1,'.csv');
filename2 = strcat(file_2,'.csv');
filename3 = strcat(file_3,'.csv');
filename4 = strcat(file_4,'.csv');
filename5 = strcat(file_5,'.csv');
filename6 = strcat(file_6,'.csv');
filename7 = strcat(file_7,'.csv');
filename8 = strcat(file_8,'.csv');
filename9 = strcat(file_9,'.csv');
filename10 = strcat(file_10,'.csv');
filename11 = strcat(file_11,'.csv');
filename12 = strcat(file_12,'.csv');
filename13 = strcat(file_13,'.csv');
filename14 = strcat(file_14,'.csv');
filename15 = strcat(file_15,'.csv');
filename16 = strcat(file_16,'.csv');
filename17 = strcat(file_17,'.csv');
filename18 = strcat(file_18,'.csv');
filename19 = strcat(file_19,'.csv');
filename20 = strcat(file_20,'.csv');
filename21 = strcat(file_21,'.csv');
filename22 = strcat(file_22,'.csv');
filename23 = strcat(file_23,'.csv');
filename24 = strcat(file_24,'.csv');

% Import file_1

count=0;

    fid1=fopen(filename1, 'r+');

    if (fid1~=-1)
        data = textscan(fid1, '%s%n', 'delimiter',',','Whitespace','\tb','commentStyle',
'"');
        dates=datenum(data{1}, 'dd/mm/yyyy HH:MM');
        chlorine=data{2};
        samples=size(dates,1);
        count=count+1;
        fclose(fid1);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of Chlorine time series: ');
    samples
```

```
 % Import file_2

    count2=0;

    fid2=fopen(filename2, 'r+');

    if (fid2~=-1)
        data2 = textscan(fid2, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates2=datenum(data2{1}, 'dd/mm/yyyy HH:MM');
        flow=data2{2};
        samples2=size(dates2,1);
        count2=count2+1;
        fclose(fid2);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of Flow time series: ');
    samples2

% Import file_3

    count3=0;

    fid3=fopen(filename3, 'r+');

    if (fid3~=-1)
        data3 = textscan(fid3, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates3=datenum(data3{1}, 'dd/mm/yyyy HH:MM');
        turbidity=data3{2};
        samples3=size(dates3,1);
        count3=count3+1;
        fclose(fid3);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of Turbidity time series: ');
    samples3

% Import file_4

count4=0;

    fid4=fopen(filename4, 'r+');

    if (fid4~=-1)
        data4 = textscan(fid4, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates4=datenum(data4{1}, 'dd/mm/yyyy HH:MM');
        chlorspot=data4{2};
        samples4=size(dates4,1);
        count4=count4+1;
        fclose(fid4);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of CLspot time series: ');
    samples4

 % Import file_5

    count5=0;

    fid5=fopen(filename5, 'r+');

    if (fid5~=-1)
        data5 = textscan(fid5, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates5=datenum(data5{1}, 'dd/mm/yyyy HH:MM');
        tempspot=data5{2};
        samples5=size(dates5,1);
        count5=count5+1;
```

```
        fclose(fid5);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of Temperature time series: ');
    samples5

% Import file_6

    count6=0;

    fid6=fopen(filename6, 'r+');

    if (fid6~=-1)
        data6 = textscan(fid6, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates6=datenum(data6{1}, 'dd/mm/yyyy HH:MM');
        HPC22=data6{2};
        samples6=size(dates6,1);
        count6=count6+1;
        fclose(fid6);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of HPC22 time series: ');
    samples6

% Import file_7

    count7=0;

    fid7=fopen(filename7, 'r+');

    if (fid7~=-1)
        data7 = textscan(fid7, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates7=datenum(data7{1}, 'dd/mm/yyyy HH:MM');
        HPC37=data7{2};
        samples7=size(dates7,1);
        count7=count7+1;
        fclose(fid7);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of HPC37 time series: ');
    samples7

% Import file_8

    count8=0;

    fid8=fopen(filename8, 'r+');

    if (fid8~=-1)
        data8 = textscan(fid8, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates8=datenum(data8{1}, 'dd/mm/yyyy HH:MM');
        colif=data8{2};
        samples8=size(dates8,1);
        count8=count8+1;
        fclose(fid8);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of Coliform time series: ');
    samples8

% Import file_9

count9=0;

    fid9=fopen(filename9, 'r+');
```

```
    if (fid9~=-1)
        data9 = textscan(fid9, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates9=datenum(data9{1}, 'dd/mm/yyyy HH:MM');
        chlorine2=data9{2};
        samples9=size(dates9,1);
        count9=count9+1;
        fclose(fid9);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of Chlorine2 time series: ');
    samples9

 % Import file_10

    count10=0;

    fid10=fopen(filename10, 'r+');

    if (fid10~=-1)
        data10 = textscan(fid10, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates10=datenum(data10{1}, 'dd/mm/yyyy HH:MM');
        flow2=data10{2};
        samples10=size(dates10,1);
        count10=count10+1;
        fclose(fid10);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of Flow2 time series: ');
    samples10

% Import file_11

    count11=0;

    fid11=fopen(filename11, 'r+');

    if (fid11~=-1)
        data11 = textscan(fid11, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates11=datenum(data11{1}, 'dd/mm/yyyy HH:MM');
        turbidity2=data11{2};
        samples11=size(dates11,1);
        count11=count11+1;
        fclose(fid11);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of Turbidity2 time series: ');
    samples11

% Import file_12

count12=0;

    fid12=fopen(filename12, 'r+');

    if (fid12~=-1)
        data12 = textscan(fid12, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates12=datenum(data12{1}, 'dd/mm/yyyy HH:MM');
        chlorspot2=data12{2};
        samples12=size(dates12,1);
        count12=count12+1;
        fclose(fid12);
    else
        disp('no file present')
        cd('..')
    end
```

```
    disp('Size of CLspot2 time series: ');
    samples12

 % Import file_13

    count13=0;

    fid13=fopen(filename13, 'r+');

    if (fid13~=-1)
        data13 = textscan(fid13, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates13=datenum(data13{1}, 'dd/mm/yyyy HH:MM');
        tempspot2=data13{2};
        samples13=size(dates13,1);
        count13=count13+1;
        fclose(fid13);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of Temperature2 time series: ');
    samples13

% Import file_14

    count14=0;

    fid14=fopen(filename14, 'r+');

    if (fid14~=-1)
        data14 = textscan(fid14, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates14=datenum(data14{1}, 'dd/mm/yyyy HH:MM');
        HPC22B=data14{2};
        samples14=size(dates14,1);
        count14=count14+1;
        fclose(fid14);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of HPC22B time series: ');
    samples14

% Import file_15

    count15=0;

    fid15=fopen(filename15, 'r+');

    if (fid15~=-1)
        data15 = textscan(fid15, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates15=datenum(data15{1}, 'dd/mm/yyyy HH:MM');
        HPC37B=data15{2};
        samples15=size(dates15,1);
        count15=count15+1;
        fclose(fid15);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of HPC37B time series: ');
    samples15

% Import file_16

    count16=0;

    fid16=fopen(filename16, 'r+');

    if (fid16~=-1)
        data16 = textscan(fid16, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates16=datenum(data16{1}, 'dd/mm/yyyy HH:MM');
        colif2=data16{2};
```

```
        samples16=size(dates16,1);
        count16=count16+1;
        fclose(fid16);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of Coliform2 time series: ');
    samples16

% Import file_17

count17=0;

    fid17=fopen(filename17, 'r+');

    if (fid17~=-1)
        data17 = textscan(fid17, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates17=datenum(data17{1}, 'dd/mm/yyyy HH:MM');
        chlorine3=data17{2};
        samples17=size(dates17,1);
        count17=count17+1;
        fclose(fid17);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of Chlorine3 time series: ');
    samples17

 % Import file_18

    count18=0;

    fid18=fopen(filename18, 'r+');

    if (fid18~=-1)
        data18 = textscan(fid18, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates18=datenum(data18{1}, 'dd/mm/yyyy HH:MM');
        flow3=data18{2};
        samples18=size(dates18,1);
        count18=count18+1;
        fclose(fid18);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of Flow3 time series: ');
    samples18

% Import file_19

    count19=0;

    fid19=fopen(filename19, 'r+');

    if (fid19~=-1)
        data19 = textscan(fid19, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates19=datenum(data19{1}, 'dd/mm/yyyy HH:MM');
        turbidity3=data19{2};
        samples19=size(dates19,1);
        count19=count19+1;
        fclose(fid19);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of Turbidity3 time series: ');
    samples19

% Import file_20

count20=0;
```

```
    fid20=fopen(filename20, 'r+');

    if (fid20~=-1)
        data20 = textscan(fid20, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates20=datenum(data20{1}, 'dd/mm/yyyy HH:MM');
        chlorspot3=data20{2};
        samples20=size(dates20,1);
        count20=count20+1;
        fclose(fid20);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of CLspot3 time series: ');
    samples20

 % Import file_21

    count21=0;

    fid21=fopen(filename21, 'r+');

    if (fid21~=-1)
        data21 = textscan(fid21, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates21=datenum(data21{1}, 'dd/mm/yyyy HH:MM');
        tempspot3=data21{2};
        samples21=size(dates21,1);
        count21=count21+1;
        fclose(fid21);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of Temperature3 time series: ');
    samples21

% Import file_22

    count22=0;

    fid22=fopen(filename22, 'r+');

    if (fid22~=-1)
        data22 = textscan(fid22, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates22=datenum(data22{1}, 'dd/mm/yyyy HH:MM');
        HPC22C=data22{2};
        samples22=size(dates22,1);
        count22=count22+1;
        fclose(fid22);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of HPC22C time series: ');
    samples22

% Import file_23

    count23=0;

    fid23=fopen(filename23, 'r+');

    if (fid23~=-1)
        data23 = textscan(fid23, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates23=datenum(data23{1}, 'dd/mm/yyyy HH:MM');
        HPC37C=data23{2};
        samples23=size(dates23,1);
        count23=count23+1;
        fclose(fid23);
    else
        disp('no file present')
        cd('..')
```

```
    end

    disp('Size of HPC37C time series: ');
    samples23

% Import file_24

    count24=0;

    fid24=fopen(filename24, 'r+');

    if (fid24~=-1)
        data24 = textscan(fid24, '%s%n',
'delimiter',',','Whitespace','\tb','commentStyle', '"');
        dates24=datenum(data24{1}, 'dd/mm/yyyy HH:MM');
        colif3=data24{2};
        samples24=size(dates24,1);
        count24=count24+1;
        fclose(fid24);
    else
        disp('no file present')
        cd('..')
    end

    disp('Size of Coliform3 time series: ');
    samples24

%% Specify key and variable for each file

    monit1=dataset(dates, chlorine, 'VarNames',{'Date' 'Chlorine'});

    monit2=dataset(dates2, flow, 'VarNames',{'Date' 'Flow'});

    monit3=dataset(dates3, turbidity, 'VarNames',{'Date' 'Turbidity'});

    CLspot=dataset(dates4, chlorspot, 'VarNames',{'Date' 'ChlorineSpot'});

    temp=dataset(dates5, tempspot, 'VarNames',{'Date' 'Temperature'});

    bacti1=dataset(dates6, HPC22, 'VarNames',{'Date' 'HPC22'});

    bacti2=dataset(dates7, HPC37, 'VarNames',{'Date' 'HPC37'});

    bacti3=dataset(dates8, colif, 'VarNames',{'Date' 'Coliforms'});

    monit4=dataset(dates9, chlorine2, 'VarNames',{'Date' 'Chlorine'});

    monit5=dataset(dates10, flow2, 'VarNames',{'Date' 'Flow'});

    monit6=dataset(dates11, turbidity2, 'VarNames',{'Date' 'Turbidity'});

    CLspot2=dataset(dates12, chlorspot2, 'VarNames',{'Date' 'ChlorineSpot'});

    temp2=dataset(dates13, tempspot2, 'VarNames',{'Date' 'Temperature'});

    bacti4=dataset(dates14, HPC22B, 'VarNames',{'Date' 'HPC22'});

    bacti5=dataset(dates15, HPC37B, 'VarNames',{'Date' 'HPC37'});

    bacti6=dataset(dates16, colif2, 'VarNames',{'Date' 'Coliforms'});

    monit7=dataset(dates17, chlorine3, 'VarNames',{'Date' 'Chlorine'});

    monit8=dataset(dates18, flow3, 'VarNames',{'Date' 'Flow'});

    monit9=dataset(dates19, turbidity3, 'VarNames',{'Date' 'Turbidity'});

    CLspot3=dataset(dates20, chlorspot3, 'VarNames',{'Date' 'ChlorineSpot'});

    temp3=dataset(dates21, tempspot3, 'VarNames',{'Date' 'Temperature'});

    bacti7=dataset(dates22, HPC22C, 'VarNames',{'Date' 'HPC22'});

    bacti8=dataset(dates23, HPC37C, 'VarNames',{'Date' 'HPC37'});

    bacti9=dataset(dates24, colif3, 'VarNames',{'Date' 'Coliforms'});

    disp('Keys and variables specified');

%% Full-outer Join 1 (HPC22 and HPC37 - 2011, 2012 and 2012B)
```

```
% Join a and b, merging the key values as a single variable in the result.

HPC22and37 = join(bacti1,bacti2,'key','Date','Type','outer',...
   'MergeKeys',true);

HPC22and37B = join(bacti4,bacti5,'key','Date','Type','outer',...
   'MergeKeys',true);

HPC22and37C = join(bacti7,bacti8,'key','Date','Type','outer',...
   'MergeKeys',true);

disp('Now look at HPC22and37, HPC22and37B and HPC22and37C - data combined');

%% Full-outer Join 2 (HPC22and37 and colif - 2011, 2012 and 2012B)

bactispot = join(HPC22and37,bacti3,'key','Date','Type','outer',...
        'MergeKeys', true);

bactispot2 = join(HPC22and37B,bacti6,'key','Date','Type','outer',...
        'MergeKeys', true);

bactispot3 = join(HPC22and37C,bacti9,'key','Date','Type','outer',...
        'MergeKeys', true);

    disp('Now look at bactispot, bactispot2 and bactispot3 - spot sampling data
combined');

%% Interpolate flow - 2011, 2012 and 2012B

intFlow = interp1(monit2.Date, monit2.Flow, monit1.Date, 'linear', 'extrap');

intFlow2 = interp1(monit5.Date, monit5.Flow, monit4.Date, 'linear', 'extrap');

intFlow3 = interp1(monit8.Date, monit8.Flow, monit7.Date, 'linear', 'extrap');

    disp('Look at intFlow, intFlow2 and intFlow3')

%% Interpolate turbidity - 2011, 2012 and 2012B

intTurb = interp1(monit3.Date, monit3.Turbidity, monit1.Date, 'linear', 'extrap');

intTurb2 = interp1(monit6.Date, monit6.Turbidity, monit4.Date, 'linear', 'extrap');

intTurb3 = interp1(monit9.Date, monit9.Turbidity, monit7.Date, 'linear', 'extrap');

    disp('Look at intTurb, intTurb2 and intTurb3')

%% Interpolate spot temperature - 2011, 2012 and 2012B

intTemp = interp1(temp.Date, temp.Temperature, monit1.Date, 'linear', 'extrap');

intTemp2 = interp1(temp2.Date, temp2.Temperature, monit4.Date, 'linear', 'extrap');

intTemp3 = interp1(temp3.Date, temp3.Temperature, monit7.Date, 'linear', 'extrap');

    disp('Look at intTemp, intTemp2 and intTemp3')

%% Interpolate spot chlorine - 2011, 2012 and 2012B

intChlor = interp1(CLspot.Date, CLspot.ChlorineSpot, monit1.Date, 'linear', 'extrap');

intChlor2 = interp1(CLspot2.Date, CLspot2.ChlorineSpot, monit4.Date, 'linear',
'extrap');

intChlor3 = interp1(CLspot3.Date, CLspot3.ChlorineSpot, monit7.Date, 'linear',
'extrap');

    disp('Look at intChlor, intChlor2 and intChlor3')

%% Start joining the files together - 2011, 2012 and 2012B

MytheA = monit1;
MytheA.Flow = intFlow;
MytheA.Turbidity = intTurb;
MytheA.TempSpot = intTemp;
MytheA.ChlorSpot = intChlor;


MytheB = monit4;
MytheB.Flow = intFlow2;
```

```
MytheB.Turbidity = intTurb2;
MytheB.TempSpot = intTemp2;
MytheB.ChlorSpot = intChlor2;

MytheC = monit7;
MytheC.Flow = intFlow3;
MytheC.Turbidity = intTurb3;
MytheC.TempSpot = intTemp3;
MytheC.ChlorSpot = intChlor3;

disp('Chlorine and interpolated monitor data combined')

%% Full-outer Join 3 (MytheA and bactispot - 2011, MytheB and bactispot2 - 2012
% and MytheC and bactispot 3 - 2012B)

% 2011
    Mythe2011 = join(MytheA,bactispot,'key','Date','Type','outer',...
        'MergeKeys', true);

    Mythe2011.HPC22(isnan(Mythe2011.HPC22)) = 0;
    Mythe2011.HPC37(isnan(Mythe2011.HPC37)) = 0;
    Mythe2011.Coliforms(isnan(Mythe2011.Coliforms)) = 0;

% 2012
    Mythe2012 = join(MytheB,bactispot2,'key','Date','Type','outer',...
        'MergeKeys', true);

    Mythe2012.HPC22(isnan(Mythe2012.HPC22)) = 0;
    Mythe2012.HPC37(isnan(Mythe2012.HPC37)) = 0;
    Mythe2012.Coliforms(isnan(Mythe2012.Coliforms)) = 0;

% 2012B
    Mythe2012B = join(MytheC,bactispot3,'key','Date','Type','outer',...
        'MergeKeys', true);

    Mythe2012B.HPC22(isnan(Mythe2012B.HPC22)) = 0;
    Mythe2012B.HPC37(isnan(Mythe2012B.HPC37)) = 0;
    Mythe2012B.Coliforms(isnan(Mythe2012B.Coliforms)) = 0;

    disp('Now look at Mythe2011, Mythe2012 and Mythe2012B')

%% Create and add Month field

    [~, Mythe_Month, ~, ~, ~] = datevec(Mythe2011.Date);
    Mythe2011.Date2 = Mythe_Month;

    [~, Mythe_Month2, ~, ~, ~] = datevec(Mythe2012.Date);
    Mythe2012.Date2 = Mythe_Month2;

    [~, Mythe_Month3, ~, ~, ~] = datevec(Mythe2012B.Date);
    Mythe2012B.Date2 = Mythe_Month3;

    disp('Now look at Mythe2011, Mythe2012 and Mythe2012B - all data combined')

%% Cross-correlation - 1

    CLxCLsp = xcorr(Mythe2011.Chlorine, Mythe2011.ChlorSpot);
    CLxCLsp2 = xcorr(Mythe2012.Chlorine, Mythe2012.ChlorSpot);
    CLxCLsp3 = xcorr(Mythe2012B.Chlorine, Mythe2012B.ChlorSpot);

    disp('Now look at CLxCLsp, CLxCLsp2 and CLxCLsp3');

    figure, subplot(3,1,1); plot(CLxCLsp);
        hold on
        title('Plot of XCORR result - chlorine and chlorine spot 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(CLxCLsp2);
        hold on
        title('Plot of XCORR result - chlorine and chlorine spot 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(CLxCLsp3);
        hold on
        title('Plot of XCORR result - chlorine and chlorine spot 2012B')
        xlabel('Lags')
```

```
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 1')

%% Cross-correlation - 2

    CLxHPC22 = xcorr(Mythe2011.Chlorine, Mythe2011.HPC22);
    CLxHPC22B = xcorr(Mythe2012.Chlorine, Mythe2012.HPC22);
    CLxHPC22C = xcorr(Mythe2012B.Chlorine, Mythe2012B.HPC22);

    disp('Now look at CLxHPC22, CLxHPC22B and CLxHPC22C');

    figure, subplot(3,1,1); plot(CLxHPC22);
        hold on
        title('Plot of XCORR result - chlorine and HPC22 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(CLxHPC22B);
        hold on
        title('Plot of XCORR result - chlorine and HPC22 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(CLxHPC22C);
        hold on
        title('Plot of XCORR result - chlorine and HPC22 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 2')

    %% Cross-correlation - 3

    CLxHPC37 = xcorr(Mythe2011.Chlorine, Mythe2011.HPC37);
    CLxHPC37B = xcorr(Mythe2012.Chlorine, Mythe2012.HPC37);
    CLxHPC37C = xcorr(Mythe2012B.Chlorine, Mythe2012B.HPC37);

    disp('Now look at CLxHPC37, CLxHPC37B and CLxHPC22C');

    figure, subplot(3,1,1); plot(CLxHPC37);
        hold on
        title('Plot of XCORR result - chlorine and HPC37 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(CLxHPC37B);
        hold on
        title('Plot of XCORR result - chlorine and HPC37 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(CLxHPC37C);
        hold on
        title('Plot of XCORR result - chlorine and HPC37 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 3')

    %% Cross-correlation - 4

    CLxCO = xcorr(Mythe2011.Chlorine, Mythe2011.Coliforms);
    CLxCO2 = xcorr(Mythe2012.Chlorine, Mythe2012.Coliforms);
    CLxCO3 = xcorr(Mythe2012B.Chlorine, Mythe2012B.Coliforms);

    disp('Now look at CLxCO, CLxCO2 and CLxCO3');

    figure, subplot(3,1,1); plot(CLxCO);
        hold on
```

```
        title('Plot of XCORR result - chlorine and coliforms 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(CLxCO2);
        hold on
        title('Plot of XCORR result - chlorine and coliforms 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(CLxCO3);
        hold on
        title('Plot of XCORR result - chlorine and coliforms 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 4')

%% Cross-correlation - 5

    FLxCL = xcorr(Mythe2011.Flow, Mythe2011.Chlorine);
    FLxCL2 = xcorr(Mythe2012.Flow, Mythe2012.Chlorine);
    FLxCL3 = xcorr(Mythe2012B.Flow, Mythe2012B.Chlorine);

    disp('Now look at FLxCL, FLxCL2 and FLxCL3');

    figure, subplot(3,1,1); plot(FLxCL);
        hold on
        title('Plot of XCORR result - flow and chlorine 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(FLxCL2);
        hold on
        title('Plot of XCORR result - flow and chlorine 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(FLxCL3);
        hold on
        title('Plot of XCORR result - flow and chlorine 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 5')

%% Cross-correlation - 6

    FLxTU = xcorr(Mythe2011.Flow, Mythe2011.Turbidity);
    FLxTU2 = xcorr(Mythe2012.Flow, Mythe2012.Turbidity);
    FLxTU3 = xcorr(Mythe2012B.Flow, Mythe2012B.Turbidity);

    disp('Now look at FLxTU, FLxTU2 and FLxTU3');

    figure, subplot(3,1,1); plot(FLxTU);
        hold on
        title('Plot of XCORR result - flow and turbidity 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(FLxTU2);
        hold on
        title('Plot of XCORR result - flow and turbidity 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(FLxTU3);
        hold on
        title('Plot of XCORR result - flow and turbidity 2012B')
        xlabel('Lags')
```

