# EXAMINING SPECIES' RESPONSES TO CLIMATE CHANGE

# ACROSS MULTIPLE TAXONOMIC GROUPS

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## Abstract

Many species are responding to anthropogenic climate change by shifting their ranges to higher latitudes. Understanding the factors that drive species' responses will help ecologists and conservationists develop strategies to avoid negative climate change impacts.

I investigated shifts at the northern (cool) range margins of 1573 southerly-distributed species from 21 animal groups in Great Britain, over the past four decades. My findings confirm continued polewards range shifts (18 km decade<sup>-1</sup> over 1986-2010). I then concentrated on 347 British species from 14 invertebrate taxa, discovering considerable variation in the distances moved within each taxonomic group (but not between groups). I used land cover data and distribution records to determine each species' habitat specialism, and to quantify habitat availability. Habitat availability explained up to half of the range shift variation. I conclude that interactions between species' attributes and the environment are important determinants of range shifts.

Abundance data are used to study species' responses to environmental changes but, unlike distribution records, are not available for many taxa. Data from 33 British butterflies revealed a strong correlation between mean year-to-year changes in total number of distribution records and mean year-to-year change in abundance, suggesting that distribution data can be used to identify species' population variability, and ecologists can investigate the influence of climate change on species' populations without abundance data.

I conclude that rates of range shifting are highly variable among species, suggesting that understanding species-specific range shifts is necessary to assess species' responses to climate change. The availability of habitat at the range margin strongly influence rates of range shifting which suggests the need for habitat management aimed at facilitating species' dispersal and population establishment. Citizen science data have potential to assist ecologists in examining species' responses to climate change and in identifying, predicting and mitigating climate change impacts in the future.

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## Declaration

I declare that this thesis is a presentation of original work and I am the sole author. This work has not previously been presented for an award at this, or any other, University. All sources are acknowledged as References.

This thesis involved collaborations with various researchers: below I present the contributions of other researchers to each of my chapters, with the following shorthand: Professor Jane Hill (JKH), Professor Chris Thomas (CDT), Dr Tom Oliver (THO), Dr Gary Powney (GDP), Dr Georgina Palmer (GP), Dr Phil Platt (PP), Richard Fox (RF), Simon Gillings (SG), Tom Brereton (TB). The work produced in this thesis was supported by NERC grant NE/K003 81X/1.

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## Chapter 1

## General Introduction

In this thesis, I examine species responses to climate change. Redistribution of species under climate change has been observed globally, and has consequences for maintaining biodiversity and ecosystems. Climate change also has positive and negative impacts upon species population dynamics, which need to be examined to assess species' vulnerability. In this first chapter, I introduce the key topics of my thesis. First, I provide the context for my thesis, anthropogenic climate change (section 1.1). I discuss species associations with the climate (climatic niches), and how these associations can vary over space and time (section 1.2). I briefly discuss different evolutionary and ecological responses to climate change (section 1.3) and focus on range shifts, a response of interest (section 1.4). I consider the population changes that drive this response, before examining the impact of habitat availability upon species' rates of range shift (section 1.5). I present the biological records data used to measure range shifts and to create proxies for abundance in this thesis (section 1.6). Finally, I set out the research questions I address in this thesis and I provide an overview of each subsequent chapter (section 1.7).

### 1.1 Anthropogenic climate change

The global climate has always been changing, as evidenced by records of oxygen isotopes, pollen, and fossils (Shackleton, 1987; Jackson *et al.*, 2000; Davis & Shaw, 2001). Since the industrial revolution, there has been an increase in the rate of climatic warming (Karl & Trenberth, 2003), termed 'anthropogenic climate change', or climate change driven by human activity. This activity has been extensive, and the term 'Anthropocene' is used to describe the current epoch which has a range of proposed start dates, ranging from the 1800's (Steffen *et al.*, 2011) to the mid-20<sup>th</sup> Century (Waters *et al.*, 2016). Anthropogenic climate change is driven by greenhouse gases (GHGs), defined by the IPCC as "those gaseous constituents of the atmosphere, both natural and anthropogenic, that absorb and emit radiation at specific wavelengths within the spectrum of thermal infrared radiation emitted by the Earth's surface, the atmosphere itself, and by clouds" (IPCC, 2014). By absorbing radiation, GHSs act as an insulator, trapping heat and warming the earth. GHGs include water vapour,  $CO<sub>2</sub>$ , CH<sub>4</sub>, O<sub>3</sub> and N<sub>2</sub>O. In 2011, CO<sub>2</sub> concentrations in the atmosphere were 40% higher than they were before the industrial revolution and  $CO<sub>2</sub>$ , CH<sub>4</sub>, and N<sub>2</sub>O