```
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 6')

%% Cross-correlation - 7

    FLxCLsp = xcorr(Mythe2011.Flow, Mythe2011.ChlorSpot);
    FLxCLsp2 = xcorr(Mythe2012.Flow, Mythe2012.ChlorSpot);
    FLxCLsp3 = xcorr(Mythe2012B.Flow, Mythe2012B.ChlorSpot);

    disp('Now look at FLxCLsp, and FLxCLsp2 and FLxCLsp3');

    figure, subplot(3,1,1); plot(FLxCLsp);
        hold on
        title('Plot of XCORR result - flow and chlorine spot 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(FLxCLsp2);
        hold on
        title('Plot of XCORR result - flow and chlorine spot 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(FLxCLsp3);
        hold on
        title('Plot of XCORR result - flow and chlorine spot 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 7')

%% Cross-correlation - 8

    FLxHPC22 = xcorr(Mythe2011.Flow, Mythe2011.HPC22);
    FLxHPC22B = xcorr(Mythe2012.Flow, Mythe2012.HPC22);
    FLxHPC22C = xcorr(Mythe2012B.Flow, Mythe2012B.HPC22);

    disp('Now look at FLxHPC22, FLxHPC22B and FLxHPC22C');

    figure, subplot(3,1,1); plot(FLxHPC22);
        hold on
        title('Plot of XCORR result - flow and HPC22 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(FLxHPC22B);
        hold on
        title('Plot of XCORR result - flow and HPC22 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(FLxHPC22C);
        hold on
        title('Plot of XCORR result - flow and HPC22 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 8')

%% Cross-correlation - 9

    FLxHPC37 = xcorr(Mythe2011.Flow, Mythe2011.HPC37);
    FLxHPC37B = xcorr(Mythe2012.Flow, Mythe2012.HPC37);
    FLxHPC37C = xcorr(Mythe2012B.Flow, Mythe2012B.HPC37);

    disp('Now look at FLxHPC37, FLxHPC37B FLxHPC37C');

    figure, subplot(3,1,1); plot(FLxHPC37);
        hold on
```

```
        title('Plot of XCORR result - flow and HPC37 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(FLxHPC37B);
        hold on
        title('Plot of XCORR result - flow and HPC37 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(FLxHPC37C);
        hold on
        title('Plot of XCORR result - flow and HPC37 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 9')

%% Cross-correlation - 10

    FLxCO = xcorr(Mythe2011.Flow, Mythe2011.Coliforms);
    FLxCO2 = xcorr(Mythe2012.Flow, Mythe2012.Coliforms);
    FLxCO3 = xcorr(Mythe2012B.Flow, Mythe2012B.Coliforms);

    disp('Now look at FLxCO, FLxCO2 and FLxCO3');

    figure, subplot(3,1,1); plot(FLxCO);
        hold on
        title('Plot of XCORR result - flow and coliforms 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(FLxCO2);
        hold on
        title('Plot of XCORR result - flow and coliforms 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(FLxCO3);
        hold on
        title('Plot of XCORR result - flow and coliforms 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 10')

%% Cross-correlation - 11

    TUxCL = xcorr(Mythe2011.Turbidity, Mythe2011.Chlorine);
    TUxCL2 = xcorr(Mythe2012.Turbidity, Mythe2012.Chlorine);
    TUxCL3 = xcorr(Mythe2012B.Turbidity, Mythe2012B.Chlorine);

    disp('Now look at TUxCL, TUxCL2 and TUxCL3');

    figure, subplot(3,1,1); plot(TUxCL);
        hold on
        title('Plot of XCORR result - turbidity and chlorine 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(TUxCL2);
        hold on
        title('Plot of XCORR result - turbidity and chlorine 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(TUxCL3);
        hold on
        title('Plot of XCORR result - turbidity and chlorine 2012B')
        xlabel('Lags')
```

```
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 11')

%% Cross-correlation - 12

    TUxCLsp = xcorr(Mythe2011.Turbidity, Mythe2011.ChlorSpot);
    TUxCLsp2 = xcorr(Mythe2012.Turbidity, Mythe2012.ChlorSpot);
    TUxCLsp3 = xcorr(Mythe2012B.Turbidity, Mythe2012B.ChlorSpot);

    disp('Now look at TUxCLsp, TUxCLsp2 and TUxCLsp3');

    figure, subplot(3,1,1); plot(TUxCLsp);
        hold on
        title('Plot of XCORR result - turbidity and chlorine spot 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(TUxCLsp2);
        hold on
        title('Plot of XCORR result - turbidity and chlorine spot 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(TUxCLsp3);
        hold on
        title('Plot of XCORR result - turbidity and chlorine spot 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 12')

%% Cross-correlation - 13

    TUxHPC22 = xcorr(Mythe2011.Turbidity, Mythe2011.HPC22);
    TUxHPC22B = xcorr(Mythe2012.Turbidity, Mythe2012.HPC22);
    TUxHPC22C = xcorr(Mythe2012B.Turbidity, Mythe2012B.HPC22);

    disp('Now look at TUxHPC22, TUxHPC22B and TUxHPC22C');

    figure, subplot(3,1,1); plot(TUxHPC22);
        hold on
        title('Plot of XCORR result - turbidity and HPC22 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(TUxHPC22B);
        hold on
        title('Plot of XCORR result - turbidity and HPC22 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(TUxHPC22C);
        hold on
        title('Plot of XCORR result - turbidity and HPC22 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 13')

%% Cross-correlation - 14

    TUxHPC37 = xcorr(Mythe2011.Turbidity, Mythe2011.HPC37);
    TUxHPC37B = xcorr(Mythe2012.Turbidity, Mythe2012.HPC37);
    TUxHPC37C = xcorr(Mythe2012B.Turbidity, Mythe2012B.HPC37);

    disp('Now look at TUxHPC37, TUxHPC37B and TUxHPC37C');

    figure, subplot(3,1,1); plot(TUxHPC37);
        hold on
```

```
        title('Plot of XCORR result - turbidity and HPC37 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(TUxHPC37B);
        hold on
        title('Plot of XCORR result - turbidity and HPC37 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(TUxHPC37C);
        hold on
        title('Plot of XCORR result - turbidity and HPC37 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 14')

%% Cross-correlation - 15

    TUxCO = xcorr(Mythe2011.Turbidity, Mythe2011.Coliforms);
    TUxCO2 = xcorr(Mythe2012.Turbidity, Mythe2012.Coliforms);
    TUxCO3 = xcorr(Mythe2012B.Turbidity, Mythe2012B.Coliforms);

    disp('Now look at TUxCO, TUxCO2 and TUxCO3');

    figure, subplot(3,1,1); plot(TUxCO);
        hold on
        title('Plot of XCORR result - turbidity and coliforms 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(TUxCO2);
        hold on
        title('Plot of XCORR result - turbidity and coliforms 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(TUxCO3);
        hold on
        title('Plot of XCORR result - turbidity and coliforms 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 15')

%% Cross-correlation - 16

    TEspxCL = xcorr(Mythe2011.TempSpot, Mythe2011.Chlorine);
    TEspxCL2 = xcorr(Mythe2012.TempSpot, Mythe2012.Chlorine);
    TEspxCL3 = xcorr(Mythe2012B.TempSpot, Mythe2012B.Chlorine);

    disp('Now look at TEspxCL, TEspxCL2 and TEspxCL3');

    figure, subplot(3,1,1); plot(TEspxCL);
        hold on
        title('Plot of XCORR result - temp spot and chlorine 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(TEspxCL2);
        hold on
        title('Plot of XCORR result - temp spot and chlorine 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(TEspxCL3);
        hold on
        title('Plot of XCORR result - temp spot and chlorine 2012B')
        xlabel('Lags')
```

```
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 16')

%% Cross-correlation - 17

    TEspxTU = xcorr(Mythe2011.TempSpot, Mythe2011.Turbidity);
    TEspxTU2 = xcorr(Mythe2012.TempSpot, Mythe2012.Turbidity);
    TEspxTU3 = xcorr(Mythe2012B.TempSpot, Mythe2012B.Turbidity);

    disp('Now look at TEspxTU, TEspxTU2 and TEspxTU3');

    figure, subplot(3,1,1); plot(TEspxTU);
        hold on
        title('Plot of XCORR result - temp spot and turbidity 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(TEspxTU2);
        hold on
        title('Plot of XCORR result - temp spot and turbidity 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(TEspxTU3);
        hold on
        title('Plot of XCORR result - temp spot and turbidity 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 17')

%% Cross-correlation - 18

    TEspxCLsp = xcorr(Mythe2011.TempSpot, Mythe2011.ChlorSpot);
    TEspxCLsp2 = xcorr(Mythe2012.TempSpot, Mythe2012.ChlorSpot);
    TEspxCLsp3 = xcorr(Mythe2012B.TempSpot, Mythe2012B.ChlorSpot);

    disp('Now look at TEspxCLsp, TEspxCLsp2 and TEspxCLsp3');

    figure, subplot(3,1,1); plot(TEspxCLsp);
        hold on
        title('Plot of XCORR result - temp spot and chlorine spot 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(TEspxCLsp2);
        hold on
        title('Plot of XCORR result - temp spot and chlorine spot 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(TEspxCLsp3);
        hold on
        title('Plot of XCORR result - temp spot and chlorine spot 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 18')

%% Cross-correlation - 19

    TEspxHPC22 = xcorr(Mythe2011.TempSpot, Mythe2011.HPC22);
    TEspxHPC22B = xcorr(Mythe2012.TempSpot, Mythe2012.HPC22);
    TEspxHPC22C = xcorr(Mythe2012B.TempSpot, Mythe2012B.HPC22);

    disp('Now look at TEspxHPC22, TEspxHPC22B and TEspxHPC22C');

    figure, subplot(3,1,1); plot(TEspxHPC22);
        hold on
```

```
        title('Plot of XCORR result - temp spot and HPC22 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(TEspxHPC22B);
        hold on
        title('Plot of XCORR result - temp spot and HPC22 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(TEspxHPC22C);
        hold on
        title('Plot of XCORR result - temp spot and HPC22 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 19')

%% Cross-correlation - 20

    TEspxHPC37 = xcorr(Mythe2011.TempSpot, Mythe2011.HPC37);
    TEspxHPC37B = xcorr(Mythe2012.TempSpot, Mythe2012.HPC37);
    TEspxHPC37C = xcorr(Mythe2012B.TempSpot, Mythe2012B.HPC37);

    disp('Now look at TEspxHPC37, TEspxHPC37B and TEspxHPC37C');

    figure, subplot(3,1,1); plot(TEspxHPC37);
        hold on
        title('Plot of XCORR result - temp spot and HPC37 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(TEspxHPC37B);
        hold on
        title('Plot of XCORR result - temp spot and HPC37 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(TEspxHPC37C);
        hold on
        title('Plot of XCORR result - temp spot and HPC37 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 20')

%% Cross-correlation - 21

    TEspxCO = xcorr(Mythe2011.TempSpot, Mythe2011.Coliforms);
    TEspxCO2 = xcorr(Mythe2012.TempSpot, Mythe2012.Coliforms);
    TEspxCO3 = xcorr(Mythe2012B.TempSpot, Mythe2012B.Coliforms);

    disp('Now look at TEspxCO, TEspxCO2 and TEspxCO3');

    figure, subplot(3,1,1); plot(TEspxCO);
        hold on
        title('Plot of XCORR result - temp spot and coliforms 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(TEspxCO2);
        hold on
        title('Plot of XCORR result - temp spot and coliforms 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(TEspxCO3);
        hold on
        title('Plot of XCORR result - temp spot and coliforms 2012B')
        xlabel('Lags')
```

```
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 21')

%% Cross-correlation - 22

    CLspxHPC22 = xcorr(Mythe2011.ChlorSpot, Mythe2011.HPC22);
    CLspxHPC22B = xcorr(Mythe2012.ChlorSpot, Mythe2012.HPC22);
    CLspxHPC22C = xcorr(Mythe2012B.ChlorSpot, Mythe2012B.HPC22);

    disp('Now look at CLspxHPC22, CLspxHPC22B and CLspxHPC22C');

    figure, subplot(3,1,1); plot(CLspxHPC22);
        hold on
        title('Plot of XCORR result - chlorine spot and HPC22 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(CLspxHPC22B);
        hold on
        title('Plot of XCORR result - chlorine spot and HPC22 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(CLspxHPC22C);
        hold on
        title('Plot of XCORR result - chlorine spot and HPC22 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 22')

%% Cross-correlation - 23

    CLspxHPC37 = xcorr(Mythe2011.ChlorSpot, Mythe2011.HPC37);
    CLspxHPC37B = xcorr(Mythe2012.ChlorSpot, Mythe2012.HPC37);
    CLspxHPC37C = xcorr(Mythe2012B.ChlorSpot, Mythe2012B.HPC37);

    disp('Now look at CLspxHPC37, CLspxHPC37B and CLspxHPC37C');

    figure, subplot(3,1,1); plot(CLspxHPC37);
        hold on
        title('Plot of XCORR result - chlorine spot and HPC37 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(CLspxHPC37B);
        hold on
        title('Plot of XCORR result - chlorine spot and HPC37 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(CLspxHPC37C);
        hold on
        title('Plot of XCORR result - chlorine spot and HPC37 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 23')

%% Cross-correlation - 24

    CLspxCO = xcorr(Mythe2011.ChlorSpot, Mythe2011.Coliforms);
    CLspxCO2 = xcorr(Mythe2012.ChlorSpot, Mythe2012.Coliforms);
    CLspxCO3 = xcorr(Mythe2012B.ChlorSpot, Mythe2012B.Coliforms);

    disp('Now look at CLspxCO, CLspxCO2 and CLspxCO3');

    figure, subplot(3,1,1); plot(CLspxCO);
        hold on
```

```
        title('Plot of XCORR result - chlorine spot and coliforms 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(CLspxCO2);
        hold on
        title('Plot of XCORR result - chlorine spot and coliforms 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(CLspxCO3);
        hold on
        title('Plot of XCORR result - chlorine spot and coliforms 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 24')

%% Cross-correlation - 25

    HPC22xHPC37 = xcorr(Mythe2011.HPC22, Mythe2011.HPC37);
    HPC22xHPC37B = xcorr(Mythe2012.HPC22, Mythe2012.HPC37);
    HPC22xHPC37C = xcorr(Mythe2012B.HPC22, Mythe2012B.HPC37);

    disp('Now look at HPC22xHPC37, HPC22xHPC37B and HPC22xHPC37C');

    figure, subplot(3,1,1); plot(HPC22xHPC37);
        hold on
        title('Plot of XCORR result - HPC22 and HPC37 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(HPC22xHPC37B);
        hold on
        title('Plot of XCORR result - HPC22 and HPC37 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(HPC22xHPC37C);
        hold on
        title('Plot of XCORR result - HPC22 and HPC37 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 25')

%% Cross-correlation - 26

    HPC22xCO = xcorr(Mythe2011.HPC22, Mythe2011.Coliforms);
    HPC22xCO2 = xcorr(Mythe2012.HPC22, Mythe2012.Coliforms);
    HPC22xCO3 = xcorr(Mythe2012B.HPC22, Mythe2012B.Coliforms);

    disp('Now look at HPC22xCO, HPC22xCO2 and HPC22xCO3');

    figure, subplot(3,1,1); plot(HPC22xCO);
        hold on
        title('Plot of XCORR result - HPC22 and coliforms 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(HPC22xCO2);
        hold on
        title('Plot of XCORR result - HPC22 and coliforms 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(HPC22xCO3);
        hold on
        title('Plot of XCORR result - HPC22 and coliforms 2012B')
        xlabel('Lags')
```

```
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 26')

%% Cross-correlation - 27

    HPC37xCO = xcorr(Mythe2011.HPC37, Mythe2011.Coliforms);
    HPC37xCO2 = xcorr(Mythe2012.HPC37, Mythe2012.Coliforms);
    HPC37xCO3 = xcorr(Mythe2012B.HPC37, Mythe2012B.Coliforms);

    disp('Now look at HPC37xCO, HPC37xCO2 and HPC37xCO3');

    figure, subplot(3,1,1); plot(HPC37xCO);
        hold on
        title('Plot of XCORR result - HPC37 and coliforms 2011')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,2); plot(HPC37xCO2);
        hold on
        title('Plot of XCORR result - HPC37 and coliforms 2012')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off
    subplot(3,1,3); plot(HPC37xCO3);
        hold on
        title('Plot of XCORR result - HPC37 and coliforms 2012B')
        xlabel('Lags')
        ylabel('Result')
        legend('XCORR result')
        hold off

    disp('See figure 27')

%% Cross-correlation results

% CLxCLsp 2011
[lagc, index] = max(CLxCLsp);
lagmax = (size(CLxCLsp,1))+1;
lagmid = lagmax/2;
this_lag = lagmid - index;
time_lag_in_hr = this_lag/60;

% CLxHPC22 2011
[lagc2, index2] = max(CLxHPC22);
lagmax2 = (size(CLxHPC22,1))+1;
lagmid2 = lagmax2/2;
this_lag2 = lagmid2 - index2;
time_lag_in_hr2 = this_lag2/60;

% CLxHPC37 2011
[lagc3, index3] = max(CLxHPC37);
lagmax3 = (size(CLxHPC37,1))+1;
lagmid3 = lagmax3/2;
this_lag3 = lagmid3 - index3;
time_lag_in_hr3 = this_lag3/60;

% CLxCO 2011
[lagc4, index4] = max(CLxCO);
lagmax4 = (size(CLxCO,1))+1;
lagmid4 = lagmax4/2;
this_lag4 = lagmid4 - index4;
time_lag_in_hr4 = this_lag4/60;

% FLxCL 2011
[lagc5, index5] = max(FLxCL);
lagmax5 = (size(FLxCL,1))+1;
lagmid5 = lagmax5/2;
this_lag5 = lagmid5 - index5;
time_lag_in_hr5 = this_lag5/60;

% FLxTU 2011
[lagc6, index6] = max(FLxTU);
lagmax6 = (size(FLxTU,1))+1;
lagmid6 = lagmax6/2;
this_lag6 = lagmid6 - index6;
```

```
time_lag_in_hr6 = this_lag6/60;

% FLxCLsp 2011
[lagc7, index7] = max(FLxCLsp);
lagmax7= (size(FLxCLsp,1))+1;
lagmid7 = lagmax7/2;
this_lag7 = lagmid7 - index7;
time_lag_in_hr7 = this_lag7/60;

% FLxHPC22 2011
[lagc8, index8] = max(FLxHPC22);
lagmax8 = (size(FLxHPC22,1))+1;
lagmid8 = lagmax8/2;
this_lag8 = lagmid8 - index8;
time_lag_in_hr8 = this_lag8/60;

% FLxHPC37 2011
[lagc9, index9] = max(FLxHPC37);
lagmax9 = (size(FLxHPC37,1))+1;
lagmid9 = lagmax9/2;
this_lag9 = lagmid9 - index9;
time_lag_in_hr9 = this_lag9/60;

% FLxCO 2011
[lagc10, index10] = max(FLxCO);
lagmax10 = (size(FLxCO,1))+1;
lagmid10 = lagmax10/2;
this_lag10 = lagmid10 - index10;
time_lag_in_hr10 = this_lag10/60;

% TUxCL 2011
[lagc11, index11] = max(TUxCL);
lagmax11 = (size(TUxCL,1))+1;
lagmid11 = lagmax11/2;
this_lag11 = lagmid11 - index11;
time_lag_in_hr11 = this_lag11/60;

% TUxCLsp 2011
[lagc12, index12] = max(TUxCLsp);
lagmax12 = (size(TUxCLsp,1))+1;
lagmid12 = lagmax12/2;
this_lag12 = lagmid12 - index12;
time_lag_in_hr12 = this_lag12/60;

% TUxHPC22 2011
[lagc13, index13] = max(TUxHPC22);
lagmax13 = (size(TUxHPC22,1))+1;
lagmid13 = lagmax13/2;
this_lag13 = lagmid13 - index13;
time_lag_in_hr13 = this_lag13/60;

% TUxHPC37 2011
[lagc14, index14] = max(TUxHPC37);
lagmax14 = (size(TUxHPC37,1))+1;
lagmid14 = lagmax14/2;
this_lag14 = lagmid14 - index14;
time_lag_in_hr14 = this_lag14/60;

% TUxCO 2011
[lagc15, index15] = max(TUxCO);
lagmax15 = (size(TUxCO,1))+1;
lagmid15 = lagmax15/2;
this_lag15 = lagmid15 - index15;
time_lag_in_hr15 = this_lag15/60;

% TEspxCL 2011
[lagc16, index16] = max(TEspxCL);
lagmax16 = (size(TEspxCL,1))+1;
lagmid16 = lagmax16/2;
this_lag16 = lagmid16 - index16;
time_lag_in_hr16 = this_lag16/60;

% TEspxTU 2011
[lagc17, index17] = max(TEspxTU);
lagmax17 = (size(TEspxTU,1))+1;
lagmid17 = lagmax17/2;
this_lag17 = lagmid17 - index17;
time_lag_in_hr17 = this_lag17/60;

% TEspxCLsp 2011
```

```
[lagc18, index18] = max(TEspxCLsp);
lagmax18 = (size(TEspxCLsp,1))+1;
lagmid18 = lagmax18/2;
this_lag18 = lagmid18 - index18;
time_lag_in_hr18 = this_lag18/60;

% TEspxHPC22 2011
[lagc19, index19] = max(TEspxHPC22);
lagmax19 = (size(TEspxHPC22,1))+1;
lagmid19 = lagmax19/2;
this_lag19 = lagmid19 - index19;
time_lag_in_hr19 = this_lag19/60;

% TEspxHPC37 2011
[lagc20, index20] = max(TEspxHPC37);
lagmax20 = (size(TEspxHPC37,1))+1;
lagmid20 = lagmax20/2;
this_lag20 = lagmid20 - index20;
time_lag_in_hr20 = this_lag20/60;

% TEspxCO 2011
[lagc21, index21] = max(TEspxCO);
lagmax21 = (size(TEspxCO,1))+1;
lagmid21 = lagmax21/2;
this_lag21 = lagmid21 - index21;
time_lag_in_hr21 = this_lag21/60;

% CLspxHPC22 2011
[lagc22, index22] = max(CLspxHPC22);
lagmax22 = (size(CLspxHPC22,1))+1;
lagmid22 = lagmax22/2;
this_lag22 = lagmid22 - index22;
time_lag_in_hr22 = this_lag22/60;

% CLspxHPC37 2011
[lagc23, index23] = max(CLspxHPC37);
lagmax23 = (size(CLspxHPC37,1))+1;
lagmid23 = lagmax23/2;
this_lag23 = lagmid23 - index23;
time_lag_in_hr23 = this_lag23/60;

% CLspxCO 2011
[lagc24, index24] = max(CLspxCO);
lagmax24 = (size(CLspxCO,1))+1;
lagmid24 = lagmax24/2;
this_lag24 = lagmid24 - index24;
time_lag_in_hr24 = this_lag24/60;

% HPC22xHPC37 2011
[lagc25, index25] = max(HPC22xHPC37);
lagmax25 = (size(HPC22xHPC37,1))+1;
lagmid25 = lagmax25/2;
this_lag25 = lagmid25 - index25;
time_lag_in_hr25 = this_lag25/60;

% HPC22xCO 2011
[lagc26, index26] = max(HPC22xCO);
lagmax26 = (size(HPC22xCO,1))+1;
lagmid26 = lagmax26/2;
this_lag26 = lagmid26 - index26;
time_lag_in_hr26 = this_lag26/60;

% HPC37xCO 2011
[lagc27, index27] = max(HPC37xCO);
lagmax27 = (size(HPC37xCO,1))+1;
lagmid27 = lagmax27/2;
this_lag27 = lagmid27 - index27;
time_lag_in_hr27 = this_lag27/60;

% CLxCLsp 2012
[lagc28, index28] = max(CLxCLsp2);
lagmax28 = (size(CLxCLsp2,1))+1;
lagmid28 = lagmax28/2;
this_lag28 = lagmid28 - index28;
time_lag_in_hr28 = this_lag28/60;

% CLxHPC22 2012
[lagc29, index29] = max(CLxHPC22B);
lagmax29 = (size(CLxHPC22B,1))+1;
lagmid29 = lagmax29/2;
```

```
this_lag29 = lagmid29 - index29;
time_lag_in_hr29 = this_lag29/60;

% CLxHPC37 2012
[lagc30, index30] = max(CLxHPC37B);
lagmax30 = (size(CLxHPC37B,1))+1;
lagmid30 = lagmax30/2;
this_lag30 = lagmid30 - index30;
time_lag_in_hr30 = this_lag30/60;

% CLxCO 2012
[lagc31, index31] = max(CLxCO2);
lagmax31 = (size(CLxCO2,1))+1;
lagmid31 = lagmax31/2;
this_lag31 = lagmid31 - index31;
time_lag_in_hr31 = this_lag31/60;

% FLxCL 2012
[lagc32, index32] = max(FLxCL2);
lagmax32 = (size(FLxCL2,1))+1;
lagmid32 = lagmax32/2;
this_lag32 = lagmid32 - index32;
time_lag_in_hr32 = this_lag32/60;

% FLxTU 2012
[lagc33, index33] = max(FLxTU2);
lagmax33 = (size(FLxTU2,1))+1;
lagmid33 = lagmax33/2;
this_lag33 = lagmid33 - index33;
time_lag_in_hr33 = this_lag33/60;

% FLxCLsp 2012
[lagc34, index34] = max(FLxCLsp2);
lagmax34 = (size(FLxCLsp2,1))+1;
lagmid34 = lagmax34/2;
this_lag34 = lagmid34 - index34;
time_lag_in_hr34 = this_lag34/60;

% FLxHPC22 2012
[lagc35, index35] = max(FLxHPC22B);
lagmax35 = (size(FLxHPC22B,1))+1;
lagmid35 = lagmax35/2;
this_lag35 = lagmid35 - index35;
time_lag_in_hr35 = this_lag35/60;

% FLxHPC37 2012
[lagc36, index36] = max(FLxHPC37B);
lagmax36 = (size(FLxHPC37B,1))+1;
lagmid36 = lagmax36/2;
this_lag36 = lagmid36 - index36;
time_lag_in_hr36 = this_lag36/60;

% FLxCO 2012
[lagc37, index37] = max(FLxCO2);
lagmax37 = (size(FLxCO2,1))+1;
lagmid37 = lagmax37/2;
this_lag37 = lagmid37 - index37;
time_lag_in_hr37 = this_lag37/60;

% TUxCL 2012
[lagc38, index38] = max(TUxCL2);
lagmax38 = (size(TUxCL2,1))+1;
lagmid38 = lagmax38/2;
this_lag38 = lagmid38 - index38;
time_lag_in_hr38 = this_lag38/60;

% TUxCLsp 2012
[lagc39, index39] = max(TUxCLsp2);
lagmax39 = (size(TUxCLsp2,1))+1;
lagmid39 = lagmax39/2;
this_lag39 = lagmid39 - index39;
time_lag_in_hr39 = this_lag39/60;

% TUxHPC22 2012
[lagc40, index40] = max(TUxHPC22B);
lagmax40 = (size(TUxHPC22B,1))+1;
lagmid40 = lagmax40/2;
this_lag40 = lagmid40 - index40;
time_lag_in_hr40 = this_lag40/60;
```

```
% TUxHPC37 2012
[lagc41, index41] = max(TUxHPC37B);
lagmax41 = (size(TUxHPC37B,1))+1;
lagmid41 = lagmax41/2;
this_lag41 = lagmid41 - index41;
time_lag_in_hr41 = this_lag41/60;

% TUxCO 2012
[lagc42, index42] = max(TUxCO2);
lagmax42 = (size(TUxCO2,1))+1;
lagmid42 = lagmax42/2;
this_lag42 = lagmid42 - index42;
time_lag_in_hr42 = this_lag42/60;

% TEspxCL 2012
[lagc43, index43] = max(TEspxCL2);
lagmax43 = (size(TEspxCL2,1))+1;
lagmid43 = lagmax43/2;
this_lag43 = lagmid43 - index43;
time_lag_in_hr43 = this_lag43/60;

% TEspxTU 2012
[lagc44, index44] = max(TEspxTU2);
lagmax44 = (size(TEspxTU2,1))+1;
lagmid44 = lagmax44/2;
this_lag44 = lagmid44 - index44;
time_lag_in_hr44 = this_lag44/60;

% TEspxCLsp 2012
[lagc45, index45] = max(TEspxCLsp2);
lagmax45 = (size(TEspxCLsp2,1))+1;
lagmid45 = lagmax45/2;
this_lag45 = lagmid45 - index45;
time_lag_in_hr45 = this_lag45/60;

% TEspxHPC22 2012
[lagc46, index46] = max(TEspxHPC22B);
lagmax46 = (size(TEspxHPC22B,1))+1;
lagmid46 = lagmax46/2;
this_lag46 = lagmid46 - index46;
time_lag_in_hr46 = this_lag46/60;

% TEspxHPC37 2012
[lagc47, index47] = max(TEspxHPC37B);
lagmax47 = (size(TEspxHPC37B,1))+1;
lagmid47 = lagmax47/2;
this_lag47 = lagmid47 - index47;
time_lag_in_hr47 = this_lag47/60;

% TEspxCO 2012
[lagc48, index48] = max(TEspxCO2);
lagmax48 = (size(TEspxCO2,1))+1;
lagmid48 = lagmax48/2;
this_lag48 = lagmid48 - index48;
time_lag_in_hr48 = this_lag48/60;

% CLspxHPC22 2012
[lagc49, index49] = max(CLspxHPC22B);
lagmax49 = (size(CLspxHPC22B,1))+1;
lagmid49 = lagmax49/2;
this_lag49 = lagmid49 - index49;
time_lag_in_hr49 = this_lag49/60;

% CLspxHPC37 2012
[lagc50, index50] = max(CLspxHPC37B);
lagmax50 = (size(CLspxHPC37B,1))+1;
lagmid50 = lagmax50/2;
this_lag50 = lagmid50 - index50;
time_lag_in_hr50 = this_lag50/60;

% CLspxCO 2012
[lagc51, index51] = max(CLspxCO2);
lagmax51 = (size(CLspxCO2,1))+1;
lagmid51 = lagmax51/2;
this_lag51 = lagmid51 - index51;
time_lag_in_hr51 = this_lag51/60;

% HPC22xHPC37 2012
[lagc52, index52] = max(HPC22xHPC37B);
lagmax52 = (size(HPC22xHPC37B,1))+1;
```

```
lagmid52 = lagmax52/2;
this_lag52 = lagmid52 - index52;
time_lag_in_hr52 = this_lag52/60;

% HPC22xCO 2012
[lagc53, index53] = max(HPC22xCO2);
lagmax53 = (size(HPC22xCO2,1))+1;
lagmid53 = lagmax53/2;
this_lag53 = lagmid53 - index53;
time_lag_in_hr53 = this_lag53/60;

% HPC37xCO 2012
[lagc54, index54] = max(HPC37xCO2);
lagmax54 = (size(HPC37xCO2,1))+1;
lagmid54 = lagmax54/2;
this_lag54 = lagmid54 - index54;
time_lag_in_hr54 = this_lag54/60;

% CLxCLsp 2012B
[lagc55, index55] = max(CLxCLsp3);
lagmax55 = (size(CLxCLsp3,1))+1;
lagmid55 = lagmax55/2;
this_lag55 = lagmid55 - index55;
time_lag_in_hr55 = this_lag55/60;

% CLxHPC22 2012B
[lagc56, index56] = max(CLxHPC22C);
lagmax56 = (size(CLxHPC22B,1))+1;
lagmid56 = lagmax56/2;
this_lag56 = lagmid56 - index56;
time_lag_in_hr56 = this_lag56/60;

% CLxHPC37 2012B
[lagc57, index57] = max(CLxHPC37C);
lagmax57 = (size(CLxHPC37C,1))+1;
lagmid57 = lagmax57/2;
this_lag57 = lagmid57 - index57;
time_lag_in_hr57 = this_lag57/60;

% CLxCO 2012B
[lagc58, index58] = max(CLxCO3);
lagmax58 = (size(CLxCO3,1))+1;
lagmid58 = lagmax58/2;
this_lag58 = lagmid58 - index58;
time_lag_in_hr58 = this_lag58/60;

% FLxCL 2012B
[lagc59, index59] = max(FLxCL3);
lagmax59 = (size(FLxCL3,1))+1;
lagmid59 = lagmax59/2;
this_lag59 = lagmid59 - index59;
time_lag_in_hr59 = this_lag59/60;

% FLxTU 2012B
[lagc60, index60] = max(FLxTU3);
lagmax60 = (size(FLxTU3,1))+1;
lagmid60 = lagmax60/2;
this_lag60 = lagmid60 - index60;
time_lag_in_hr60 = this_lag60/60;

% FLxCLsp 2012B
[lagc61, index61] = max(FLxCLsp3);
lagmax61 = (size(FLxCLsp3,1))+1;
lagmid61 = lagmax61/2;
this_lag61 = lagmid61 - index61;
time_lag_in_hr61 = this_lag61/60;

% FLxHPC22 2012B
[lagc62, index62] = max(FLxHPC22C);
lagmax62 = (size(FLxHPC22C,1))+1;
lagmid62 = lagmax62/2;
this_lag62 = lagmid62 - index62;
time_lag_in_hr62 = this_lag62/60;

% FLxHPC37 2012B
[lagc63, index63] = max(FLxHPC37C);
lagmax63 = (size(FLxHPC37C,1))+1;
lagmid63 = lagmax63/2;
this_lag63 = lagmid63 - index63;
time_lag_in_hr63 = this_lag63/60;
```

```
% FLxCO 2012B
[lagc64, index64] = max(FLxCO3);
lagmax64 = (size(FLxCO3,1))+1;
lagmid64 = lagmax64/2;
this_lag64 = lagmid64 - index64;
time_lag_in_hr64 = this_lag64/60;

% TUxCL 2012B
[lagc65, index65] = max(TUxCL3);
lagmax65 = (size(TUxCL3,1))+1;
lagmid65 = lagmax65/2;
this_lag65 = lagmid65 - index65;
time_lag_in_hr65 = this_lag65/60;

% TUxCLsp 2012B
[lagc66, index66] = max(TUxCLsp3);
lagmax66 = (size(TUxCLsp3,1))+1;
lagmid66 = lagmax66/2;
this_lag66 = lagmid66 - index66;
time_lag_in_hr66 = this_lag66/60;

% TUxHPC22 2012B
[lagc67, index67] = max(TUxHPC22C);
lagmax67 = (size(TUxHPC22C,1))+1;
lagmid67 = lagmax67/2;
this_lag67 = lagmid67 - index67;
time_lag_in_hr67 = this_lag67/60;

% TUxHPC37 2012B
[lagc68, index68] = max(TUxHPC37C);
lagmax68 = (size(TUxHPC37C,1))+1;
lagmid68 = lagmax68/2;
this_lag68 = lagmid68 - index68;
time_lag_in_hr68 = this_lag68/60;

% TUxCO 2012B
[lagc69, index69] = max(TUxCO3);
lagmax69 = (size(TUxCO3,1))+1;
lagmid69 = lagmax69/2;
this_lag69 = lagmid69 - index69;
time_lag_in_hr69 = this_lag69/60;

% TEspxCL 2012B
[lagc70, index70] = max(TEspxCL3);
lagmax70 = (size(TEspxCL3,1))+1;
lagmid70 = lagmax70/2;
this_lag70 = lagmid70 - index70;
time_lag_in_hr70 = this_lag70/60;

% TEspxTU 2012B
[lagc71, index71] = max(TEspxTU3);
lagmax71 = (size(TEspxTU3,1))+1;
lagmid71 = lagmax71/2;
this_lag71 = lagmid71 - index71;
time_lag_in_hr71 = this_lag71/60;

% TEspxCLsp 2012B
[lagc72, index72] = max(TEspxCLsp3);
lagmax72 = (size(TEspxCLsp3,1))+1;
lagmid72 = lagmax72/2;
this_lag72 = lagmid72 - index72;
time_lag_in_hr72 = this_lag72/60;

% TEspxHPC22 2012B
[lagc73, index73] = max(TEspxHPC22C);
lagmax73 = (size(TEspxHPC22C,1))+1;
lagmid73 = lagmax73/2;
this_lag73 = lagmid73 - index73;
time_lag_in_hr73 = this_lag73/60;

% TEspxHPC37 2012B
[lagc74, index74] = max(TEspxHPC37C);
lagmax74 = (size(TEspxHPC37C,1))+1;
lagmid74 = lagmax74/2;
this_lag74 = lagmid74 - index74;
time_lag_in_hr74 = this_lag74/60;

% TEspxCO 2012B
[lagc75, index75] = max(TEspxCO3);
```

```
lagmax75 = (size(TEspxCO3,1))+1;
lagmid75 = lagmax75/2;
this_lag75 = lagmid75 - index75;
time_lag_in_hr75 = this_lag75/60;

% CLspxHPC22 2012B
[lagc76, index76] = max(CLspxHPC22C);
lagmax76 = (size(CLspxHPC22C,1))+1;
lagmid76 = lagmax76/2;
this_lag76 = lagmid76- index76;
time_lag_in_hr76 = this_lag76/60;

% CLspxHPC37 2012B
[lagc77, index77] = max(CLspxHPC37C);
lagmax77 = (size(CLspxHPC37C,1))+1;
lagmid77 = lagmax77/2;
this_lag77 = lagmid77 - index77;
time_lag_in_hr77 = this_lag77/60;

% CLspxCO 2012B
[lagc78, index78] = max(CLspxCO3);
lagmax78 = (size(CLspxCO3,1))+1;
lagmid78 = lagmax78/2;
this_lag78 = lagmid78 - index78;
time_lag_in_hr78 = this_lag78/60;

% HPC22xHPC37 2012B
[lagc79, index79] = max(HPC22xHPC37C);
lagmax79 = (size(HPC22xHPC37C,1))+1;
lagmid79 = lagmax79/2;
this_lag79 = lagmid79 - index79;
time_lag_in_hr79 = this_lag79/60;

% HPC22xCO 2012B
[lagc80, index80] = max(HPC22xCO3);
lagmax80 = (size(HPC22xCO3,1))+1;
lagmid80 = lagmax80/2;
this_lag80 = lagmid80 - index80;
time_lag_in_hr80 = this_lag80/60;

% HPC37xCO 2012B
[lagc81, index81] = max(HPC37xCO3);
lagmax81 = (size(HPC37xCO3,1))+1;
lagmid81 = lagmax81/2;
this_lag81 = lagmid81 - index81;
time_lag_in_hr81 = this_lag81/60;

% Compiling output file
XCORRname = {'CLxCLsp'; 'CLxHPC22'; 'CLxHPC37'; 'CLxCO'; 'FLxCL';...
    'FLxTU'; 'FLxCLsp'; 'FLxHPC22'; 'FLxHPC37'; 'FLxCO'; 'TUxCL';...
    'TUxCLsp'; 'TUxHPC22'; 'TUxHPC37'; 'TUxCO'; 'TEspxCL'; 'TEspxTU';...
    'TEspxCLsp'; 'TEspxHPC22'; 'TEspxHPC37'; 'TEspxCO'; 'CLspxHPC22';...
    'CLspxHPC37';'CLspxCO';'HPC22xHPC37';'HPC22xCO';'HPC37xCO';...
    'CLxCLsp2'; 'CLxHPC22B'; 'CLxHPC37B'; 'CLxCO2'; 'FLxCL2'; 'FLxTU2';...
    'FLxCLsp2'; 'FLxHPC22B'; 'FLxHPC37B'; 'FLxCO2'; 'TUxCL2';...
    'TUxCLsp2'; 'TUxHPC22B'; 'TUxHPC37B'; 'TUxCO2'; 'TEspxCL2'; 'TEspxTU2';...
    'TEspxCLsp2'; 'TEspxHPC22B'; 'TEspxHPC37B'; 'TEspxCO2'; 'CLspxHPC22B';...
    'CLspxHPC37B'; 'CLspxCO2'; 'HPC22xHPC37B'; 'HPC22xCO2';'HPC37xCO2';...
    'CLxCLsp3'; 'CLxHPC22C'; 'CLxHPC37C'; 'CLxCO3'; 'FLxCL3'; 'FLxTU3';...
    'FLxCLsp3'; 'FLxHPC22C'; 'FLxHPC37C'; 'FLxCO3'; 'TUxCL3';...
    'TUxCLsp3'; 'TUxHPC22C'; 'TUxHPC37C'; 'TUxCO3'; 'TEspxCL3'; 'TEspxTU3';...
    'TEspxCLsp3'; 'TEspxHPC22C'; 'TEspxHPC37C'; 'TEspxCO3'; 'CLspxHPC22C';...
    'CLspxHPC37C'; 'CLspxCO3'; 'HPC22xHPC37C'; 'HPC22xCO3'; 'HPC37xCO3'};
MaxXCORR = [lagc; lagc2; lagc3; lagc4; lagc5; lagc6; lagc7; lagc8; lagc9; lagc10;...
    lagc11; lagc12; lagc13; lagc14; lagc15; lagc16; lagc17; lagc18; lagc19;...
    lagc20; lagc21; lagc22; lagc23; lagc24; lagc25; lagc26; lagc27; lagc28;...
    lagc29; lagc30; lagc31; lagc32; lagc33; lagc34; lagc35; lagc36; lagc37;...
    lagc38; lagc39; lagc40; lagc41; lagc42; lagc43; lagc44; lagc45; lagc46;...
    lagc47; lagc48; lagc49; lagc50; lagc51; lagc52; lagc53; lagc54; lagc55;...
    lagc56; lagc57; lagc58; lagc59; lagc60; lagc61; lagc62; lagc63; lagc64;...
    lagc65; lagc66; lagc67; lagc68; lagc69; lagc70; lagc71; lagc72; lagc73;...
    lagc74; lagc75; lagc76; lagc77; lagc78; lagc79; lagc80; lagc81];
TimeLagHr = [time_lag_in_hr; time_lag_in_hr2; time_lag_in_hr3; time_lag_in_hr4;...
    time_lag_in_hr5; time_lag_in_hr6; time_lag_in_hr7; time_lag_in_hr8;...
    time_lag_in_hr9; time_lag_in_hr10; time_lag_in_hr11; time_lag_in_hr12;...
    time_lag_in_hr13; time_lag_in_hr14; time_lag_in_hr15; time_lag_in_hr16;...
    time_lag_in_hr17; time_lag_in_hr18; time_lag_in_hr19; time_lag_in_hr20;...
    time_lag_in_hr21; time_lag_in_hr22; time_lag_in_hr23; time_lag_in_hr24;...
    time_lag_in_hr25; time_lag_in_hr26; time_lag_in_hr27; time_lag_in_hr28;...
    time_lag_in_hr29; time_lag_in_hr30; time_lag_in_hr31; time_lag_in_hr32;...
```

```
    time_lag_in_hr33; time_lag_in_hr34; time_lag_in_hr35; time_lag_in_hr36;...
    time_lag_in_hr37; time_lag_in_hr38; time_lag_in_hr39; time_lag_in_hr40;...
    time_lag_in_hr41; time_lag_in_hr42; time_lag_in_hr43; time_lag_in_hr44;...
    time_lag_in_hr45; time_lag_in_hr46; time_lag_in_hr47; time_lag_in_hr48;...
    time_lag_in_hr49; time_lag_in_hr50; time_lag_in_hr51; time_lag_in_hr52;...
    time_lag_in_hr53; time_lag_in_hr54; time_lag_in_hr55; time_lag_in_hr56;...
    time_lag_in_hr57; time_lag_in_hr58; time_lag_in_hr59; time_lag_in_hr60;...
    time_lag_in_hr61; time_lag_in_hr62; time_lag_in_hr63; time_lag_in_hr64;...
    time_lag_in_hr65; time_lag_in_hr66; time_lag_in_hr67; time_lag_in_hr68;...
    time_lag_in_hr69; time_lag_in_hr70; time_lag_in_hr71; time_lag_in_hr72;...
    time_lag_in_hr73; time_lag_in_hr74; time_lag_in_hr75; time_lag_in_hr76;...
    time_lag_in_hr77; time_lag_in_hr78; time_lag_in_hr79; time_lag_in_hr80;...
    time_lag_in_hr81];
xcorrRES = dataset(XCORRname, MaxXCORR, TimeLagHr, 'VarNames', {'Cross_CORR',...
    'MaxXCORR', 'TimeLagHr'});

disp('XCORR output file ready to view: xcorrRES')

%% Indexes results between 0 and 24 hr (+ve)
xcorrBEST = xcorrRES(xcorrRES.TimeLagHr >=0 & xcorrRES.TimeLagHr <=24,:);
xcorrBEST(:,{'Cross_CORR','MaxXCORR','TimeLagHr'});

disp('Best XCORR results ready to view: xcorrBEST')

%% Self-Organising Maps

% Mythe 2011
   TRAIN_CORE =[Mythe2011.Flow Mythe2011.Turbidity Mythe2011.Chlorine ...
       Mythe2011.ChlorSpot Mythe2011.TempSpot Mythe2011.HPC22 ...
       Mythe2011.HPC37 Mythe2011.Coliforms];

   sData=som_data_struct(TRAIN_CORE);

   sData=som_normalize(sData,'range');%also histogram equalisation and logarithmic
scaling
   sM = som_make((sData), 'msize', [60 40]); %performs rough training with large initial
% neighbourhood and large initial training and then fine training.
% By default linear initialisation used and batch training

sM.comp_names{1}='Flow_11';
sM.comp_names{2}='Turbidity_11';
sM.comp_names{3}='Chlorine_11';
sM.comp_names{4}='ChlorSpot_11';
sM.comp_names{5}='TempSpot_11';
sM.comp_names{6}='HPC22_11';
sM.comp_names{7}='HPC37_11';
sM.comp_names{8}='Coliforms_11';

figure, som_show(sM);