concentrations were noted to "exceed the highest concentrations recorded in ice cores during the past 800,000 years" (IPCC, 2013). Human activities are contributing to GHG emissions through energy production, other industrial activities and land use change (Turner *et al.*, 1994; Ramankutty & Foley, 1999; Christidis *et al.*, 2013). There is a consensus in the literature that the global-scale warming trend since the mid  $20<sup>th</sup>$  century has mainly been caused by anthropogenic emissions (Oreskes, 2005; Jenkins *et al.*, 2008; IPCC, 2013). The rapid proliferation of technology and exploitation of the Earth's resources (e.g. fossil fuel energy) have led to increased GHG emissions. In future, human activities are likely to intensify as our rising population (now estimated globally at 7,550 million people: see United Nations report, 2017) demands an increasing supply of resources. As concentrations of atmospheric GHGs continue to rise, climatic conditions will change affecting the Earth's ecosystems and the species that live there.

Atmospheric and oceanic temperature increases are a consequence of GHGs warming the planet by trapping radiation (Karl & Trenberth, 2003). At a worldwide scale, a globally averaged warming of 0.85°C has been observed from 1880 to 2012 for land and ocean surface temperatures combined (IPCC, 2013). Increases in the frequency of extreme events are predicted to occur under climate change (Easterling, 2000; Cai *et al.*, 2014). Extreme record-breaking temperatures are increasingly observed (Lhotka *et al.*, 2016), with 2017 being the second hottest year on record for the US (NOAA National Centers for Environmental Information, 2017). Warmer temperatures result in higher rates of evaporation from the Earth's oceans, leading to greater incidence of heavy rainfall and flooding (Lenderink & van Meijgaard, 2008). However, in drier areas where there are fewer water bodies, increased temperatures may increase the risk of drought (IPCC, 2013). These extreme events are predicted to have detrimental impacts for ecosystems, causing population collapse in sensitive species (Oliver *et al.*, 2015) and reductions in habitat quality and availability (Ummenhofer & Meehl, 2017).

In this thesis, I study the responses of species in Britain to climate change. In the UK, the climate has been monitored for hundreds of years by volunteers and organisations such as the UK Met Office. Instrumental recording of monthly temperatures began with Central England Temperature (CET) data in 1600s (Parker *et al.*, 1992), and the longest continuously-active weather station has records since 1767 (Oxford University News, 2015). An analysis of UK climate changes show that all regions have experienced a trend of increased winter rainfall, the Central England Temperature (CET) has increased 1°C since

the 1970s, and severe windstorms have become more frequent (Jenkins *et al.*, 2008). The UK Climate Projections science report (Murphy *et al.*, 2009) predicts that by 2080 the UK will experience increased daily temperatures by 5.4°C in summer and 2.8°C in winter (median emissions scenario, 50% probability). The projected impact of climate change on precipitation is less clear, but includes increased winter rainfall by up to 33% in the west of the UK, decreased summer rainfall by up to 40% in southern England, and an increased risk of flash-flooding (Kendon *et al.*, 2014). The potential consequences of these changes for biodiversity are a core area of ecological research, and in this thesis, I explore species' responses to climate change, in order to understand how and why species react to changes in their environment. These analyses will not only aid understanding of species' recent responses to climate, but also help inform conservation efforts to protect species in future. The results have implications beyond the UK, for example, informing on how different species types are likely to respond to climatic change in heavily human modified landscapes, as found in many countries globally.

## 1.2 Species' associations with climate

In order to understand the impacts of anthropogenic climate change on species and ecosystems, it is important to understand the relationships between species and climate. Fundamental niches constitute the multi-dimensional array of conditions (including climate) within which a species can exist (Hutchinson, 1957; Holt, 2009). However, species may be excluded from parts of their fundamental niches, due to interspecific interactions, such as predation, competition and parasitism. This new subset of their fundamental niche is called the 'realised' niche (Hutchinson, 1957). The range of climatic conditions where species are able to survive (measured within the realised niche) can be referred to as the 'climatic niche' (Bellard *et al.*, 2012). Extinctions can occur where climate becomes unsuitable, but species may colonise new areas that become habitable under climate change. These changes in species' distributions or 'range shifts' in response to climate change are a primary focus for my thesis, and I discuss them further below (section 1.4).

A suitable climate is a vital aspect of a species' niche, and species distributions and population sizes are commonly determined by climatic conditions (Stephens *et al.*, 2016). There are defined climatic regions across the world, and biodiversity is distributed nonrandomly, peaking in moist, tropical regions. This pattern can be explained by the speciesenergy relationship (Gaston, 2000), which implies that more species will be able to persist where more energy (heat) and water is available (measured as temperature and/or

evapotranspiration). This relationship is theorised to occur because higher energy availability will boost primary productivity, which in turn supports more primary consumers, with cascading impacts through the entire ecosystem. Alternatively, extreme dry or cold environments present limits to productivity, and fewer species can persist in such conditions (Araújo *et al.*, 2013). There are many interacting processes in biodiversityrich regions, and understanding the extent to which different factors create and maintain diversity is complex (Brown, 2014).

Weather conditions influence populations by directly affecting fecundity and mortality rates, and by indirectly affecting interspecific relationships (i.e. abundance of predators or prey) and resources (e.g. host plant quantity and quality for herbivores). Temperature and rainfall are commonly examined in studies of population dynamics, because these variables are also metrics of climate change (WallisDeVries *et al.*, 2011). The impacts of these variables on species' biogeography have been studied for butterflies, a data-rich taxonomic group. Temperature is linked to fecundity in several butterfly species, because females rely on warm temperatures to seek out appropriate host plants (Kingsolver, 1989). Rainfall is beneficial for host plant growth, and some butterflies prefer moist conditions, although rainfall reduces dispersal (individuals' movement through the landscape) and may prevent foraging (Pollard, 1988). Roy *et al.* (2001) found that rainfall and temperature interacted to influence populations: the majority of butterfly species generally had positive associations with warmer summer temperatures, but for some species, droughts (caused by low rainfall) resulted in negative associations between abundance and warm summers in previous years. Given the heterogeneous impacts of weather conditions upon species populations, climate change is likely to have positive and negative impacts on populations. If temperatures rise, this may increase productivity, which will support larger populations for some species. Extreme climatic events can cause species' populations to severely decline (Oliver *et al.*, 2013) or increase in variability (Vázquez *et al.*, 2017). Increased variability in species abundances can increase risk of local extinctions (Wiens, 2016), and cause disappearances of species from larger areas (Parmesan, 2006; Stanton *et al.*, 2015). To summarise, species have strong associations with different climatic processes that directly and indirectly influence their vitality, fecundity and mortality. Until such details are known, the complexity of these interacting effects of weather on populations make it difficult to predict the longer-term impacts of climate change on species (Knape & de Valpine, 2011). However, some short-term impacts such as the effects of sudden and extreme climatic events have been observed and studied.