% Mythe 2012a
   TRAIN_CORE =[Mythe2012.Flow Mythe2012.Turbidity Mythe2012.Chlorine ...
       Mythe2012.ChlorSpot Mythe2012.TempSpot Mythe2012.HPC22 ...
       Mythe2012.HPC37 Mythe2012.Coliforms];

   sData=som_data_struct(TRAIN_CORE);

   sData=som_normalize(sData,'range');
   sM = som_make((sData), 'msize', [60 40]);

sM.comp_names{1}='Flow_12a';
sM.comp_names{2}='Turbidity_12a';
sM.comp_names{3}='Chlorine_12a';
sM.comp_names{4}='ChlorSpot_12a';
sM.comp_names{5}='TempSpot_12a';
sM.comp_names{6}='HPC22_12a';
sM.comp_names{7}='HPC37_12a';
sM.comp_names{8}='Coliforms_12a';

figure, som_show(sM);

% Mythe 2012b
   TRAIN_CORE =[Mythe2012B.Flow Mythe2012B.Turbidity Mythe2012B.Chlorine ...
       Mythe2012B.ChlorSpot Mythe2012B.TempSpot Mythe2012B.HPC22 ...
       Mythe2012B.HPC37 Mythe2012B.Coliforms];

   sData=som_data_struct(TRAIN_CORE);

   sData=som_normalize(sData,'range');
   sM = som_make((sData), 'msize', [60 40]);
```

```
sM.comp_names{1}='Flow12B';
sM.comp_names{2}='Turbidity12B';
sM.comp_names{3}='Chlorine12B';
sM.comp_names{4}='ChlorSpot12B';
sM.comp_names{5}='TempSpot12B';
sM.comp_names{6}='HPC22_12B';
sM.comp_names{7}='HPC37_12B';
sM.comp_names{8}='Coliforms12B';

figure, som_show(sM);
```

Appendix 2. Strensham cross-correlation results

Cross-correlation results for Raw coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
RawCO	RawEC	0.0	-	0.0	0.0	0.0	0.0
RawCO	RawNC	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	RawCLOS	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	RawEN	0.0	0.0	-	0.0	0.0	0.0
RawCO	RawTurb	21.4	0.0	0.0	0.0	0.0	0.0
RawCO	RawpHSpot	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	RawpHMon	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	ASettCO	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	ASettEC	3.9	0.0	0.0	0.0	0.0	0.0
RawCO	ASettNC	-	0.0	0.0	0.0	0.0	0.0
RawCO	ASettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	ASettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	BSettCO	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	BSettEC	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	BSettNC	-	0.0	0.0	0.0	0.0	0.0
RawCO	BSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	BSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	CSettCO	-	0.0	0.0	0.0	0.0	0.0
RawCO	CSettEC	0.8	0.0	0.0	0.0	0.0	0.0
RawCO	CSettNC	-	0.0	0.0	0.0	0.0	0.0
RawCO	CSettTurb	-	0.0	0.0	0.0	0.0	0.0
RawCO	CSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	DSettCO	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	DSettEC	-	0.0	0.0	0.0	0.0	0.0
RawCO	DSettNC	-	0.0	0.0	0.0	0.0	0.0
RawCO	DSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	DSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	ABCFiltEC	0.1	0.0	0.0	0.0	0.0	0.0
RawCO	ABCFiltNC	-	0.0	0.0	0.0	0.0	0.0
RawCO	ABCFiltTurb	-	0.0	0.0	0.0	0.0	0.0
RawCO	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	DFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	DFiltEC	1.5	0.0	0.0	0.0	0.0	0.0
RawCO	DFiltNC	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	DFiltTurb	-	-	0.0	0.0	0.0	0.0
RawCO	DFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	GACCO	0.0	-	0.0	0.0	-	0.0
RawCO	GACEC	-	-	-	10.7	-	-
RawCO	GACNC	-	-	0.0	0.0	-	-
RawCO	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	CONTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	BALTurb	4.0	0.0	0.0	0.0	5.4	0.0
RawCO	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
RawCO	FINHPC37	21.8	-	-	-	-	-
RawCO	FINNC1L	-	-	-	-	23.7	-
RawCO	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawCO	FINpH	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Raw *E. coli* that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
RawEC	RawCO	0.0	4.6	0.0	0.0	0.0	0.0
RawEC	RawNC	2.2	11.8	0.0	0.0	0.0	0.0
RawEC	RawCLOS	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	RawEN	22.9	0.0	-	0.0	0.0	0.0
RawEC	RawTurb	1.6	0.0	0.0	0.0	0.0	0.0
RawEC	RawpHSpot	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	RawpHMon	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	ASettCO	12.2	1.4	0.0	0.0	0.0	0.0
RawEC	ASettEC	13.9	0.0	0.0	-	0.0	0.0
RawEC	ASettNC	-	0.0	0.0	0.0	0.0	0.0
RawEC	ASettTurb	-	0.0	0.0	0.0	0.0	0.0
RawEC	ASettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	BSettCO	-	3.3	0.0	-	0.0	0.0
RawEC	BSettEC	4.2	-	0.0	-	0.0	0.0
RawEC	BSettNC	-	-	0.0	-	0.0	0.0
RawEC	BSettTurb	-	0.0	0.0	0.0	0.0	0.0
RawEC	BSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	CSettCO	-	0.0	0.0	-	0.0	0.0
RawEC	CSettEC	17.8	15.2	0.0	-	0.0	-
RawEC	CSettNC	-	0.0	0.0	-	0.0	0.0
RawEC	CSettTurb	-	0.0	-	0.0	0.0	0.0
RawEC	CSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	DSettCO	8.1	10.5	0.0	-	0.0	0.0
RawEC	DSettEC	0.8	0.0	0.0	0.0	0.0	0.0
RawEC	DSettNC	-	-	0.0	0.0	0.0	0.0
RawEC	DSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	DSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	ABCFiltEC	4.7	3.8	0.0	-	0.0	0.0
RawEC	ABCFiltNC	-	0.0	-	0.0	0.0	0.0
RawEC	ABCFiltTurb	-	0.0	0.0	0.0	0.0	0.0
RawEC	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	DFiltCO	0.1	0.0	0.0	0.0	0.0	0.0
RawEC	DFiltEC	5.7	5.3	0.0	0.0	0.0	0.0
RawEC	DFiltNC	-	0.0	-	0.0	0.0	0.0
RawEC	DFiltTurb	-	-	0.0	0.0	0.0	0.0
RawEC	DFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	GACCO	-	0.0	0.0	-	0.0	-
RawEC	GACNC	-	-	0.0	-	-	-
RawEC	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	CONTurb	-	0.9	0.0	0.0	0.0	0.0
RawEC	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	BALTurb	-	0.0	-	-	0.0	0.0
RawEC	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	FINFlow	-	0.0	-	0.0	0.0	0.0
RawEC	FINTurbMon	-	14.0	-	0.0	0.0	0.0
RawEC	FINCO	-	20.3	-	-	-	-
RawEC	FINCO1L	-	-	-	-	12.3	-
RawEC	FINFreeCL	2.0	0.0	0.0	0.0	0.0	0.0
RawEC	FINTurb	-	0.0	0.0	0.0	0.0	0.0
RawEC	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
RawEC	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Raw non-coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
RawNC	RawCO	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	RawEC	-	-	0.0	0.0	0.0	0.0
RawNC	RawCLOS	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	RawEN	-	0.0	-	0.0	0.0	0.0
RawNC	RawTurb	-	0.0	0.0	0.0	0.0	0.0
RawNC	RawpHSpot	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	RawpHMon	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	ASettCO	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	ASettEC	5.0	0.0	0.0	-	0.0	0.0
RawNC	ASettNC	-	0.0	0.0	0.0	0.0	0.0
RawNC	ASettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	ASettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	BSettCO	0.0	0.0	0.0	-	0.0	0.0
RawNC	BSettEC	6.5	0.0	0.0	-	0.0	0.0
RawNC	BSettNC	-	0.0	0.0	-	0.0	0.0
RawNC	BSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	BSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	CSettCO	0.0	0.0	0.0	-	0.0	0.0
RawNC	CSettEC	7.7	0.0	0.0	-	0.0	0.0
RawNC	CSettNC	-	0.0	0.0	-	0.0	0.0
RawNC	CSettTurb	-	0.0	0.0	0.0	0.0	0.0
RawNC	CSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	DSettCO	-	0.0	0.0	-	0.0	0.0
RawNC	DSettEC	-	0.0	0.0	0.0	0.0	0.0
RawNC	DSettNC	-	0.0	0.0	0.0	0.0	0.0
RawNC	DSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	DSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	ABCFiltCO	1.7	0.0	0.0	0.0	0.0	0.0
RawNC	ABCFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	ABCFiltNC	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	ABCFiltTurb	-	0.0	0.0	0.0	0.0	0.0
RawNC	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	DFiltCO	1.2	0.0	0.0	0.0	0.0	0.0
RawNC	DFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	DFiltNC	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	DFiltTurb	-	0.0	0.0	0.0	0.0	0.0
RawNC	DFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	GACCO	-	-	0.0	-	-	0.1
RawNC	GACNC	-	0.0	0.0	-	-	5.3
RawNC	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	CONTurb	-	0.0	0.0	0.0	0.0	0.0
RawNC	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	CONTotalCL	0.1	0.0	0.0	0.0	0.0	0.0
RawNC	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	BALTurb	-	0.0	0.0	-	0.0	0.0
RawNC	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	FINFlow	8.7	0.0	0.0	0.0	0.0	0.0
RawNC	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
RawNC	FINFreeCL	8.1	0.0	0.0	0.0	0.0	0.0
RawNC	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
RawNC	FINTotalCL	3.5	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Raw turbidity that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
RawTurb	RawCO	-	0.0	0.0	0.0	0.0	0.0
RawTurb	RawEC	-	0.0	0.0	0.0	0.0	0.0
RawTurb	RawNC	-	0.0	0.0	0.0	0.0	0.0
RawTurb	RawCLOS	0.0	0.0	0.0	0.0	0.0	0.0
RawTurb	RawEN	-	0.0	-	0.0	0.0	0.0
RawTurb	RawpHSpot	-	0.0	0.0	0.0	0.0	0.0
RawTurb	RawpHMon	-	0.0	0.0	0.0	0.0	0.0
RawTurb	ASettCO	-	0.0	0.0	0.0	0.0	0.0
RawTurb	ASettEC	-	0.0	0.0	-	0.0	0.0
RawTurb	ASettNC	-	0.0	0.0	-	0.0	0.0
RawTurb	ASettTurb	-	0.0	0.0	0.0	0.0	0.0
RawTurb	ASettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawTurb	BSettCO	-	0.0	0.0	-	0.0	0.0
RawTurb	BSettEC	-	0.0	0.0	-	0.0	0.0
RawTurb	BSettNC	-	0.0	0.0	-	0.0	0.0
RawTurb	BSettTurb	-	0.0	0.0	0.0	0.0	0.0
RawTurb	BSettpH	-	0.0	0.0	0.0	0.0	0.0
RawTurb	CSettCO	-	0.0	0.0	-	0.0	0.0
RawTurb	CSettEC	-	0.0	0.0	-	0.0	0.0
RawTurb	CSettNC	-	0.0	0.0	-	0.0	0.0
RawTurb	CSettTurb	-	0.0	0.0	0.0	0.0	0.0
RawTurb	CSettpH	-	0.0	0.0	0.0	0.0	0.0
RawTurb	DSettCO	-	0.0	0.0	0.0	0.0	0.0
RawTurb	DSettEC	-	0.0	0.0	0.0	0.0	0.0
RawTurb	DSettNC	-	0.0	0.0	-	0.0	0.0
RawTurb	DSettTurb	-	0.0	0.0	-	0.0	0.0
RawTurb	DSettpH	-	0.0	0.0	0.0	0.0	0.0
RawTurb	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
RawTurb	ABCFiltEC	-	0.0	0.0	-	0.0	0.0
RawTurb	ABCFiltNC	-	0.0	0.0	0.0	0.0	0.0
RawTurb	ABCFiltTurb	-	0.0	0.0	0.0	0.0	0.0
RawTurb	ABCFiltpH	-	0.0	0.0	0.0	0.0	0.0
RawTurb	DFiltCO	-	0.0	0.0	0.0	0.0	0.0
RawTurb	DFiltEC	-	0.0	0.0	-	0.0	0.0
RawTurb	DFiltNC	-	0.0	0.0	0.0	0.0	0.0
RawTurb	DFiltTurb	-	0.0	0.0	0.0	0.0	0.0
RawTurb	DFiltpH	-	0.0	0.0	0.0	0.0	0.0
RawTurb	GACCO	-	-	0.0	-	-	0.0
RawTurb	GACNC	-	-	0.0	-	-	-
RawTurb	GACpH	-	0.0	0.0	0.0	0.0	0.0
RawTurb	CONFreeCL	-	0.0	0.0	0.0	0.0	0.0
RawTurb	CONTurb	-	0.0	0.0	-	0.0	0.0
RawTurb	CONpH	-	0.0	0.0	0.0	0.0	0.0
RawTurb	CONTotalCL	-	0.0	0.0	0.0	0.0	0.0
RawTurb	BALFreeCL	-	0.0	0.0	0.0	0.0	0.0
RawTurb	BALTurb	-	0.0	0.0	-	0.0	0.0
RawTurb	BALpH	-	0.0	0.0	0.0	0.0	0.0
RawTurb	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
RawTurb	FINCLMon	-	0.0	0.0	0.0	0.0	0.0
RawTurb	FINFlow	-	0.0	0.0	0.0	0.0	0.0
RawTurb	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
RawTurb	FINCO	-	20.3	-	-	-	-
RawTurb	FINNC1L	-	-	-	-	23.7	-
RawTurb	FINFreeCL	-	0.0	0.0	0.0	0.0	0.0
RawTurb	FINTurb	-	0.0	0.0	0.0	0.0	0.0
RawTurb	FINpH	-	0.0	0.0	0.0	0.0	0.0
RawTurb	FINTotalCL	-	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Raw spot-sampled pH that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
RawpHSpot	RawCO	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	RawEC	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	RawNC	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	RawCLOS	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	RawEN	-	0.0	-	0.0	0.0	0.0
RawpHSpot	RawTurb	17.3	0.0	0.0	0.0	0.0	0.0
RawpHSpot	RawpHMon	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	ASettCO	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	ASettEC	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	ASettNC	-	0.0	0.0	0.0	0.0	0.0
RawpHSpot	ASettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	ASettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	BSettCO	-	0.0	0.0	0.0	0.0	0.0
RawpHSpot	BSettEC	3.9	0.0	0.0	0.0	0.0	0.0
RawpHSpot	BSettNC	6.1	0.0	0.0	0.0	0.0	0.0
RawpHSpot	BSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	BSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	CSettCO	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	CSettEC	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	CSettNC	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	CSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	CSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	DSettCO	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	DSettEC	-	0.0	0.0	0.0	0.0	0.0
RawpHSpot	DSettNC	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	DSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	DSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	ABCFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	ABCFiltNC	-	0.0	0.0	0.0	0.0	0.0
RawpHSpot	ABCFiltTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	DFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	DFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	DFiltNC	-	0.0	0.0	0.0	0.0	0.0
RawpHSpot	DFiltTurb	10.9	0.0	0.0	0.0	0.0	0.0
RawpHSpot	DFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	GACCO	-	0.0	0.0	0.0	0.0	0.6
RawpHSpot	GACNC	-	0.0	0.0	0.0	0.0	-
RawpHSpot	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	CONHPC37	-	-	23.7	-	-	-
RawpHSpot	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	CONTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	FINTurbMon	7.4	0.0	0.0	0.0	0.0	0.0
RawpHSpot	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHSpot	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Raw monitor pH that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
RawpHMon	RawCO	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	RawEC	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	RawNC	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	RawCLOS	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	RawEN	-	0.0	-	0.0	0.0	0.0
RawpHMon	RawTurb	-	0.0	0.0	0.0	0.0	0.0
RawpHMon	RawpHSpot	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	ASettCO	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	ASettEC	0.0	0.0	1.6	0.0	0.0	0.0
RawpHMon	ASettNC	-	0.0	0.0	0.0	0.0	0.0
RawpHMon	ASettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	ASettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	BSettCO	-	0.0	0.0	0.0	0.0	0.0
RawpHMon	BSettEC	-	0.0	0.0	0.0	0.0	0.0
RawpHMon	BSettNC	-	0.0	0.0	0.0	0.0	0.0
RawpHMon	BSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	BSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	CSettCO	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	CSettEC	0.0	0.0	3.3	0.0	0.0	0.0
RawpHMon	CSettNC	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	CSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	CSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	DSettCO	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	DSettEC	-	0.0	0.0	0.0	0.0	0.0
RawpHMon	DSettNC	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	DSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	DSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	ABCFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	ABCFiltNC	-	0.0	0.0	0.0	0.0	0.0
RawpHMon	ABCFiltTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	DFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	DFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	DFiltNC	-	0.0	0.0	0.0	0.0	0.0
RawpHMon	DFiltTurb	16.4	0.0	0.0	0.0	0.0	0.0
RawpHMon	DFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	GACCO	-	0.0	0.0	0.0	0.0	0.3
RawpHMon	GACEC	-	-	-	0.0	-	15.0
RawpHMon	GACNC	-	0.0	0.0	0.0	0.0	17.9
RawpHMon	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	CONTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	FINTurbMon	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
RawpHMon	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Raw water temperature that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
RawTemp	RawCO	-	0.0	0.0	0.0	0.0	0.0
RawTemp	RawEC	-	0.0	0.0	0.0	0.0	0.0
RawTemp	RawNC	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	RawCLOS	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	RawTurb	-	0.0	0.0	0.0	0.0	0.0
RawTemp	RawpHSpot	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	RawpHMon	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	ASettCO	-	0.0	0.0	0.0	0.0	0.0
RawTemp	ASettEC	-	0.0	3.4	0.0	0.0	0.0
RawTemp	ASettNC	-	0.0	0.0	0.0	0.0	0.0
RawTemp	ASettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	ASettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	BSettCO	-	-	0.0	0.0	0.0	0.0
RawTemp	BSettEC	-	9.5	0.0	0.0	0.0	0.0
RawTemp	BSettNC	-	10.3	0.0	0.0	0.0	0.0
RawTemp	BSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	BSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	CSettCO	-	0.0	0.0	0.0	0.0	0.0
RawTemp	CSettEC	-	-	5.8	0.0	0.0	0.0
RawTemp	CSettNC	-	0.0	0.0	0.0	0.0	0.0
RawTemp	CSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	CSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	DSettCO	-	-	0.0	0.0	0.0	0.0
RawTemp	DSettEC	-	9.0	0.0	0.0	0.0	0.0
RawTemp	DSettNC	-	0.0	0.0	0.0	0.0	0.0
RawTemp	DSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	DSettpH	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	ABCFiltEC	-	0.0	0.0	0.0	0.0	0.0
RawTemp	ABCFiltNC	-	0.0	0.0	0.0	0.0	0.0
RawTemp	ABCFiltTurb	-	0.0	0.0	0.0	0.0	0.0
RawTemp	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	DFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	DFiltEC	-	0.0	0.0	0.0	0.0	0.0
RawTemp	DFiltNC	-	0.0	0.0	0.0	0.0	0.0
RawTemp	DFiltTurb	17.2	6.2	0.0	0.0	0.0	0.0
RawTemp	DFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	GACCO	-	-	0.0	0.0	-	0.0
RawTemp	GACNC	-	0.0	0.0	0.0	0.0	0.0
RawTemp	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	CONTurb	11.6	0.0	0.0	0.0	0.0	0.0
RawTemp	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	BALTurb	4.0	0.0	0.0	0.0	0.0	0.0
RawTemp	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
RawTemp	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
RawTemp	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Settlement Tank A coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
ASettCO	ASettEC	0.0	0.0	0.0	0.0	0.0	0.0
ASettCO	ASettNC	-	0.0	0.0	0.0	0.0	0.0
ASettCO	ASettTurb	0.0	0.0	0.0	0.0	0.0	0.0
ASettCO	ASettpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettCO	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
ASettCO	ABCFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