Climate change, in addition to impacting the persistence of species populations, may also affect species' climate associations. Under climate change, these associations may remain constant (niche conservatism), resulting in species shifting their ranges, or be altered (niche shifts) if species adapt *in situ* to changing climates (Holt, 2009). Under the assumption of conservatism, niches can be inferred from occupancy-environment relationships, whereby species persistence is determined by the suitability of its environment (Pearman *et al.*, 2008). In addition, conservatism rests on the assumption that species are in equilibrium with their environment, and will shift their ranges to track their climatic niche (La Sorte & Jetz, 2012). By contrast, niche shifts have been observed when species invade new areas and encounter new environmental conditions (Tingley *et al.*, 2014). While a species' realised niche can be used to predict whether that species might invade a new area, the niche can be inadequate for predicting future distributions (Broennimann *et al.*, 2007). Whether niches are conserved or altered over time is important for understanding whether the species will successfully shift its range and establish in new areas or not. For example, Yackulic *et al.* (2015) concluded that temporal variation in climatic conditions and colonisation and extinction events can result in species' occupancy-environment relationships changing over time. Most researchers consider that static occupancyenvironment relationships, and the correlative models that utilise them, are over-simplistic for predicting species responses to climate change (Schurr *et al.*, 2012; Yackulic *et al.*, 2015). Species may not always be at equilibrium with their environment (such as at the edges of the range where exposure to changes in environmental conditions can make populations rapidly increase or decrease), and there may be delays or lags in response to climate change, but creating models that are reflective of the true occupancy-environment relationship of species is extremely challenging. In conclusion, species climate associations are not necessarily static; some species may contract or expand their realised and even fundamental niches over time, and thus adjust to climate change in different ways.

### 1.3 Species' responses to climate change

Across continents, a wide range of species' responses to climate change have been detected (Parmesan, 2006; Sutherland *et al.*, 2010). These are genetic, evolutionary responses (e.g. microevolution, (Parmesan, 2006; Bellard *et al.*, 2012; Vedder *et al.*, 2013), and ecological responses. Ecological responses include phenotypic plasticity, which is the ability of a genotype to express different phenotypes under different conditions, phenological changes, changes in population dynamics and range shifts (moving to new locations as species track suitable conditions), and while framed as species reactions to

changes in the environment, these responses can have evolutionary bases (see below). In this section, I discuss the relationship between evolutionary and ecological responses, examples of genetic and phenotypical responses, and how population dynamics (e.g. changes in size) are used to monitor species' sensitivity to climate, before focussing on range shifts in more depth in the next section (1.4).

Understanding the mechanisms of species responses to climate change can be immensely difficult, as it is often unclear whether responses have a genetic underpinning, or are a result of phenotypic adaptations. Most studies of climate change responses do not test for genetic changes in species and populations (Gienapp *et al.*, 2008). Thus, evidence of evolutionary responses to climate change tends to be limited and many responses are inconclusively theorised to be evolutionary. Some phenotypic responses such as plasticity could be evolutionary responses to a changing environment (Vázquez *et al.*, 2017); alternatively, adaptations which are thought to be genetic may actually be driven by ecological processes (Gienapp *et al.*, 2008). Species may demonstrate both genetic and phenotypical adaptations under climate change. While these adaptations may enable species to respond to climate change, many studies do not explicitly identify climate as the selective driving force of the adaption (Gienapp *et al.*, 2008). With these issues in mind, I will now discuss case studies of evolutionary and ecological responses to climate change.

Evolutionary responses to climate change can facilitate species' successful colonisation of newly-suitable locations, or enable persistence of altered climate conditions *in situ* (Chevin & Hoffmann, 2016). For example, some British cricket species (*Concephalus discolor* and *Metrioptera roseii*) have short- and long-winged forms, and the longer-winged, more dispersive individuals have been observed more frequently in newly established populations (Thomas *et al.*, 2001; Simmons & Thomas, 2004). Temperature influences the form that individuals will mature into (as demonstrated by Sänger & Helfert, 1975), and climate change acts as a driving force for range expansion (Hochkirch & Damerau, 2009; also see below). Therefore, it is likely that climate has acted as a selective pressure to increase the proportion of the population with longer wings, because long distance dispersers are more likely to establish new populations in regions that have recently become climatically suitable for them. Once established, a costly dispersal strategy is unnecessary for individuals, and the incidence of long-winged forms declines over time; this demonstrates how evolutionary processes can cause short-lived changes in species' behaviour in response to climate change (Simmons & Thomas, 2004).