ASettCO	ABCFiltNC	-	0.0	-	0.0	0.0	0.0
ASettCO	ABCFiltTurb	-	0.0	0.0	0.0	0.0	0.0
ASettCO	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettCO	GACCO	-	-	0.0	4.6	0.0	-
ASettCO	GACEC	-	-	-	11.4	-	-
ASettCO	GACNC	-	-	0.0	2.4	-	-
ASettCO	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettCO	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettCO	CONTurb	-	0.0	0.0	0.0	0.0	0.0
ASettCO	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettCO	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettCO	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettCO	BALTurb	-	0.0	0.0	0.0	9.4	0.0
ASettCO	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettCO	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettCO	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
ASettCO	FINFlow	-	-	0.0	0.0	0.0	0.0
ASettCO	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
ASettCO	FINCO	-	23.4	-	-	-	-
ASettCO	FINCO1L	-	-	-	23.8	-	-
ASettCO	FINNC1L	-	-	-	-	23.7	-
ASettCO	FINFreeCL	-	0.0	0.0	0.0	0.0	0.0
ASettCO	FINTurb	-	0.0	0.0	0.0	0.0	0.0
ASettCO	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettCO	FINTotalCL	-	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Settlement Tank A *E. coli* that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
ASettEC	ASettCO	0.0	0.0	0.0	0.0	0.0	0.0
ASettEC	ASettNC	-	0.0	0.0	0.0	0.0	0.0
ASettEC	ASettTurb	0.0	0.0	-	-	0.0	0.0
ASettEC	ASettpH	0.0	0.0	-	0.0	0.0	0.0
ASettEC	ABCFiltCO	-	0.0	0.0	0.0	0.0	0.0
ASettEC	ABCFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
ASettEC	ABCFiltNC	-	0.0	-	0.0	0.0	0.0
ASettEC	ABCFiltTurb	-	0.0	0.0	0.0	0.0	0.0
ASettEC	ABCFiltpH	0.0	0.0	-	0.0	0.0	0.0
ASettEC	GACCO	-	0.0	0.0	-	-	0.0
ASettEC	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettEC	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettEC	CONTurb	-	0.0	-	0.0	0.0	0.0
ASettEC	CONpH	0.0	0.0	-	0.0	0.0	0.0
ASettEC	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettEC	BALFreeCL	-	0.0	0.0	0.0	0.0	0.0
ASettEC	BALTurb	0.0	0.0	-	0.0	0.0	0.0
ASettEC	BALpH	0.0	0.0	-	0.0	0.0	0.0
ASettEC	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettEC	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
ASettEC	FINFlow	-	0.0	-	0.0	0.0	0.0
ASettEC	FINTurbMon	-	0.0	-	0.0	0.0	0.0
ASettEC	FINCO	-	23.4	-	-	-	-
ASettEC	FINFreeCL	-	0.0	0.0	21.4	0.0	0.0
ASettEC	FINTurb	-	0.0	0.0	0.0	0.0	0.0
ASettEC	FINpH	0.0	0.0	-	0.0	0.0	0.0
ASettEC	FINTotalCL	-	0.0	0.0	20.0	0.0	0.0

Cross-correlation results for Settlement Tank A non-coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
ASettNC	ASettCO	13.0	0.0	0.0	0.0	0.0	0.0
ASettNC	ASettEC	5.7	0.0	0.0	0.0	0.0	0.0
ASettNC	ASettTurb	0.0	0.0	0.0	0.0	0.0	0.0
ASettNC	ASettpH	4.5	0.0	0.0	0.0	0.0	0.0
ASettNC	ABCFiltCO	2.0	0.0	0.0	0.0	0.0	0.0
ASettNC	ABCFiltEC	19.9	0.0	0.0	0.0	0.0	0.0
ASettNC	ABCFiltNC	-	0.0	0.0	0.0	0.0	0.0
ASettNC	ABCFiltTurb	13.5	0.0	0.0	0.0	0.0	-
ASettNC	ABCFiltpH	4.2	0.0	0.0	0.0	0.0	0.0
ASettNC	GACCO	-	-	0.0	-	-	-
ASettNC	GACNC	-	0.0	0.0	-	-	-
ASettNC	GACpH	4.8	0.0	0.0	0.0	0.0	0.0
ASettNC	CONFreeCL	11.5	0.0	0.0	0.0	0.0	0.0
ASettNC	CONTurb	9.1	0.0	0.0	0.0	0.0	0.0
ASettNC	CONpH	4.9	0.0	0.0	0.0	0.0	0.0
ASettNC	CONTotalCL	11.5	0.0	0.0	0.0	0.0	0.0
ASettNC	BALFreeCL	2.1	0.0	0.0	0.0	0.0	0.0
ASettNC	BALTurb	7.7	0.0	0.0	0.0	0.0	0.0
ASettNC	BALpH	3.7	0.0	0.0	0.0	0.0	0.0
ASettNC	BALTotalCL	3.8	0.0	0.0	0.0	0.0	0.0
ASettNC	FINCLMon	4.5	0.0	0.0	0.0	0.0	0.0
ASettNC	FINFlow	-	0.0	0.0	0.0	0.0	0.0
ASettNC	FINTurbMon	-	0.0	0.0	0.0	0.0	-
ASettNC	FINFreeCL	0.5	0.0	0.0	0.0	0.0	0.0
ASettNC	FINTurb	-	0.0	0.0	0.0	0.0	0.0
ASettNC	FINpH	4.7	0.0	0.0	0.0	0.0	0.0
ASettNC	FINTotalCL	1.5	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Settlement Tank A turbidity that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
ASettTurb	ASettCO	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	ASettEC	0.0	0.0	7.5	-	0.0	0.0
ASettTurb	ASettNC	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	ASettpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	ABCFiltEC	-	0.0	0.0	-	0.0	0.0
ASettTurb	ABCFiltNC	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	ABCFiltTurb	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	GACCO	-	0.0	0.0	-	0.0	5.7
ASettTurb	GACEC	-	-	-	-	-	13.7
ASettTurb	GACNC	-	0.0	0.0	-	-	9.9
ASettTurb	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	CONTurb	0.0	0.0	0.0	-	0.0	0.0
ASettTurb	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	BALTurb	0.0	0.0	0.0	-	0.0	0.0
ASettTurb	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
ASettTurb	FINNC1L	-	-	-	-	23.7	-
ASettTurb	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettTurb	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Settlement Tank A pH that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
ASettpH	ASettCO	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	ASettEC	0.0	0.0	0.6	0.0	0.0	0.0
ASettpH	ASettNC	-	0.0	0.0	0.0	0.0	0.0
ASettpH	ASettTurb	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	ABCFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	ABCFiltNC	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	ABCFiltTurb	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	GACCO	0.0	-	0.0	0.0	0.0	0.2
ASettpH	GACEC	-	-	-	-	-	4.2
ASettpH	GACNC	-	-	0.0	0.0	16.6	4.5
ASettpH	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	CONTurb	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	FINTurbMon	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
ASettpH	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Settlement Tank B coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
BSettCO	BSettEC	-	0.0	0.0	-	0.0	0.0
BSettCO	BSettNC	-	0.0	0.0	-	0.0	0.0
BSettCO	BSettTurb	0.0	0.0	0.0	0.0	0.0	-
BSettCO	BSettpH	-	0.0	0.0	0.0	0.0	0.0
BSettCO	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
BSettCO	ABCFiltEC	0.0	0.0	0.0	-	0.0	0.0
BSettCO	ABCFiltNC	-	0.0	-	0.0	0.0	0.0
BSettCO	ABCFiltTurb	-	0.0	0.0	0.0	0.0	-
BSettCO	ABCFiltpH	-	0.0	0.0	0.0	0.0	0.0
BSettCO	GACCO	-	-	0.0	7.4	0.0	-
BSettCO	GACEC	-	-	-	7.0	-	-
BSettCO	GACNC	-	-	0.0	5.2	-	-
BSettCO	GACpH	-	0.0	0.0	0.0	0.0	0.0
BSettCO	CONFreeCL	-	0.0	0.0	0.0	0.0	0.0
BSettCO	CONTurb	-	0.0	0.0	0.0	0.0	0.0
BSettCO	CONpH	-	0.0	0.0	0.0	0.0	0.0
BSettCO	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
BSettCO	BALFreeCL	-	0.0	0.0	0.0	0.0	0.0
BSettCO	BALTurb	0.0	0.0	0.0	0.0	7.7	0.0
BSettCO	BALpH	-	0.0	0.0	0.0	0.0	0.0
BSettCO	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
BSettCO	FINCLMon	-	0.0	0.0	0.0	0.0	0.0
BSettCO	FINFlow	-	-	-	22.4	0.0	0.0
BSettCO	FINTurbMon	-	0.0	0.0	0.0	0.0	-
BSettCO	FINCO1L	23.4	-	-	23.4	-	-
BSettCO	FINNC1L	-	-	-	-	23.7	-
BSettCO	FINFreeCL	-	0.0	0.0	10.2	0.0	0.0
BSettCO	FINTurb	-	0.0	0.0	0.0	0.0	0.0
BSettCO	FINpH	-	0.0	0.0	0.0	0.0	0.0
BSettCO	FINTotalCL	-	0.0	0.0	10.6	0.0	0.0

Cross-correlation results for Settlement Tank B *E. coli* that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
BSettEC	BSettCO	1.3	0.0	0.0	5.3	0.0	0.0
BSettEC	BSettNC	-	0.0	0.0	0.0	0.0	0.0
BSettEC	BSettTurb	9.5	0.0	0.0	11.1	0.0	0.0
BSettEC	BSettpH	-	0.0	0.0	0.0	0.0	0.0
BSettEC	ABCFiltCO	-	0.0	0.0	0.0	0.0	0.0
BSettEC	ABCFiltEC	0.1	0.0	0.0	0.0	0.0	0.0
BSettEC	ABCFiltNC	-	0.0	-	0.0	0.0	0.0
BSettEC	ABCFiltTurb	-	0.0	0.0	0.0	0.0	0.0
BSettEC	ABCFiltpH	-	0.0	0.0	0.0	0.0	0.0
BSettEC	GACCO	-	-	0.0	16.7	-	-
BSettEC	GACNC	-	-	0.0	9.8	-	-
BSettEC	GACpH	-	0.0	0.0	0.0	0.0	0.0
BSettEC	CONHPC37	-	-	-	10.2	-	-
BSettEC	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
BSettEC	CONTurb	-	0.0	0.0	0.0	0.0	0.0
BSettEC	CONpH	-	0.0	0.0	0.0	0.0	0.0
BSettEC	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
BSettEC	BALFreeCL	-	0.0	0.0	0.0	0.0	0.0
BSettEC	BALTurb	-	0.0	-	0.0	11.6	0.0
BSettEC	BALpH	-	0.0	0.0	0.0	0.0	0.0
BSettEC	BALTotalCL	-	0.0	0.0	0.0	0.0	0.0
BSettEC	FINCLMon	-	0.0	0.0	0.0	0.0	0.0
BSettEC	FINFlow	-	-	-	10.3	0.0	0.0
BSettEC	FINTurbMon	-	0.0	-	0.0	0.0	-
BSettEC	FINNC1L	-	-	-	-	23.7	-
BSettEC	FINFreeCL	-	0.0	0.0	20.5	0.0	0.0
BSettEC	FINTurb	-	0.0	0.0	0.0	3.0	0.0
BSettEC	FINpH	-	0.0	0.0	0.0	0.0	0.0
BSettEC	FINTotalCL	-	0.0	0.0	19.0	0.0	0.0

Cross-correlation results for Settlement Tank B non-coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
BSettNC	BSettCO	5.6	0.0	0.0	0.5	0.0	0.0
BSettNC	BSettEC	10.6	0.0	0.0	0.0	0.0	0.0
BSettNC	BSettTurb	15.7	0.0	0.0	0.6	0.0	
BSettNC	BSettpH	0.0	0.0	0.0	0.0	0.0	0.0
BSettNC	ABCFiltCO	7.5	0.0	0.0	0.0	0.0	0.0
BSettNC	ABCFiltEC	6.0	0.0	0.0	0.0	0.0	0.0
BSettNC	ABCFiltNC		0.0	0.0	0.0	0.0	0.0
BSettNC	ABCFiltTurb		0.0	0.0	0.0	0.0	
BSettNC	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
BSettNC	GACCO			0.0	11.1		
BSettNC	GACEC				15.0		
BSettNC	GACNC			0.0	6.8		
BSettNC	GACpH	1.8	0.0	0.0	0.0	0.0	0.0
BSettNC	CONFreeCL	9.0	0.0	0.0	0.0	0.0	0.0
BSettNC	CONTurb		0.0	0.0	0.0	0.0	0.0
BSettNC	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
BSettNC	CONTotalCL	9.5	0.0	0.0	0.0	0.0	0.0
BSettNC	BALFreeCL		0.0	0.0	0.0	0.0	0.0
BSettNC	BALTurb	12.6	0.0	0.0	0.0	7.1	0.0
BSettNC	BALpH		0.0	0.0	0.0	0.0	0.0
BSettNC	BALTotalCL	2.4	0.0	0.0	0.0	0.0	0.0
BSettNC	FINCLMon		0.0	0.0	0.0	0.0	0.0
BSettNC	FINFlow			0.0	1.0	0.0	0.0
BSettNC	FINTurbMon			0.0	0.0	0.0	
BSettNC	FINCO1L				23.4		
BSettNC	FINNC1L					23.7	
BSettNC	FINFreeCL	3.4	0.0	0.0	12.0	0.0	0.0
BSettNC	FINTurb		0.0	0.0	0.0	0.0	0.0
BSettNC	FINpH	0.1	0.0	0.0	0.0	0.0	0.0
BSettNC	FINTotalCL	3.7	0.0	0.0	11.2	0.0	0.0

Cross-correlation results for Settlement Tank B turbidity that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
BSettTurb	BSettCO	0.0	0.0	0.0	0.0	0.0	10.2
BSettTurb	BSettEC	-	0.0	0.0	-	0.0	0.0
BSettTurb	BSettNC	-	0.0	0.0	-	0.0	-
BSettTurb	BSettpH	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	ABCFiltEC	-	0.0	0.0	0.0	0.0	9.8
BSettTurb	ABCFiltNC	-	0.0	0.0	0.0	0.0	0.0
BSettTurb	ABCFiltTurb	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	GACCO	-	-	0.0	0.0	-	4.3
BSettTurb	GACEC	-	-	-	6.2	-	1.5
BSettTurb	GACNC	-	0.0	0.0	0.0	-	6.8
BSettTurb	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	CONTurb	3.4	0.0	0.0	0.0	0.0	0.0
BSettTurb	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	BALCO	0.4	-	-	-	-	-
BSettTurb	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	BALTurb	0.4	0.0	0.0	0.0	0.0	0.0
BSettTurb	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
BSettTurb	FINCO1L	-	-	-	23.4	-	-
BSettTurb	FINNC1L	-	-	-	-	23.7	-
BSettTurb	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
BSettTurb	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Settlement Tank B pH that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
BSettpH	BSettCO	-	0.0	0.0	0.0	0.0	0.0
BSettpH	BSettEC	-	0.0	0.0	0.0	0.0	0.0
BSettpH	BSettNC	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	BSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	ABCFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	ABCFiltNC	-	0.0	0.0	0.0	0.0	0.0
BSettpH	ABCFiltTurb	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	GACCO	0.0	0.0	0.0	0.0	0.0	0.4
BSettpH	GACEC	-	-	-	-	-	3.6
BSettpH	GACNC	-	0.0	0.0	0.0	0.0	5.5
BSettpH	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	CONTurb	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	FINTurbMon	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
BSettpH	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Settlement Tank C coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
CSettCO	CSettEC	7.0	0.0	0.0	0.0	0.0	
CSettCO	CSettNC	-	0.0	0.0	0.0	0.0	0.0
CSettCO	CSettTurb	9.3	0.0	0.0	0.0	0.0	0.0
CSettCO	CSettpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettCO	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
CSettCO	ABCFiltEC	5.6	0.0	0.0	0.0	0.0	0.0
CSettCO	ABCFiltNC	-	0.0	-	0.0	0.0	0.0
CSettCO	ABCFiltTurb	-	0.0	0.0	0.0	0.0	0.0
CSettCO	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettCO	GACCO	-	0.0	0.0	7.7	-	-
CSettCO	GACEC	-	-	-	8.6	-	-
CSettCO	GACNC	-	-	0.0	5.3	-	-
CSettCO	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettCO	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettCO	CONTurb	-	0.0	0.0	0.0	0.0	0.0
CSettCO	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettCO	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettCO	BALFreeCL	-	0.0	0.0	0.0	0.0	0.0
CSettCO	BALTurb	6.7	0.0	-	0.0	11.5	0.0
CSettCO	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettCO	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettCO	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
CSettCO	FINFlow	-	-	0.0	8.1	0.0	0.0
CSettCO	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
CSettCO	FINCO	-	20.2	-	-	-	-
CSettCO	FINCO1L	-	-	-	23.6	-	-
CSettCO	FINNC1L	-	-	-	-	23.7	-
CSettCO	FINFreeCL	-	0.0	0.0	11.1	0.0	0.0
CSettCO	FINTurb	-	0.0	0.0	0.0	2.9	0.0
CSettCO	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettCO	FINTotalCL	-	0.0	0.0	11.0	0.0	0.0

Cross-correlation results for Settlement Tank C *E. coli* that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
CSettEC	CSettCO	-	0.0	0.0	0.0	0.0	18.9
CSettEC	CSettNC	-	0.0	0.0	0.0	0.0	16.4
CSettEC	CSettTurb	0.0	0.0	-	0.0	0.0	0.0
CSettEC	CSettpH	0.0	0.0	-	0.0	0.0	0.0
CSettEC	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
CSettEC	ABCFiltEC	0.0	0.0	0.0	0.0	0.0	20.6
CSettEC	ABCFiltNC	-	0.0	-	0.0	0.0	2.9
CSettEC	ABCFiltTurb	0.0	0.0	0.0	0.0	0.0	0.0
CSettEC	ABCFiltpH	0.0	0.0	-	0.0	0.0	0.0
CSettEC	GACCO	-	-	0.0	-	0.0	0.0
CSettEC	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettEC	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettEC	CONTurb	-	0.0	0.0	0.0	0.0	0.0
CSettEC	CONpH	0.0	0.0	-	0.0	0.0	0.0
CSettEC	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettEC	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettEC	BALTurb	0.0	0.0	-	0.0	8.1	0.0
CSettEC	BALpH	0.0	0.0	-	0.0	0.0	0.0
CSettEC	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettEC	FINCLMon	-	0.0	0.0	0.0	0.0	0.0
CSettEC	FINFlow	-	-	-	9.0	0.0	0.0
CSettEC	FINTurbMon	-	0.0	-	0.0	0.0	-
CSettEC	FINNC1L	-	-	-	-	23.7	-
CSettEC	FINFreeCL	-	0.0	0.0	20.7	0.0	0.0
CSettEC	FINTurb	-	0.0	0.0	0.0	0.0	0.0
CSettEC	FINpH	0.0	0.0	-	0.0	0.0	0.0
CSettEC	FINTotalCL	-	0.0	0.0	19.4	0.0	0.0

Cross-correlation results for Settlement Tank C non-coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
CSettNC	CSettCO	-	0.0	0.0	0.0	0.0	0.0
CSettNC	CSettEC	-	0.0	0.0	0.0	0.0	-
CSettNC	CSettTurb	-	0.0	0.0	0.0	0.0	0.0
CSettNC	CSettpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettNC	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
CSettNC	ABCFiltEC	-	0.0	0.0	0.0	0.0	0.0
CSettNC	ABCFiltNC	-	0.0	0.0	0.0	0.0	0.0
CSettNC	ABCFiltTurb	-	0.0	0.0	0.0	0.0	-
CSettNC	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettNC	GACCO	-	-	0.0	-	-	-
CSettNC	GACNC	-	-	0.0	-	-	-
CSettNC	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettNC	CONFreeCL	-	0.0	0.0	0.0	0.0	0.0
CSettNC	CONTurb	-	0.0	0.0	0.0	0.0	0.0
CSettNC	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettNC	CONTotalCL	-	0.0	0.0	0.0	0.0	0.0
CSettNC	BALFreeCL	-	0.0	0.0	0.0	0.0	0.0
CSettNC	BALTurb	4.9	0.0	0.0	0.0	11.4	0.0
CSettNC	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettNC	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettNC	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
CSettNC	FINFlow	-	0.0	0.0	0.0	0.0	0.0
CSettNC	FINTurbMon	-	0.0	0.0	0.0	0.0	-
CSettNC	FINNC1L	-	-	-	-	23.7	-
CSettNC	FINFreeCL	0.0	0.0	0.0	14.9	0.0	0.0
CSettNC	FINTurb	0.0	0.0	0.0	0.0	1.5	0.0
CSettNC	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettNC	FINTotalCL	0.0	0.0	0.0	13.9	0.0	0.0

Cross-correlation results for Settlement Tank C turbidity that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
CSettTurb	CSettCO	-	0.0	0.0	0.0	0.0	0.0
CSettTurb	CSettEC	0.0	0.0	12.3	0.0	0.0	0.0
CSettTurb	CSettNC	-	0.0	0.0	0.0	0.0	0.0
CSettTurb	CSettpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettTurb	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
CSettTurb	ABCFiltEC	-	0.0	0.0	0.0	0.0	0.0
CSettTurb	ABCFiltNC	-	0.0	0.0	0.0	0.0	0.0
CSettTurb	ABCFiltTurb	0.0	0.0	0.0	0.0	0.0	0.0
CSettTurb	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettTurb	GACCO	-	-	0.0	-	-	0.0
CSettTurb	GACNC	-	0.0	0.0	-	-	-
CSettTurb	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettTurb	CONHPC37	-	-	23.5	-	-	-
CSettTurb	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettTurb	CONTurb	-	0.0	0.0	0.0	0.0	0.0
CSettTurb	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettTurb	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettTurb	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettTurb	BALTurb	-	0.0	0.0	0.0	0.0	0.0
CSettTurb	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettTurb	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettTurb	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
CSettTurb	FINFlow	-	0.0	0.0	0.0	0.0	0.0
CSettTurb	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
CSettTurb	FINNC1L	-	-	-	-	23.7	-
CSettTurb	FINFreeCL	-	0.0	0.0	0.0	0.0	0.0
CSettTurb	FINTurb	-	0.0	0.0	0.0	0.0	0.0
CSettTurb	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettTurb	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Settlement Tank C pH that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
CSettpH	CSettCO	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	CSettEC	0.0	0.0	2.4	0.0	0.0	0.0
CSettpH	CSettNC	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	CSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	ABCFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	ABCFiltNC	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	ABCFiltTurb	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	GACCO	0.0	0.0	0.0	0.0	0.0	0.3
CSettpH	GACEC	-	-	-	-	-	12.7
CSettpH	GACNC	-	0.0	0.0	0.0	0.0	10.4
CSettpH	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	CONTurb	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	FINTurbMon	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
CSettpH	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Settlement Tank D coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
DSettCO	DSettEC	-	-	0.0	0.0	0.0	0.0
DSettCO	DSettNC	-	0.0	0.0	0.0	0.0	0.0
DSettCO	DSettTurb	-	0.0	0.0	0.0	0.0	0.0
DSettCO	DSettpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettCO	DFiltCO	-	0.0	0.0	0.0	0.0	0.0
DSettCO	DFiltEC	2.8	0.0	0.0	0.0	0.0	0.0
DSettCO	DFiltNC	-	0.0	-	0.0	0.0	0.0
DSettCO	DFiltTurb	-	-	0.0	0.0	0.0	0.0
DSettCO	DFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettCO	GACCO	0.0	-	0.0	-	-	-
DSettCO	GACNC	-	-	0.0	-	-	-
DSettCO	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettCO	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DSettCO	CONTurb	12.6	0.0	0.0	0.0	0.0	0.0
DSettCO	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettCO	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
DSettCO	BALFreeCL	-	0.0	0.0	0.0	0.0	0.0
DSettCO	BALTurb	12.3	0.0	0.0	0.0	3.6	0.0
DSettCO	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettCO	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
DSettCO	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
DSettCO	FINFlow	-	-	-	0.0	0.0	0.0
DSettCO	FINTurbMon	-	0.0	0.0	0.0	0.0	-
DSettCO	FINCO	-	21.8	-	-	-	-
DSettCO	FINNC1L	-	-	-	-	23.7	-
DSettCO	FINFreeCL	-	0.0	0.0	11.2	0.0	0.0
DSettCO	FINTurb	-	0.0	0.0	0.0	0.0	0.0
DSettCO	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettCO	FINTotalCL	-	0.0	0.0	10.6	0.0	0.0

Cross-correlation results for Settlement Tank D *E. coli* that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
DSettEC	DSettCO	7.3	10.6	0.0	0.0	0.0	0.0
DSettEC	DSettNC	-	0.0	0.0	0.0	0.0	0.0
DSettEC	DSettTurb	-	0.0	-	0.0	0.0	0.0
DSettEC	DSettpH	-	0.0	0.0	0.0	0.0	0.0
DSettEC	DFiltCO	3.9	0.0	0.0	0.0	0.0	0.0
DSettEC	DFiltEC	12.8	0.0	0.0	0.0	0.0	0.0
DSettEC	DFiltNC	-	0.0	-	0.0	0.0	0.0
DSettEC	DFiltTurb	-	-	0.0	0.0	0.0	0.0
DSettEC	DFiltpH	-	0.0	0.0	0.0	0.0	0.0
DSettEC	GACCO	-	-	0.0	-	-	-
DSettEC	GACNC	-	-	0.0	4.3	-	-
DSettEC	GACpH	-	0.0	0.0	0.0	0.0	0.0
DSettEC	CONFreeCL	4.5	0.0	0.0	0.0	0.0	0.0
DSettEC	CONTurb	-	0.0	0.0	0.0	8.1	0.0
DSettEC	CONpH	-	0.0	0.0	0.0	0.0	0.0
DSettEC	CONTotalCL	3.7	0.0	0.0	0.0	0.0	0.0
DSettEC	BALFreeCL	-	0.0	0.0	0.0	0.0	0.0
DSettEC	BALTurb	-	0.0	-	0.0	16.0	0.0
DSettEC	BALpH	1.7	0.0	0.0	0.0	0.0	0.0
DSettEC	BALTotalCL	-	0.0	0.0	0.0	0.0	0.0
DSettEC	FINCLMon	-	0.0	0.0	0.0	0.0	0.0
DSettEC	FINFlow	-	-	-	0.0	-	0.0
DSettEC	FINTurbMon	-	0.0	-	0.0	0.0	-
DSettEC	FINCO	-	21.8	-	-	-	-
DSettEC	FINNC1L	-	-	-	-	23.7	-
DSettEC	FINFreeCL	-	0.0	0.0	0.0	0.0	0.0
DSettEC	FINTurb	-	0.0	0.0	0.0	12.8	0.0
DSettEC	FINpH	-	0.0	0.0	0.0	0.0	0.0
DSettEC	FINTotalCL	-	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Settlement Tank D non-coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
DSettNC	DSettCO	4.2	0.0	0.0	0.0	0.0	0.0
DSettNC	DSettEC	4.5	0.0	0.0	0.0	0.0	0.0
DSettNC	DSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
DSettNC	DSettpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettNC	DFiltCO	-	0.0	0.0	0.0	0.0	0.0
DSettNC	DFiltEC	-	0.0	0.0	0.0	0.0	0.0
DSettNC	DFiltNC	-	0.0	0.0	0.0	0.0	0.0
DSettNC	DFiltTurb	-	-	0.0	0.0	0.0	-
DSettNC	DFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettNC	GACCO	-	-	0.0	-	0.0	-
DSettNC	GACNC	-	-	0.0	-	-	-
DSettNC	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettNC	CONHPC37	-	-	-	22.8	-	-
DSettNC	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DSettNC	CONTurb	18.4	0.0	0.0	0.0	0.0	0.0
DSettNC	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettNC	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
DSettNC	BALFreeCL	-	0.0	0.0	0.0	0.0	0.0
DSettNC	BALTurb	8.9	0.0	0.0	0.0	4.0	0.0
DSettNC	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettNC	BALTotalCL	-	0.0	0.0	0.0	0.0	0.0
DSettNC	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
DSettNC	FINFlow	-	0.0	0.0	0.0	0.0	0.0
DSettNC	FINTurbMon	-	0.0	0.0	0.0	0.0	-
DSettNC	FINNC1L	-	-	-	-	23.7	-
DSettNC	FINFreeCL	0.0	0.0	0.0	11.2	0.0	0.0
DSettNC	FINTurb	-	0.0	0.0	0.0	0.0	0.0
DSettNC	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettNC	FINTotalCL	0.0	0.0	0.0	10.2	0.0	0.0

Cross-correlation results for Settlement Tank D turbidity that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
DSettTurb	DSettCO	2.9	0.0	0.0	0.0	0.0	0.0
DSettTurb	DSettEC	-	0.0	-	0.0	0.0	0.0
DSettTurb	DSettNC	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	DSettpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	DFiltCO	0.0	0.0	3.1	0.0	0.0	0.0
DSettTurb	DFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	DFiltNC	-	0.0	0.0	0.0	0.0	0.0
DSettTurb	DFiltTurb	7.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	DFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	GACCO	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	GACEC	-	-	-	0.0	-	-
DSettTurb	GACNC	0.0	0.0	0.0	0.0	-	-
DSettTurb	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	CONTurb	13.5	0.0	0.0	0.0	0.0	0.0
DSettTurb	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	BALTurb	14.1	0.0	0.0	0.0	0.0	0.0
DSettTurb	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
DSettTurb	FINCO	-	21.8	-	-	-	-
DSettTurb	FINCO1L	-	-	-	22.2	-	-
DSettTurb	FINNC1L	-	-	-	-	23.7	-
DSettTurb	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettTurb	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Settlement Tank D pH that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
DSettpH	DSettCO	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	DSettEC	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	DSettNC	-	0.0	0.0	0.0	0.0	0.0
DSettpH	DSettTurb	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	DFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	DFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	DFiltNC	-	0.0	0.0	0.0	0.0	0.0
DSettpH	DFiltTurb	11.6	0.0	0.0	0.0	0.0	0.0
DSettpH	DFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	GACCO	0.0	0.0	0.0	0.0	0.0	0.1
DSettpH	GACEC	-	-	-	-	-	5.6
DSettpH	GACNC	-	0.0	0.0	0.0	21.6	4.9
DSettpH	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	CONTurb	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	FINTurbMon	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	FINCO1L	-	-	-	-	-	23.0
DSettpH	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
DSettpH	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for ABC Filter coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
ABCFiltCO	ABCFiltEC	2.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	ABCFiltNC	-	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	ABCFiltTurb	-	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	GACCO	-	0.0	0.0	0.0	-	0.0
ABCFiltCO	GACEC	-	-	-	21.1	-	-
ABCFiltCO	GACNC	-	0.0	0.0	0.0	-	0.0
ABCFiltCO	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	CONTurb	-	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltCO	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for ABC Filter *E. coli* that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
ABCFiltEC	ABCFiltCO	-	0.0	0.0	0.0	0.0	0.0
ABCFiltEC	ABCFiltNC	-	0.0	-	0.0	0.0	0.0
ABCFiltEC	ABCFiltTurb	-	0.0	0.0	0.0	0.0	-
ABCFiltEC	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltEC	GACCO	-	-	0.0	13.3	-	-
ABCFiltEC	GACNC	-	-	0.0	6.8	-	-
ABCFiltEC	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltEC	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltEC	CONTurb	-	0.0	0.0	0.0	0.0	0.0
ABCFiltEC	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltEC	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltEC	BALFreeCL	-	0.0	0.0	0.0	0.0	0.0
ABCFiltEC	BALTurb	0.0	0.0	0.0	0.0	10.2	0.0
ABCFiltEC	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltEC	BALTotalCL	-	0.0	0.0	0.0	0.0	0.0
ABCFiltEC	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltEC	FINFlow	-	-	-	0.0	0.0	0.0
ABCFiltEC	FINTurbMon	-	0.0	0.0	0.0	0.0	-
ABCFiltEC	FINCO	13.9	6.2	-	-	-	-
ABCFiltEC	FINNC1L	-	-	-	-	23.7	-
ABCFiltEC	FINFreeCL	-	0.0	0.0	9.8	0.0	0.0
ABCFiltEC	FINTurb	-	0.0	0.0	0.0	0.0	0.0
ABCFiltEC	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltEC	FINTotalCL	-	0.0	0.0	9.3	0.0	0.0

Cross-correlation results for ABC Filter non-coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
ABCFiltNC	ABCFiltCO	0.9	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	ABCFiltEC	-	0.0	10.1	0.0	0.0	0.0
ABCFiltNC	ABCFiltTurb	-	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	GACCO	-	0.0	0.0	0.0	-	0.0
ABCFiltNC	GACNC	-	0.0	0.0	0.0	-	0.0
ABCFiltNC	GACpH	-	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	CONFreeCL	-	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	CONTurb	-	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	CONpH	-	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	CONTotalCL	-	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	BALFreeCL	-	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	BALTurb	19.7	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	BALpH	-	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	BALTotalCL	-	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	FINCLMon	-	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	FINTurbMon	-	0.0	0.0	0.0	0.0	-
ABCFiltNC	FINHPC22	-	21.0	-	-	-	-
ABCFiltNC	FINHPC37	21.6	-	-	-	-	-
ABCFiltNC	FINCO1L	-	-	-	22.0	-	0.1
ABCFiltNC	FINNC1L	-	-	-	-	23.7	
ABCFiltNC	FINFreeCL	-	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	FINTurb	22.3	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	FINpH	-	0.0	0.0	0.0	0.0	0.0
ABCFiltNC	FINTotalCL	-	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for ABC Filter turbidity that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
ABCFiltTurb	ABCFiltCO	4.4	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	ABCFiltEC	-	0.0	0.0	0.0	0.0	9.7
ABCFiltTurb	ABCFiltNC	1.7	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	ABCFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	GACCO	-	-	0.0	-	-	4.2
ABCFiltTurb	GACNC	-	0.0	0.0	-	-	-
ABCFiltTurb	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	CONTurb	-	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	BALTurb	-	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	FINTurbMon	0.2	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltTurb	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for ABC Filter pH that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
ABCFiltpH	ABCFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	ABCFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	ABCFiltNC	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	ABCFiltTurb	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	GACCO	0.0	0.0	0.0	0.0	0.0	0.2
ABCFiltpH	GACEC	-	-	-	-	-	3.4
ABCFiltpH	GACNC	-	0.0	0.0	0.0	22.4	3.9
ABCFiltpH	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	CONTurb	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	FINTurbMon	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
ABCFiltpH	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for D Filter coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
DFiltCO	DFiltEC	0.5	0.0	0.0	0.0	0.0	0.0
DFiltCO	DFiltNC	-	0.0	-	0.0	0.0	0.0
DFiltCO	DFiltTurb	-	0.0	0.0	0.0	0.0	0.0
DFiltCO	DFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
DFiltCO	GACCO	-	0.0	0.0	0.0	0.0	0.0
DFiltCO	GACNC	-	0.0	0.0	0.0	-	0.0
DFiltCO	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
DFiltCO	CONHPC37	-	-	-	18.0	-	-
DFiltCO	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DFiltCO	CONTurb	-	0.0	0.0	0.0	0.0	0.0
DFiltCO	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
DFiltCO	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
DFiltCO	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DFiltCO	BALTurb	-	0.0	-	0.0	0.0	0.0
DFiltCO	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
DFiltCO	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
DFiltCO	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
DFiltCO	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
DFiltCO	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
DFiltCO	FINNC1L	-	-	-	-	23.7	-
DFiltCO	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DFiltCO	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
DFiltCO	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
DFiltCO	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for D Filter *E. coli* that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
DFiltEC	DFiltCO	-	0.0	0.0	0.0	0.0	0.0
DFiltEC	DFiltNC	-	0.0	0.0	0.0	0.0	0.0
DFiltEC	DFiltTurb	-	-	0.0	0.0	0.0	0.0
DFiltEC	DFiltpH	0.0	0.0	0.0	0.0	0.0	0.0
DFiltEC	GACCO	-	-	0.0	10.1	0.0	0.0
DFiltEC	GACNC	-	-	0.0	4.2	-	-
DFiltEC	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
DFiltEC	CONHPC37	-	-	-	21.9	-	-
DFiltEC	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DFiltEC	CONTurb	-	0.0	0.0	0.0	0.0	0.0
DFiltEC	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
DFiltEC	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
DFiltEC	BALFreeCL	-	0.0	0.0	0.0	0.0	0.0
DFiltEC	BALTurb	-	0.0	0.0	0.0	6.8	0.0
DFiltEC	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
DFiltEC	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
DFiltEC	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
DFiltEC	FINFlow	-	-	0.0	0.0	0.0	0.0
DFiltEC	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
DFiltEC	FINCO	16.9	18.2	-	-	-	-
DFiltEC	FINNC1L	-	-	-	-	23.7	-
DFiltEC	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DFiltEC	FINTurb	-	0.0	0.0	0.0	0.0	0.0
DFiltEC	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
DFiltEC	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for D Filter non-coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
DFiltNC	DFiltCO	3.2	0.0	9.0	0.0	0.0	0.0
DFiltNC	DFiltEC	-	0.0	0.0	0.0	0.0	0.0
DFiltNC	DFiltTurb	7.3	0.0	0.0	0.0	0.0	0.0
DFiltNC	DFiltpH	6.0	0.0	0.0	0.0	0.0	0.0
DFiltNC	GACCO	-	0.0	0.0	0.0	0.0	0.0
DFiltNC	GACNC	-	0.0	0.0	0.0	-	0.0
DFiltNC	GACpH	-	0.0	0.0	0.0	0.0	0.0
DFiltNC	CONHPC22	-	-	-	-	-	14.7
DFiltNC	CONHPC37	-	-	-	5.7	-	-
DFiltNC	CONFreeCL	-	0.0	0.0	0.0	0.0	0.0
DFiltNC	CONTurb	-	0.0	0.0	0.0	0.0	0.0
DFiltNC	CONpH	16.9	0.0	0.0	0.0	0.0	0.0
DFiltNC	CONTotalCL	-	0.0	0.0	0.0	0.0	0.0
DFiltNC	BALFreeCL	-	0.0	0.0	0.0	0.0	0.0
DFiltNC	BALTurb	8.1	0.0	0.0	0.0	0.0	0.0
DFiltNC	BALpH	-	0.0	0.0	0.0	0.0	0.0
DFiltNC	BALTotalCL	-	0.0	0.0	0.0	0.0	0.0
DFiltNC	FINCLMon	-	0.0	0.0	0.0	0.0	0.0
DFiltNC	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
DFiltNC	FINTurbMon	-	0.0	0.0	0.0	0.0	-
DFiltNC	FINHPC37	19.8	-	-	-	-	-
DFiltNC	FINNC1L	-	-	-	-	23.7	-
DFiltNC	FINFreeCL	-	0.0	0.0	0.0	0.0	0.0
DFiltNC	FINTurb	6.5	0.0	0.0	0.0	0.0	0.0
DFiltNC	FINpH	-	0.0	0.0	0.0	0.0	0.0
DFiltNC	FINTotalCL	-	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for D Filter turbidity that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
DFiltTurb	DFiltCO	4.3	0.0	0.0	0.0	0.0	0.0
DFiltTurb	DFiltEC	-	-	0.0	0.0	0.0	0.0
DFiltTurb	DFiltNC	-	0.0	0.0	0.0	0.0	0.0
DFiltTurb	DFiltpH	-	0.0	0.0	0.0	0.0	0.0
DFiltTurb	GACCO	-	-	0.0	0.0	-	6.7
DFiltTurb	GACEC	-	-	-	0.0	-	7.3
DFiltTurb	GACNC	-	-	0.0	0.0	-	11.2
DFiltTurb	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
DFiltTurb	CONFreeCL	-	0.0	0.0	0.0	0.0	0.0
DFiltTurb	CONTurb	0.5	0.0	0.0	0.0	0.0	0.0
DFiltTurb	CONpH	-	0.0	0.0	0.0	0.0	0.0
DFiltTurb	CONTotalCL	-	0.0	0.0	0.0	0.0	0.0
DFiltTurb	BALFreeCL	-	0.0	0.0	0.0	0.0	0.0
DFiltTurb	BALTurb	-	0.0	0.0	0.0	0.0	0.0
DFiltTurb	BALpH	-	0.0	0.0	0.0	0.0	0.0
DFiltTurb	BALTotalCL	-	0.0	0.0	0.0	0.0	0.0
DFiltTurb	FINCLMon	-	0.0	0.0	0.0	0.0	0.0
DFiltTurb	FINFlow	7.5	-	0.0	0.0	0.0	0.0
DFiltTurb	FINTurbMon	-	-	0.0	0.0	0.0	0.0
DFiltTurb	FINCO1L	-	-	-	22.0	-	23.2
DFiltTurb	FINNC1L	-	-	-	-	23.7	-
DFiltTurb	FINFreeCL	-	0.0	0.0	0.0	0.0	0.0
DFiltTurb	FINTurb	-	0.0	0.0	0.0	0.0	0.0
DFiltTurb	FINpH	-	0.0	0.0	0.0	0.0	0.0
DFiltTurb	FINTotalCL	-	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for D Filter pH that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