Another example of an evolutionary response to climate change is the changes observed in migration patterns of *Sylvia atricapilla*, the Eurasian blackcap. As temperatures increase, winters become warmer, changing the distribution of suitable areas where migrating birds can overwinter. Over the last 50 years, some German blackcap populations have evolved new migration patterns (Berthold *et al.*, 1992); while British populations migrate southwards, some German birds migrate westwards to Britain, where there are milder winters and an abundance of food resources in domestic gardens. Because of the closeness of this location to the species native range, birds overwintering in Britain can return to Germany sooner, and breed 2 weeks before individuals than overwinter in Africa and southern Europe. Because birds that return sooner breed with other birds do the same, there is genetic isolation between populations with different migration strategies which has enabled this rapid evolutionary change (Pulido, 2007). While there is much potential for evolutionary responses to climate change, many observed adaptations appear to be variations on normal behaviour and body size, and uniquely different phenotypes are not often observed. A lack of existing genetic variation, gene flow or new mutations may limit adaptations to climate change (Thomas, 2005).

The evidence base for adaptive responses to climate change is mostly comprised of phenotypic observations, which may be underpinned by genetic changes and/or by plasticity. Phenotypic plasticity is the phenomenon of changes in species' behaviour, thermal tolerances, physiology or other aspect of their phenotype. Climate change effects mediated through physiology can have positive or negative effects on individual fitness. For example, with regards to butterflies, warmer temperatures allow females more time to search for hostplants and to lay their eggs. Davies *et al.* (2006) studied the thermallyrestricted silver spotted skipper butterfly (*Hesperia comma*), and found that warming climates had improved habitat availability, allowing the species to disperse and utilise a variety of hostplants beyond its traditional ones. As a result, egg-laying rates increased, which in turn may boost numbers of individuals. However, climate change can also lead to lowered fitness through heat stress (McCarty, 2001), or reduced foraging time for insects due to unsuitable conditions (Andrew *et al.*, 2013).

Phenotypic plasticity can help species survive in extreme and variable climates, and therefore is of interest to ecologists and conservationists (Chevin & Hoffmann, 2016). An example of phenotypic plasticity is phenological change. Alterations in phenology (the timings of seasonal events in species' lifecycles) are *in-situ* climate change responses, which are often prompted by temperature changes (Foden *et al.*, 2013; Dickinson *et al.*, 2014) and influenced by species' life histories (Forrest, 2016). As different species have different responses to climate change, changes in phenology can lead to either trophic matches, improving or creating interspecific interactions, or tropic mismatch, where ecological interactions between species are disrupted (Thackeray *et al.*, 2010; Schweiger *et al.*, 2012). Changes in phenology may allow species to track climate change and avoid mismatches. Without adaptations like this, populations may decline. One of the best examples of phenological responses to climate change is the interaction between great tits, *Parus major* and larvae of the winter moth, *Operophtera brumata* (Visser *et al.*, 2006). Great tits lay their eggs so that the hatching of their chicks coincides with the peak abundance of larvae (Noordwijk *et al.*, 1995), which in turn hatch during the bud burst of oak trees, to feed on new leaves. Larval growth and oak bud burst depends on temperature, and changing climates might have resulted in a mismatch between when larvae are abundant, and when the great tit eggs are laid. However, in Wytham Woods, great tits demonstrated plasticity, rather than microevolution, changing their nesting behaviour to track the emergence of the larvae (Charmantier *et al.*, 2008). Other phenological responses include changes in voltinism, the number of generations a species produces. Climate change has improved the prospects of Lepidoptera species in Europe, increasing the frequency of second and third broods in many species (Altermatt, 2010). Multiple generations per year may speed up evolutionary responses to climate change, and contribute to population growth.

Here, I briefly discuss climate effects on population size. Because climate can influence species fecundity and mortality, population metrics are often used to determine the risks of climate change to species. This responsiveness of populations to climate change (often termed vulnerability in the literature) to climate change is determined by two factors: sensitivity to climate and exposure (i.e. how much the climate has changed for species, see Williams *et al.*, 2008 and Huey *et al.*, 2012). Climate sensitivity is a metric that measures how populations respond to climate change, characterised as a species' ability to persist in changed environments or dependence on unaltered climate conditions (Dawson *et al.*, 2011; Foden *et al.*, 2013; Dickinson *et al.*, 2014). While much of the literature focuses on negative impacts of climate change, warm-associated species in Britain (which are the focus

of my thesis) are set to benefit from climate change (Burns *et al.*, 2016). Populations may increase because of positive climate effects on fecundity and brood size, as stated above. Climate sensitivity is often assessed as the magnitude of changes in population size in response to climatic variables, and exposure reflects the degree of change of climate variables that the species is sensitive to (Foden *et al.*, 2013). The combined effects of sensitivity to different climatic variables and exposure to those climatic variables will determine how species respond to climatic change. The responsiveness of species populations to climate change must be measured in a clear and rigorous way (Wade *et al.*, 2017) so that ecologists can predict future outcomes for species and develop appropriate conservation management strategies (McMahon *et al.*, 2011). In this thesis, I explore a method to use distribution data to measure population variability where abundance data are lacking, potentially providing a key indicator of species responses to climate change (see section 1.6.2 below).

### 1.4 Range shifting in response to climate change

Naturalists and ecologists have observed the changing spatial distributions of species (Kaisila, 1962; Fuller et al., 1995; Brown et al., 1996). Range shifts are a well-studied response to climate change, and in this section, I discuss different patterns of range change and how they are measured, and the population processes that lead to range shifts. I finish this section by discussing the knowledge gaps that my thesis addresses.

Species responses to climate change are observed through changes in the size, shape or extent of species' ranges (Thuiller *et al.*, 2005), and changes in position of the range by latitude (Parmesan & Yohe, 2003; Hickling *et al.*, 2006; Parmesan, 2006; Walther, 2010; Poloczanska *et al.*, 2013). Changes in the longitude (Gillings *et al.*, 2015; Lenoir & Svenning, 2015; Tayleur *et al.*, 2015) and elevation of ranges are also observed (Sekercioglu *et al.*, 2008; Chen *et al.*, 2009; Menéndez *et al.*, 2014). Shifts have been measured for many different species in different biomes, at different scales, both micro- and global. Latitudinal changes in a species' ranges are most often measured at the poleward (leading-edge) range margin, though they can also be measured by the shift of the centre point (centroid) of the whole distribution (Huntley *et al.*, 2008), or by measuring ranges shifts in other directions, e.g. north-westwards (Gillings *et al.*, 2015). In this thesis, I use measure latitudinal changes in the northern range margin of species, which is normally the leading-edge of the range in Britain for species which favour warmer climates.

### 1.4.1 Population and range shifts

Range shift is a distributional change underpinned by population processes, which are commonly driven by climate change. Distribution and abundance are both influenced by climate because the two are related (Brown, 1984), as reflected in the abundanceoccupancy relationship (Gaston, 1996; Hartley, 1998; Roney *et al.*, 2015). This relationship is generally positive, but negative relationships can occur in situations where large populations of a species are highly aggregated (Webb *et al.*, 2012). Species ranges exist across geographical and climatic gradients, but none of these factors alone necessarily explains the spread of populations within ranges (Pironon *et al.*, 2015). Abundance within ranges is also influenced by inter- and intra-specific interactions, by species' ability to adapt to environmental change, and by human activity (Sagarin *et al.*, 2006).

As the climate warms, southern warm-adapted species in Britain experience range expansion. Species expand their distributions by colonisation, which involves individuals moving through landscapes (dispersal), and building populations in unoccupied habitats (establishment) at the leading-edge, (Hughes, 2000). At the leading-edge, abundance may limit colonisation of new areas (Mair *et al.*, 2014), where smaller populations produce few dispersing individuals. Some colonisations are undertaken by a few individuals over great distances, which can lead to founder effects, where the new population has low genetic diversity (Hill *et al.*, 2011). Reduced genetic variability, coupled with unfamiliar conditions, can threaten the success of the new populations by making species vulnerable to disease or extreme climatic conditions. The majority of population data on range shifts come from the leading-edge margins, and studies of periphery populations at the trailing-edge are relatively rare (Hampe & Petit, 2005). However, the population dynamics at this margin are important: this margin often contains older populations, with many genetic lineages (Hampe & Petit, 2005). These populations are sensitive to climate change, and retractions have been detected at the trailing edge margins (Franco *et al.*, 2006). Without local adaptation or population stability to enable persistence at the trailing edge, these populations may go extinct, causing the range to shift towards the leading-edge. The rate of population processes at the margins are not necessarily equal, and some species' leadingedges have been shown to expand faster than their trailing-edges contract (Chen *et al.*, 2011a).