DFiltpH	DFiltCO	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	DFiltEC	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	DFiltNC	-	0.0	0.0	0.0	0.0	0.0
DFiltpH	DFiltTurb	10.2	0.0	0.0	0.0	0.0	0.0
DFiltpH	GACCO	0.0	0.0	0.0	0.0	0.0	0.2
DFiltpH	GACEC	-	-	-	-	-	0.3
DFiltpH	GACNC	-	0.0	0.0	0.0	-	1.0
DFiltpH	GACpH	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	CONHPC37	-	-	-	22.6	-	-
DFiltpH	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	CONTurb	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	FINTurbMon	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	FINCO1L	-	-	-	-	-	23.2
DFiltpH	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
DFiltpH	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for GAC Filter coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
GACCO	GACEC	0.0	-	-	-	-	-
GACCO	GACNC	0.6	2.4	0.0	-	0.0	-
GACCO	GACpH	-	0.0	0.0	0.0	0.0	0.0
GACCO	CONFreeCL	-	0.7	0.0	0.0	0.8	0.0
GACCO	CONTurb	-	5.3	0.0	0.0	8.7	-
GACCO	CONpH	1.2	0.0	0.0	0.0	0.0	0.0
GACCO	CONTotalCL	-	1.0	0.0	0.0	1.3	0.0
GACCO	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
GACCO	BALTurb	-	3.3	0.0	0.0	-	0.0
GACCO	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
GACCO	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
GACCO	FINCLMon	-	0.1	0.0	0.0	0.5	-
GACCO	FINFlow	-	4.0	0.0	17.3	0.0	0.0
GACCO	FINTurbMon	-	14.5	0.0	0.0	2.1	-
GACCO	FINCO	-	21.0	-	-	-	-
GACCO	FINCO1L	-	-	-	21.8	-	22.8
GACCO	FINFreeCL	-	0.0	0.0	0.0	0.0	0.0
GACCO	FINTurb	-	1.3	0.0	0.0	-	0.0
GACCO	FINpH	2.7	0.0	0.0	0.0	0.0	-
GACCO	FINTotalCL	-	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for GAC Filter *E. coli* that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
GACEC	GACCO	-	-	-	0.7	-	4.8
GACEC	GACNC	2.7	-	-	-	-	0.0
GACEC	CONFreeCL	-	-	-	-	-	12.9
GACEC	CONTurb	-	-	-	-	-	1.1
GACEC	CONTotalCL	-	-	-	-	-	14.9
GACEC	BALTurb	-	-	-	-	-	0.5
GACEC	FINCO1L	-	-	-	21.8	-	22.8
GACEC	FINTurb	-	-	-	-	-	8.4

Cross-correlation results for GAC Filter non-coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
GACNC	GACCO	-	-	0.0	0.4	0.0	3.1
GACNC	GACEC	-	-	-	0.2	-	0.0
GACNC	GACpH	-	0.0	0.0	0.0	-	0.0
GACNC	CONHPC37	-	-	21.5	-	-	-
GACNC	CONFreeCL	-	0.0	0.0	0.0	-	0.0
GACNC	CONTurb	-	5.2	0.0	0.0	-	0.0
GACNC	CONpH	-	0.1	0.0	0.0	0.0	0.0
GACNC	CONTotalCL	-	0.0	0.0	0.0	-	0.0
GACNC	BALFreeCL	-	0.0	0.0	0.0	-	-
GACNC	BALTurb	-	0.5	0.0	0.0	-	0.0
GACNC	BALpH	10.9	0.0	0.0	0.0	-	-
GACNC	BALTotalCL	-	0.0	0.0	0.0	-	-
GACNC	FINCLMon	-	1.3	0.0	0.0	-	-
GACNC	FINFlow	-	0.3	0.0	17.2	3.4	-
GACNC	FINTurbMon	-	-	0.0	0.0	-	-
GACNC	FINCO1L	-	-	-	21.8	-	22.8
GACNC	FINFreeCL	-	0.0	0.0	0.0	0.0	-
GACNC	FINTurb	-	0.1	0.0	0.0	-	0.0
GACNC	FINpH	-	0.0	0.0	0.0	0.0	-
GACNC	FINTotalCL	-	0.0	0.0	0.0	0.0	-

Cross-correlation results for GAC Filter pH that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
GACpH	GACCO	-	0.0	0.0	0.0	0.0	0.0
GACpH	GACNC	-	0.0	0.0	0.0	-	0.0
GACpH	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
GACpH	CONTurb	0.0	0.0	0.0	0.0	0.0	0.0
GACpH	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
GACpH	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
GACpH	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
GACpH	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
GACpH	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
GACpH	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
GACpH	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
GACpH	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
GACpH	FINTurbMon	0.0	0.0	0.0	0.0	0.0	0.0
GACpH	FINHPC22	-	4.8	-	-	-	-
GACpH	FINNC1L	-	13.7	-	-	-	-
GACpH	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
GACpH	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
GACpH	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Contact Tank HPCs at 22 and 37 °C that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
CONHPC22	CONpH	-	-	-	-	-	0.0
CONHPC22	BALpH	-	-	-	-	-	0.5

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
CONHPC37	BALTotalCL	-	-	22.3	-	-	-
CONHPC37	FINFlow	-	-	-	11.6	-	-
CONHPC37	FINpH	20.5	-	-	-	-	-

Cross-correlation results for Contact Tank free chlorine that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
CONFreeCL	CONTurb	0.0	0.0	0.0	0.0	0.0	0.0
CONFreeCL	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
CONFreeCL	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CONFreeCL	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CONFreeCL	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
CONFreeCL	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
CONFreeCL	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CONFreeCL	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
CONFreeCL	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
CONFreeCL	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
CONFreeCL	FINCO1L	-	-	-	-	-	22.8
CONFreeCL	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CONFreeCL	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
CONFreeCL	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
CONFreeCL	FINTotalCL	0.0	0.0	0.0	0.0	0.0	-

Cross-correlation results for Contact Tank turbidity that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
CONTurb	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CONTurb	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
CONTurb	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CONTurb	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CONTurb	BALTurb	3.5	0.0	0.0	0.0	0.0	0.0
CONTurb	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
CONTurb	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CONTurb	FINCLMon	-	0.0	0.0	0.0	0.0	0.0
CONTurb	FINFlow	5.4	0.0	0.0	0.0	0.0	0.0
CONTurb	FINTurbMon	16.6	0.0	0.0	0.0	-	0.0
CONTurb	FINCO	-	20.9	-	-	-	-
CONTurb	FINCO1L	-	-	-	-	-	22.8
CONTurb	FINFreeCL	-	0.0	0.0	0.0	0.0	0.0
CONTurb	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
CONTurb	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
CONTurb	FINTotalCL		0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Contact Tank pH that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
CONpH	CONHPC22	-	-	-	-	-	0.0
CONpH	CONHPC37	-	-	-	22.1		-
CONpH	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CONpH	CONTurb	0.0	0.0	0.0	0.0	0.0	0.0
CONpH	CONTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CONpH	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CONpH	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
CONpH	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
CONpH	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CONpH	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
CONpH	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
CONpH	FINTurbMon	4.5	0.0	0.0	0.0	0.0	0.0
CONpH	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CONpH	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
CONpH	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
CONpH	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Contact Tank total chlorine that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
CONTotalCL	CONFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CONTotalCL	CONTurb	0.0	0.0	0.0	0.0	0.0	0.0
CONTotalCL	CONpH	0.0	0.0	0.0	0.0	0.0	0.0
CONTotalCL	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CONTotalCL	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
CONTotalCL	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
CONTotalCL	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
CONTotalCL	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
CONTotalCL	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
CONTotalCL	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
CONTotalCL	FINCO1L	-	-	-	-	20.2	22.8
CONTotalCL	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
CONTotalCL	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
CONTotalCL	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
CONTotalCL	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Balance Tank turbidity that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
BALTurb	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
BALTurb	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
BALTurb	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
BALTurb	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
BALTurb	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
BALTurb	FINTurbMon	-	0.0	0.0	0.0	-	0.0
BALTurb	FINCO1L	-	-	-	22.4	-	23.4
BALTurb	FINFreeCL	-	0.0	0.0	0.0	0.0	0.0
BALTurb	FINTurb	-	0.0	0.0	0.0	0.0	0.0
BALTurb	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
BALTurb	FINTotalCL	-	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Balance Tank pH that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
BALpH	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
BALpH	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
BALpH	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
BALpH	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
BALpH	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
BALpH	FINTurbMon	9.1	0.0	0.0	0.0	0.0	0.0
BALpH	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
BALpH	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
BALpH	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
BALpH	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Balance Tank coliforms and free chlorine that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
BALCO	FINFreeCL	1.7	-	-	-	-	-
BALCO	FINTotalCL	1.7	-	-	-	-	-

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
BALFreeCL	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
BALFreeCL	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
BALFreeCL	BALTotalCL	0.0	0.0	0.0	0.0	0.0	0.0
BALFreeCL	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
BALFreeCL	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
BALFreeCL	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
BALFreeCL	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
BALFreeCL	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
BALFreeCL	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
BALFreeCL	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Balance Tank total chlorine that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
BALTotalCL	BALFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
BALTotalCL	BALTurb	0.0	0.0	0.0	0.0	0.0	0.0
BALTotalCL	BALpH	0.0	0.0	0.0	0.0	0.0	0.0
BALTotalCL	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
BALTotalCL	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
BALTotalCL	FINTurbMon		0.0	0.0	0.0	0.0	0.0
BALTotalCL	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
BALTotalCL	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
BALTotalCL	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
BALTotalCL	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Final monitor chlorine that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
FINCLMon	FINFlow	-	0.0	0.0	0.0	0.0	0.0
FINCLMon	FINTurbMon	-	-	0.0	0.0	-	0.0
FINCLMon	FINHPC22	-	14.8	-	-	-	-
FINCLMon	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
FINCLMon	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
FINCLMon	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
FINCLMon	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Final flow that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
FINFlow	FINCLMon	0.3	0.0	0.0	0.0	0.0	0.0
FINFlow	FINTurbMon	-	3.3	0.0	0.0	0.0	-
FINFlow	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
FINFlow	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
FINFlow	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
FINFlow	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Final turbidity that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
FINTurb	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
FINTurb	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
FINTurb	FINTurbMon	-	0.0	0.0	0.0	23.4	0.0
FINTurb	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
FINTurb	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
FINTurb	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Final monitor turbidity that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
FINTurbMon	FINCLMon	-	0.3	0.0	0.0	0.6	0.0
FINTurbMon	FINFlow	-	-	0.0	0.0	0.0	0.4
FINTurbMon	FINCO	-	4.5	-	-	-	-
FINTurbMon	FINCO1L	-	-	-	1.5	-	-
FINTurbMon	FINNC1L	-	-	-	-	20.2	-
FINTurbMon	FINFreeCL	-	0.0	0.0	0.0	0.0	0.0
FINTurbMon	FINTurb	-	0.0	0.0	0.0	17.6	0.0
FINTurbMon	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
FINTurbMon	FINTotalCL	5.2	0.0	0.0	0.0	0.0	0.0

Cross-correlation results for Final HPCs at 22 °C, 1 L coliforms and 1 L non-coliforms that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
FINHPC22	FINNC1L	-	20.1	-	-	-	-

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
FINCO1L	FINCLMon	-	-	-	-	-	12.9

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
FINNC1L	FINCO	23.0	23.0	-	-	-	-
FINNC1L	FINHPC22	-	0.0	-	-	-	-

Cross-correlation results for Final free chlorine that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
FINFreeCL	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
FINFreeCL	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
FINFreeCL	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
FINFreeCL	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
FINFreeCL	FINpH	0.0	0.0	0.0	0.0	0.0	0.0
FINFreeCL	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

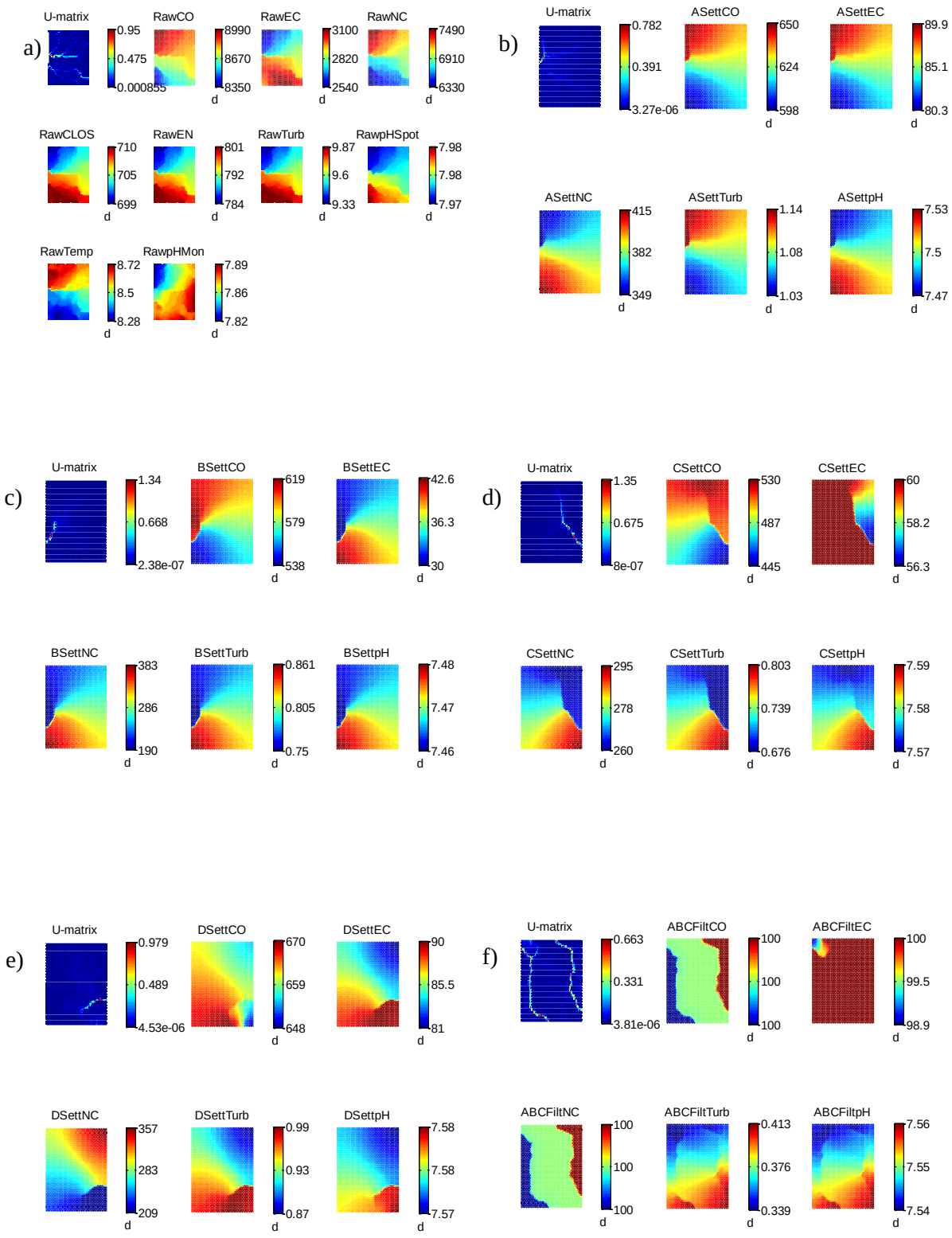
Cross-correlation results for Final total chlorine that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
FINTotalCL	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
FINTotalCL	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
FINTotalCL	FINTurbMon	-	0.0	0.0	0.0	0.0	0.0
FINTotalCL	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
FINTotalCL	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
FINTotalCL	FINpH	0.0	0.0	0.0	0.0	0.0	0.0

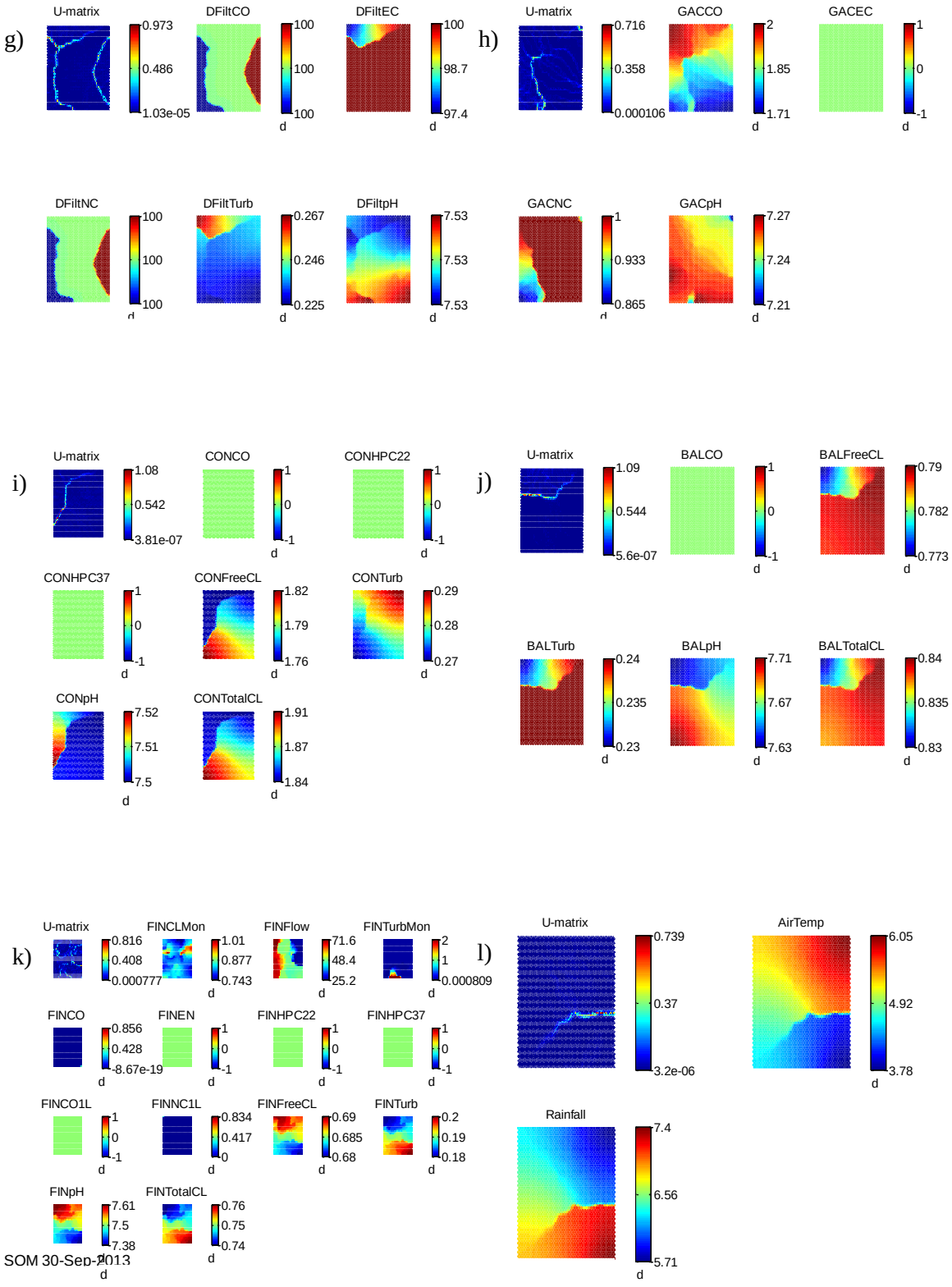
Cross-correlation results for Final pH that were both positive and between 0 and 24 h.

Parameter 1	Parameter 2	5 months	CO	EN	CO 1L (1)	CO 1L (2)	CO 1L (3)
FINpH	FINCLMon	0.0	0.0	0.0	0.0	0.0	0.0
FINpH	FINFlow	0.0	0.0	0.0	0.0	0.0	0.0
FINpH	FINTurbMon	0.0	0.0	0.0	0.0	0.0	0.0
FINpH	FINFreeCL	0.0	0.0	0.0	0.0	0.0	0.0
FINpH	FINTurb	0.0	0.0	0.0	0.0	0.0	0.0
FINpH	FINTotalCL	0.0	0.0	0.0	0.0	0.0	0.0

Appendix 3. Strensham coliform failure SOMs

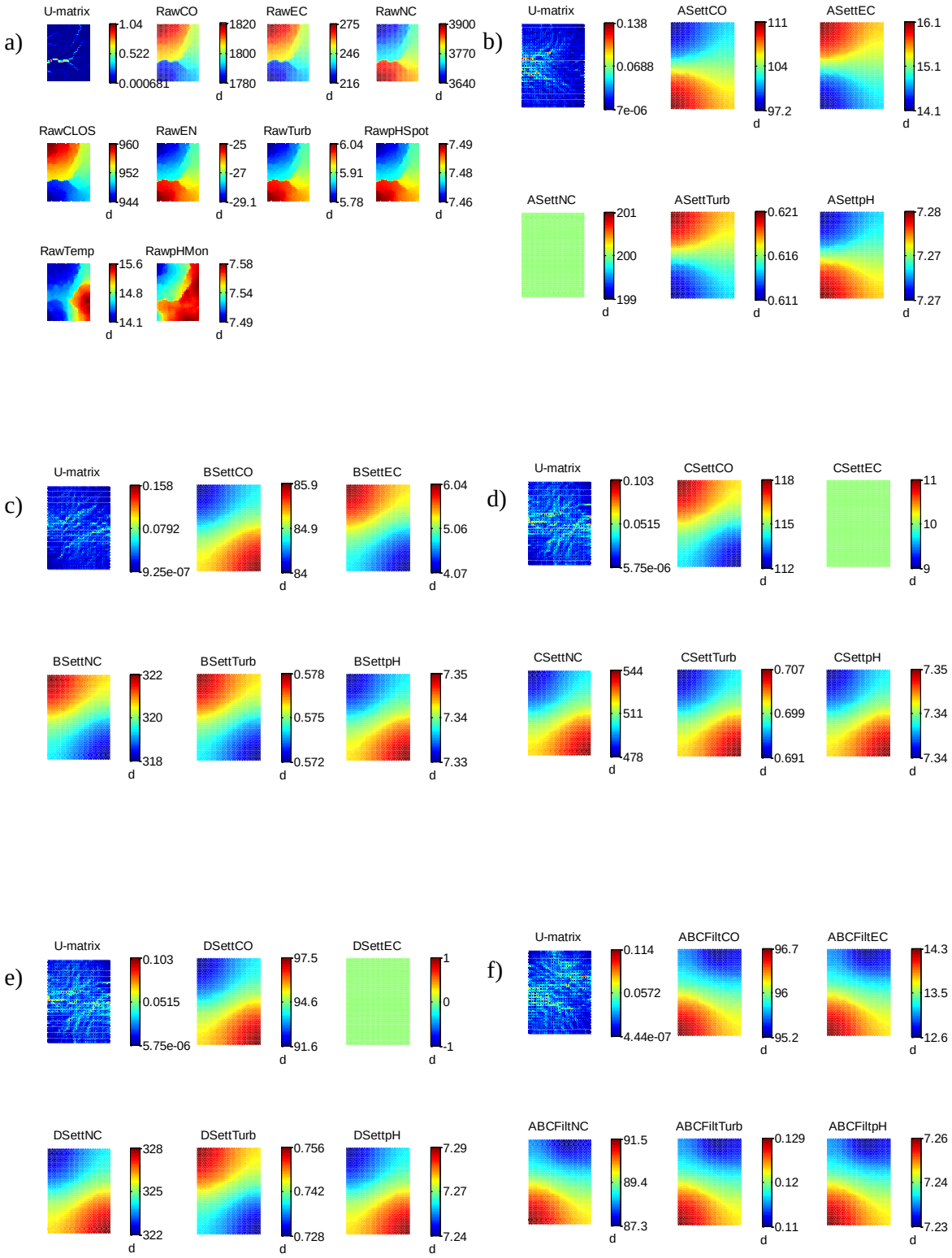


SOMs for the week of the Strensham coliform failure: a) Raw water; b) Settlement Tank A; c) Settlement Tank B; d) Settlement Tank C; e) Settlement Tank D; and f) Filter Block ABC.

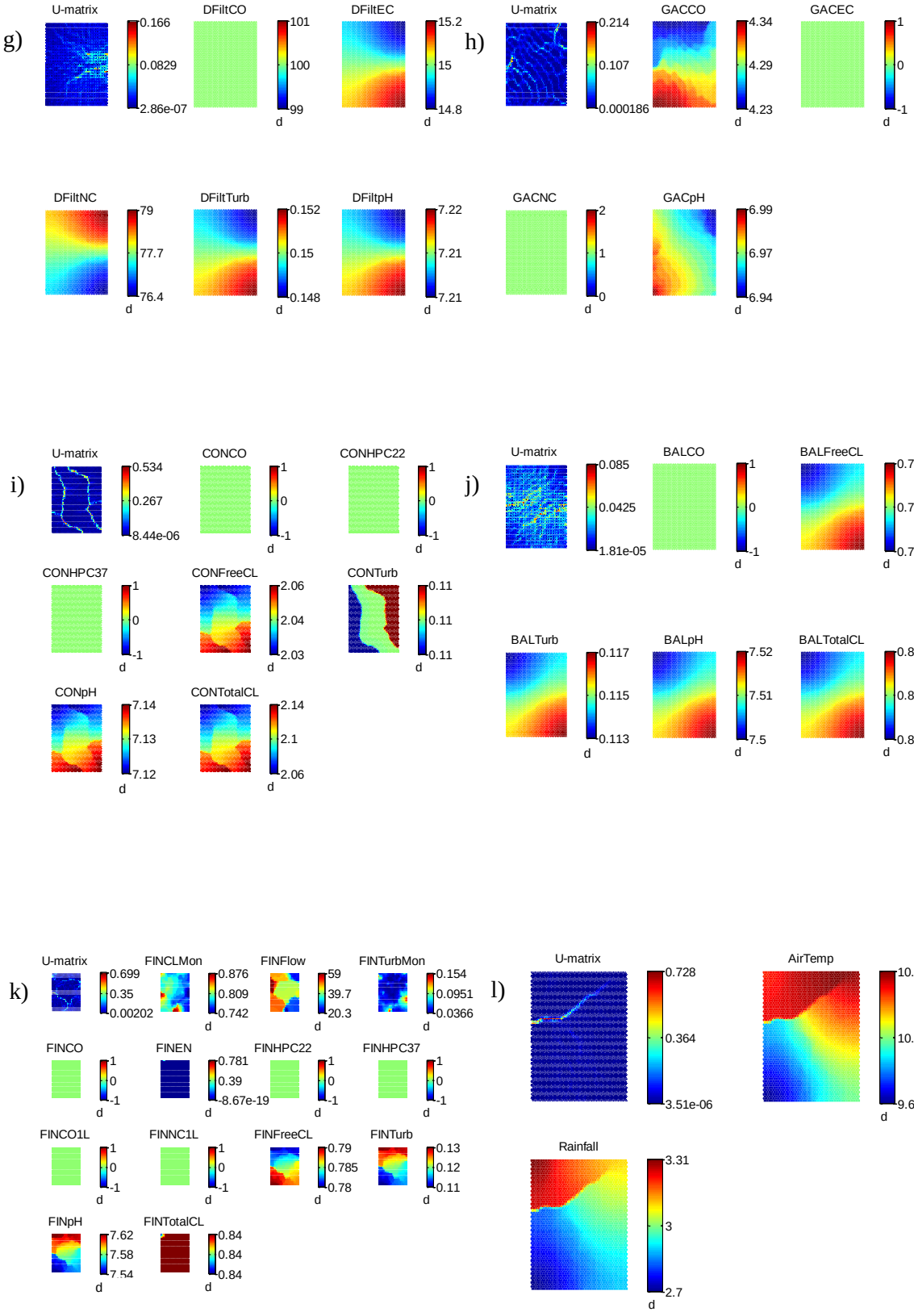


SOMs for the week of the Strensham coliform failure: g) Filter Block D; h) GAC Filters; i) Contact Tank; j) Balance Tank; k) Final water; and l) Climate.

Appendix 4. Strensham Enterococcus failure SOMs

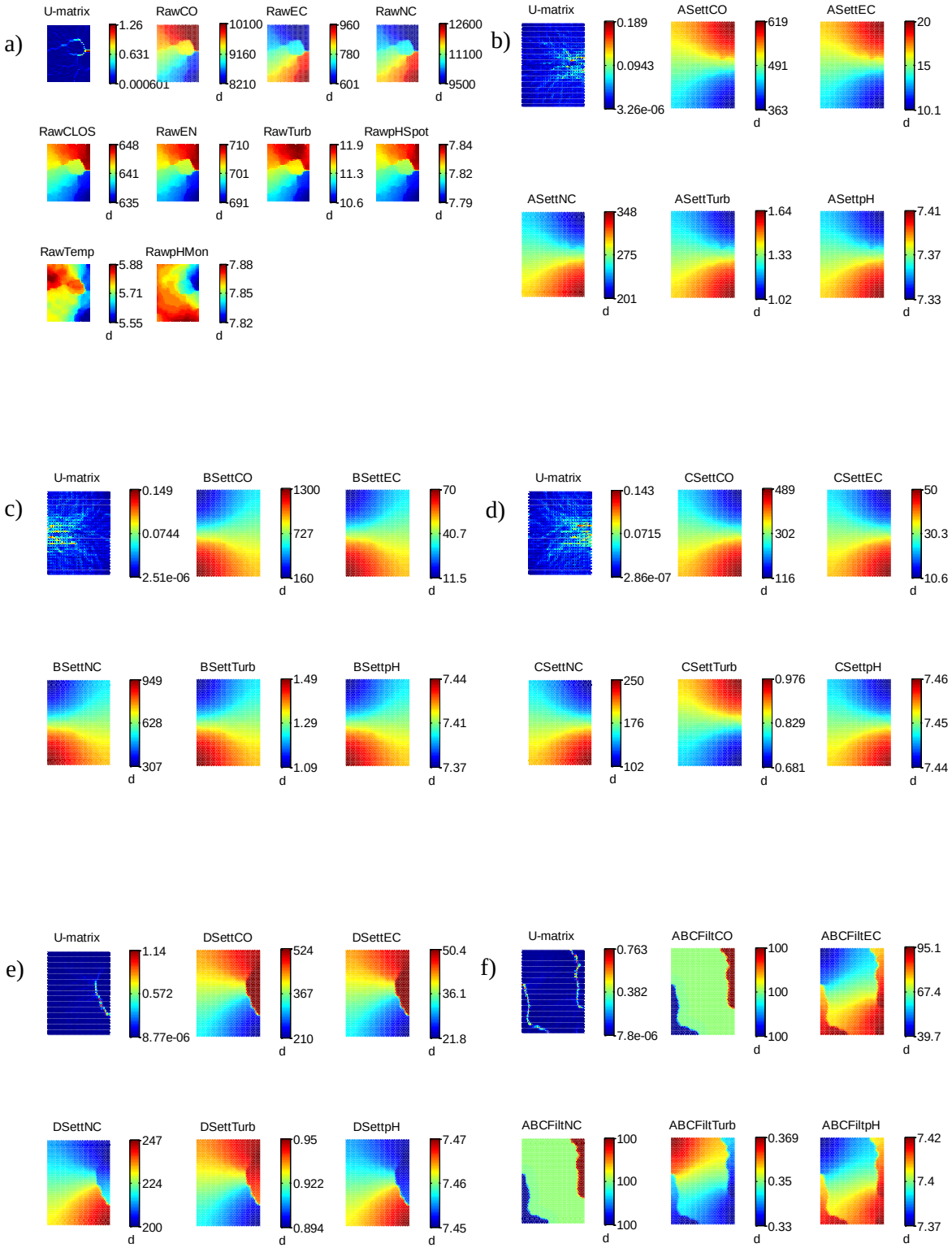


SOMs for the week of the Strensham Enterococcus failure: a) Raw water; b) Settlement Tank A; c) Settlement Tank B; d) Settlement Tank C; e) Settlement Tank D; and f) Filter Block ABC.

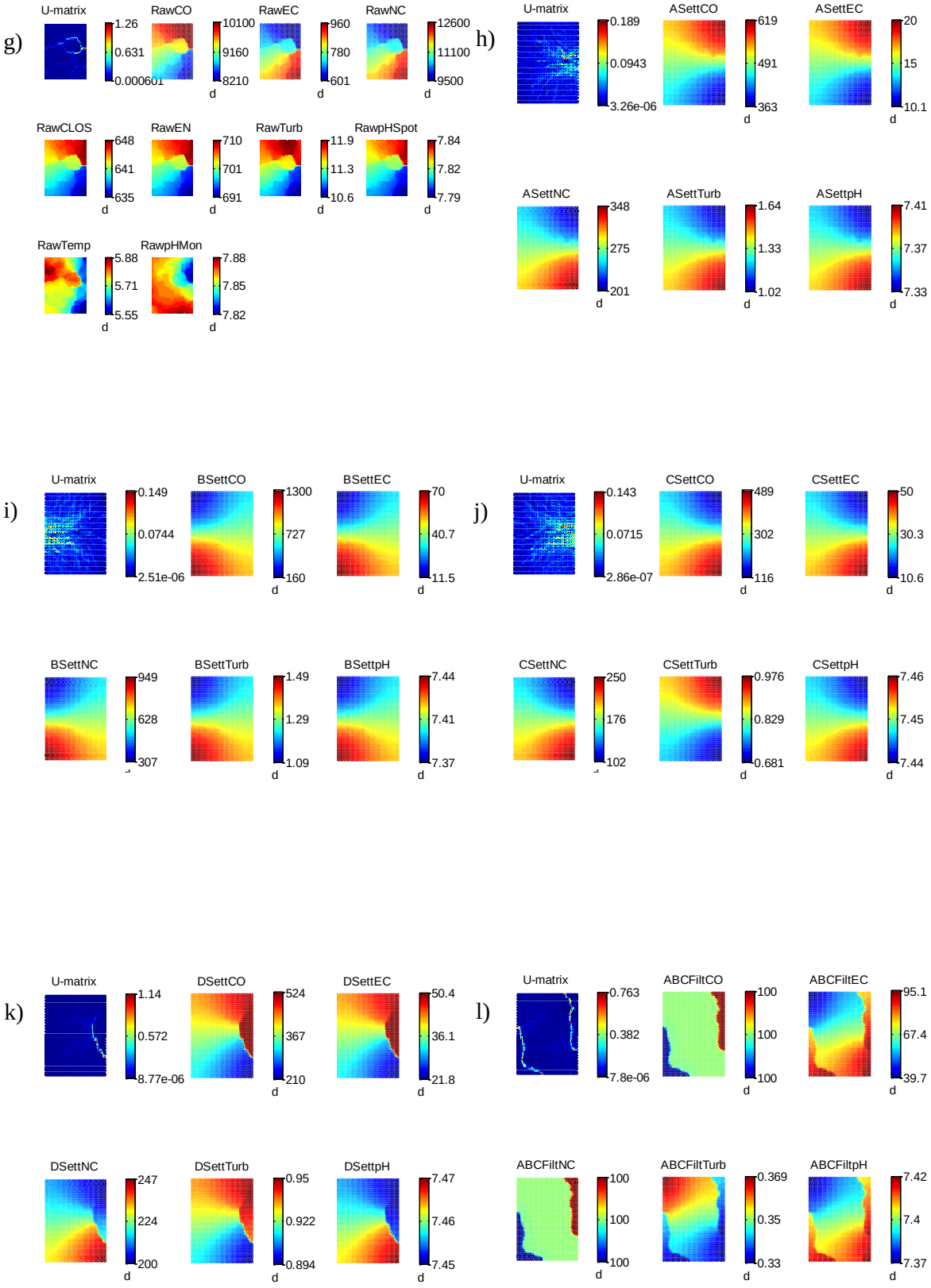


SOMs for the week of the Strensham Enterococcus failure: g) Filter Block D; h) GAC Filters; i) Contact Tank; j) Balance Tank; k) Final water; and l) Climate.

Appendix 5. Strensham first 1 L coliform failure SOMs

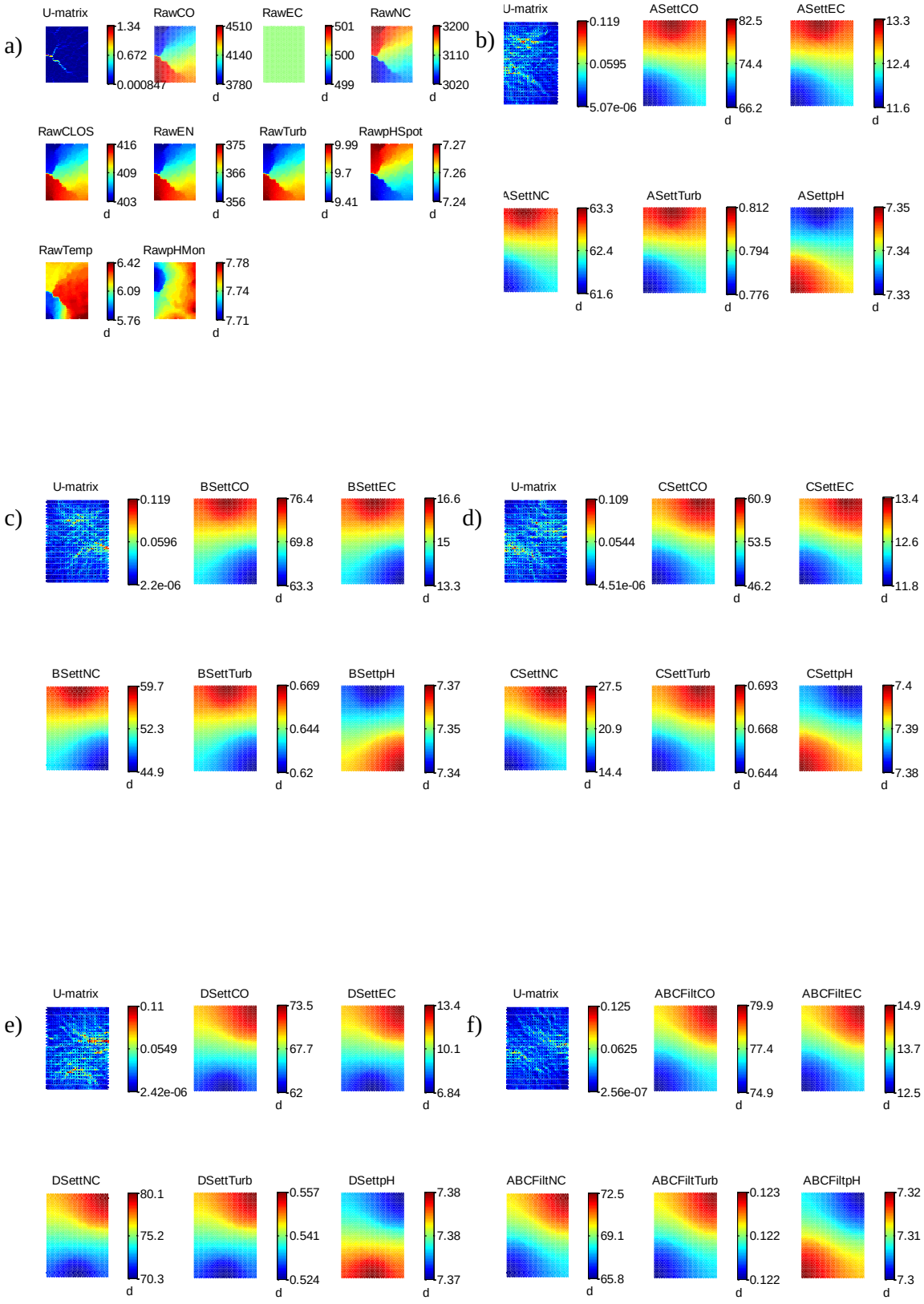


SOMs for the week of the Strensham first 1 L coliform failure: a) Raw water; b) Settlement Tank A; c) Settlement Tank B; d) Settlement Tank C; e) Settlement Tank D; and f) Filter Block ABC.

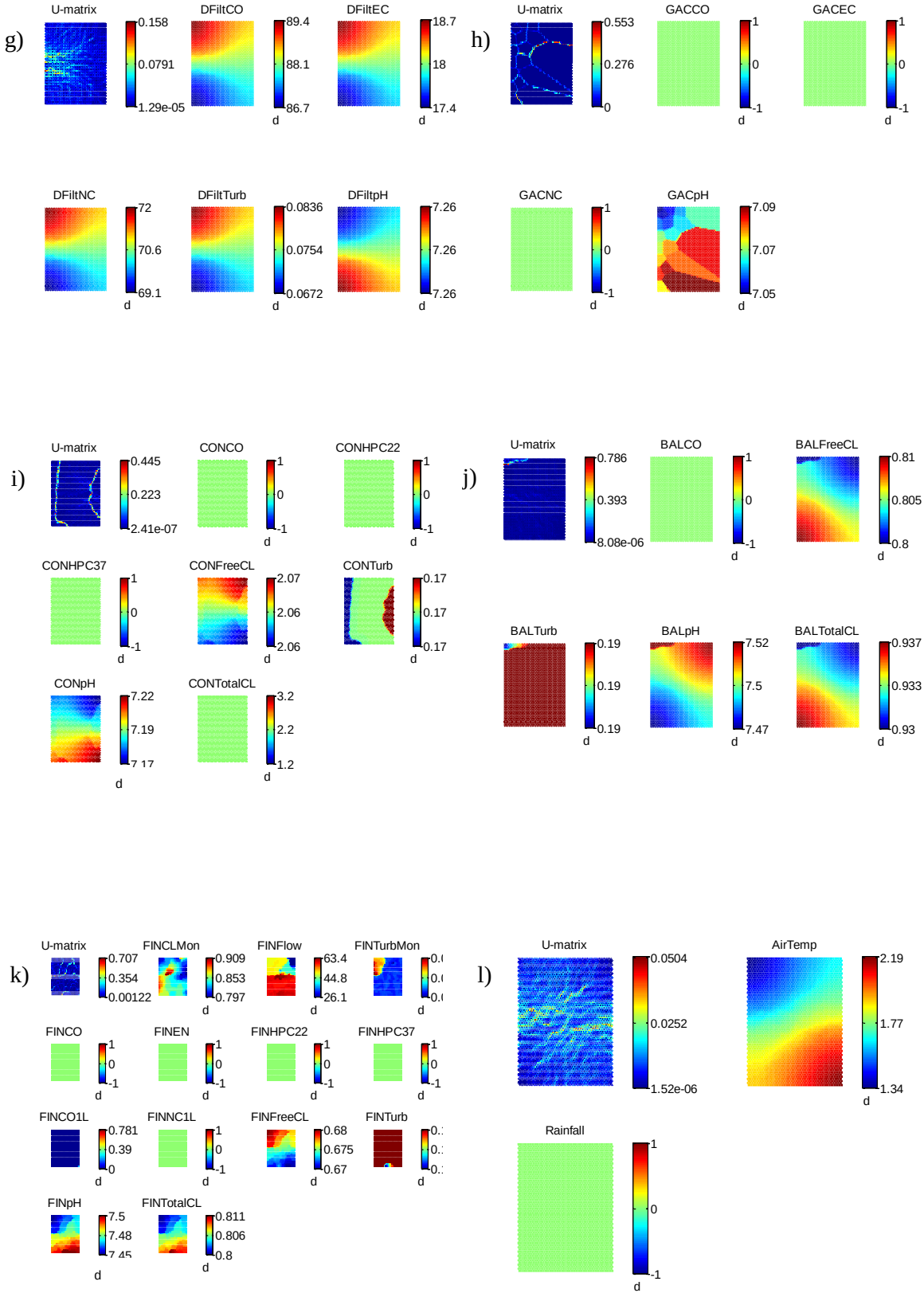


SOMs for the week of the Strensham first 1 L coliform failure: g) Filter Block D; h) GAC Filters; i) Contact Tank; j) Balance Tank; k) Final water; and l) Climate.

Appendix 6. Strensham second 1 L coliform failure SOMs

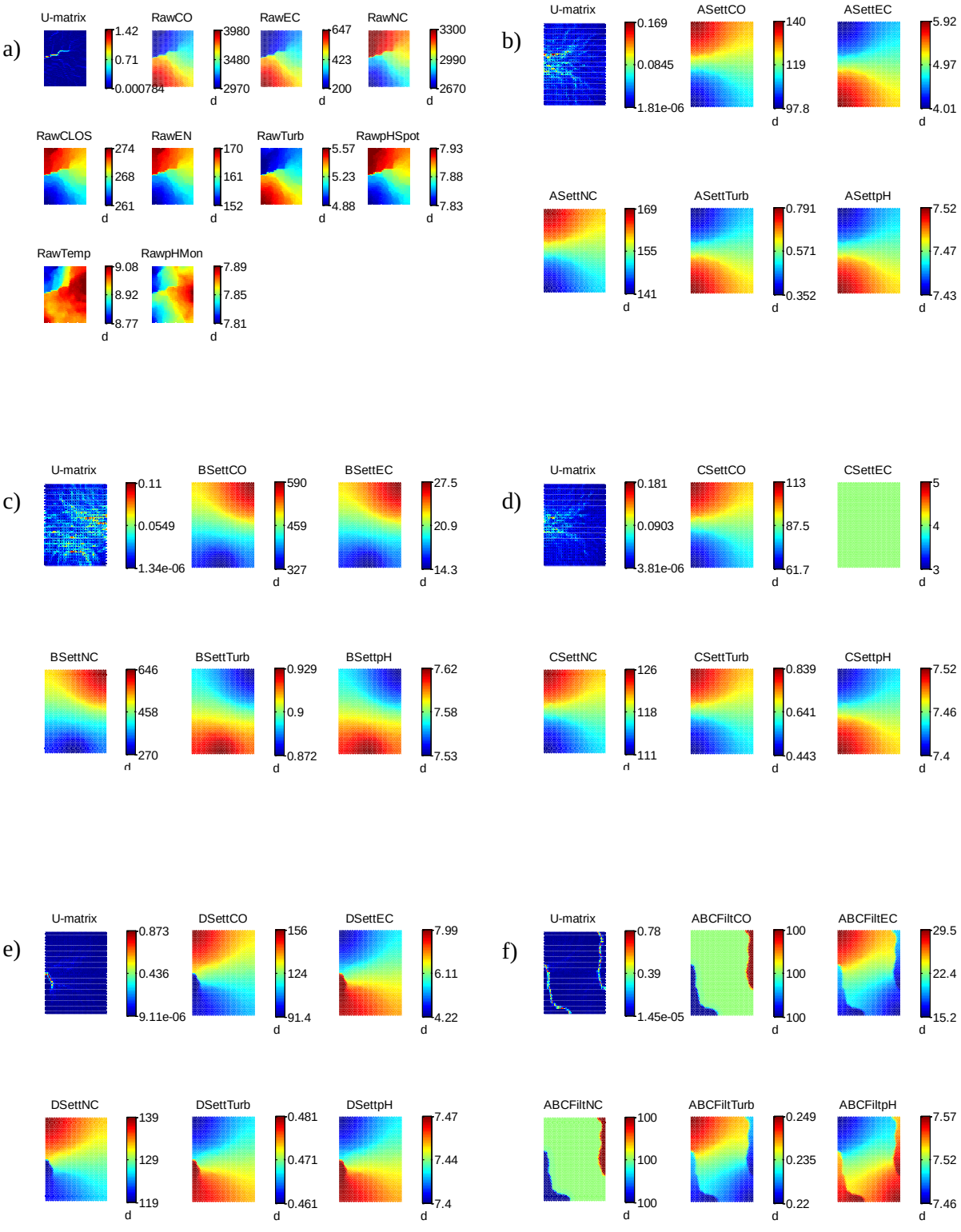


SOMs for the week of the Strensham second 1 L coliform failure: a) Raw water; b) Settlement Tank A; c) Settlement Tank B; d) Settlement Tank C; e) Settlement Tank D; and f) Filter Block ABC.

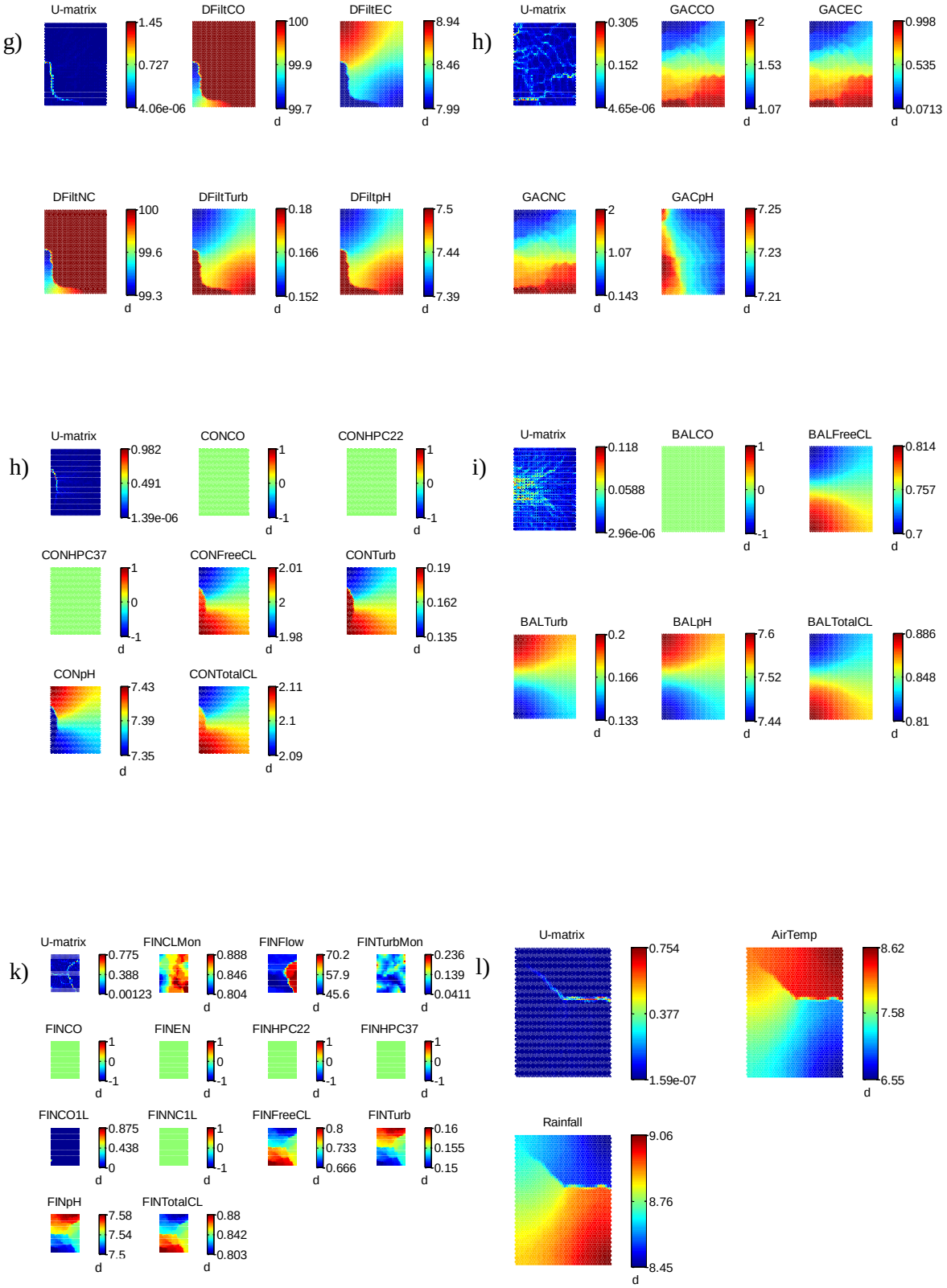


SOMs for the week of the Strensham second 1 L coliform failure: g) Filter Block D; h) GAC Filters; i) Contact Tank; j) Balance Tank; k) Final water; and l) Climate.

Appendix 7. Strensham third 1 L coliform failure SOMs



SOMs for the week of the Strensham third 1 L coliform failure: a) Raw water; b) Settlement Tank A; c) Settlement Tank B; d) Settlement Tank C; e) Settlement Tank D; and f) Filter Block ABC.



SOMs for the week of the Strensham third 1 L coliform failure: g) Filter Block D; h) GAC Filters; i) Contact Tank; j) Balance Tank; k) Final water; and l) Climate.