#### 1.4.2 Variation in range shifts amongst and within taxa

Species differ in their niches, thermal tolerances, and responses to climate change, and thus variation is expected in range shifts both within and between taxonomic groups (Parmesan & Yohe, 2003; Angert *et al.*, 2011). For example, tree and shrub species in Sweden have tracked climate change at different rates (Kullman, 2002); different species across a range of taxa show different latitudinal and elevational shifts over time (Chen *et al.*, 2011b); and British butterflies show heterogeneous distribution and abundance responses to climate change (Mair *et al.*, 2012).

Few studies examine variation in rates of range shifts across multiple taxonomic groups (Hickling *et al.*, 2006). It is important to study variation in range shifts across a wide range of groups because the range shifts of well-studied species and taxa may not be representative of shifts experienced by the full range of biodiversity. There may be differences (flight ability, body size, reproductive strategies) between groups, which could result in variable climate change responses. Within-group variation must also be assessed because apparently similar species may still exhibit a variety of climate associations and life histories. If phylogenetically similar species respond to climate change in similar ways, then (for example) one butterfly's range shift would be similar to another's. Where this is not the case, specific range shift measurements must be calculated for each species of interest.

While it is generally accepted that there is intra- and inter-taxon variation in range shifts, these types of variation are rarely assessed together. Detecting and understanding variation in range shifts across multiple taxonomic groups will help ecologists identify what types of species are likely to have limited colonisation abilities. By exploring which factors influence rates of range shift, targeted conservation strategies can be developed to help protect vulnerable species under climate change, and facilitate increases in other species. This thesis addresses the lack of multi-taxon analyses of range shifts by exploiting the rich data available for British taxa, collated by the UK Biological Records Centre.

## 1.5 Habitat factors in range shifts

In addition to specific climatic conditions, species are often associated with specific types of habitat. To respond to climate change, species require suitable habitats in order to persist, as 'stepping stones' so that they can move through landscapes, and for habitat to be available to colonise and establish populations in new regions. The presence of seminatural (Papanikolaou et al., 2017), heterogeneous (Oliver et al., 2010), or intact (Eigenbrod et al., 2015) habitat can buffer species against negative effects of climate change by promoting population stability and providing refugia which faciliate range shifts. However, suitable habitat is not always available, as the world's biotopes are being converted, polluted, and fragmented by agricultural and industrial human activities (Vitousek *et al.*, 1997; Foley *et al.*, 2005). In this section, I discuss how climate and habitat factors interact to impact species populations and distributions (1.5.1), and then consider habitat availability within fragmented landscapes (1.5.2). I investigate the role of habitat availability in multitaxon range shifts in Chapter 3.

#### 1.5.1 Interactions between climate and habitat

Habitat is an important factor to consider when studying range shifts, because species require suitable habitats to establish new populations and track climate change. Attributing ecological changes (range expansions or contractions) to climate change, habitat availability, or both of these drivers is a challenge, as these drivers interact and other factors are also involved: life history traits, intraspecific competition and diseases (Oliver & Morecroft, 2014). The relationship between land use and climate change has different forms: additive, where the impacts of each driver can simply be summed, or interactive (Oliver *et al.*, 2016; Radinger *et al.*, 2016). Interactions between habitat and climate may be synergistic or antagonistic, where one factor amplifies or buffers (reduces) the effects of the other. For example, Bradbury *et al.* (2011) found that establishment of new populations of the Dartford Warbler in the UK was influenced by warmer climates improving the suitability of higher altitude, unoccupied and available habitats. This demonstrates a synergistic interaction between the amelioration of cold winters and habitat availability at higher altitudes. Because of the variety of impacts habitat change can have, it is important to control for habitat when studying climate change impacts (Clavero *et al.*, 2011).

Key examples of climate and habitat interactions include the altered habitat associations of butterflies, e.g. the silver spotted skipper, now increasingly utilises a wider variety of microhabitats and northerly-facing habitat patches (Davies *et al.*, 2006). Pateman *et al.* (2012) examined the habitat associations of two British butterfly species, the brown argus *Aricia agestis* and the speckled wood *Pararge aegeria*. The brown argus butterfly is associated with two hostplants, rockrose and dove's-foot cranesbill. The rockrose is the favoured hostplant, supporting large, stable populations. In the 1980's, only 20% of this species population was found in cranesbill-only areas. However, warmer summers improved suitability of cranesbill habitat, promoting population growth. The cranesbill is much more abundant than the rockrose in Southern England, allowing the large numbers of individuals to expand over this area, and now over 40% of populations are found in cranesbill-only areas (Pateman *et al.*, 2012). The *Aricia agestis* case study is an example of niche constraints (climate) being relaxed, allowing the exploitation or less favoured hostplants. *Pararge aegeria* has also been shown to vary its broad habitat use under climate change. Giving this butterfly its name, the speckled wood butterfly is associated with deciduous and coniferous woodland. However, as winters and summers have warmed, and summer rainfall has increased, this species has been able to create and sustain new populations in open unsheltered grassland where chill and desiccation would have previously had negative impacts upon populations. Therefore, the degree to which species are specialised on different habitats may vary between populations and the climatic conditions those individuals experience (Suggitt *et al.*, 2012). While climate can impact species' habitat associations in this way, habitat structure can also impact the climate that species experience. For example, changes in habitat structure (e.g. vegetation height, cover and type) can influence microclimate. Various aspects of microclimate such as solar irradiation and moisture have been found to be a driver of species' occupancy, persistence and population dynamics (Suggitt *et al.*, 2015; Wilson *et al.*, 2015; Fourcade & Öckinger, 2017).

The combined impacts of land conversion and climate change may create negative impacts for some species such as range losses and extinctions, particularly in developing nations, as has been shown for birds (Jetz *et al.*, 2007), trees (García-Valdés *et al.*, 2015) and other groups including mammals, reptiles, and amphibians (Jantz *et al.*, 2015). Few studies have attempted to predict the extent of future negative impacts from the combined effects of habitat and climate on species (Titeux *et al.*, 2016). To form effective conservation strategies, ecologists need to identify drivers of distribution and population changes and understand how those drivers interact.

#### 1.5.2 Habitat availability in anthropogenic landscapes

Species' habitats are embedded within landscapes, and global landscapes have been altered by land-use change. Thus, suitable habitat patches may become too far apart for species to move between them, creating barriers to dispersal (Hill *et al.*, 2001; Warren *et al.*, 2001; Menéndez *et al.*, 2006). For range expansion to occur, suitable habitat must be sufficient in size and quality to allow the establishment and persistence of species' populations (Mortelliti *et al.*, 2012), and species need to be able to access these habitats. The ability to traverse non-habitat areas is vital for species to successfully respond to climate change (Holyoak & Heath, 2016). Species that cannot do this may experience range collapses or extinction (Thomas, 2000).

Two metrics used to assess how species move through landscapes are structural connectivity, which is the spatial distribution of (single or multi-species) habitat types, and functional connectivity, which relates to the movement of (typically) individual species across a landscape (Tischendorf & Fahrig, 2000). Structural connectivity is often used as a proxy for functional connectivity, as the structure of a landscape relates to species movement. However, structural connectivity has limited value because it makes a single generalised assessment of connectivity for a landscape, but connectivity may be specific for different species in the same landscape (Tischendorf & Fahrig, 2000). Some species can disperse through habitats they would not establish in, demonstrating disparity between structural and functional connectivity (Keeley *et al.*, 2017). High functional connectivity is important for gene flow and diversity in species' populations, and synchrony between geographically-related populations can be used as a proxy for connectivity (Powney *et al.*, 2012). In this thesis, I examine species range expansions under climate change, which is the activity of individuals dispersing and establishing in new areas. Lawson *et al.* (2012) demonstrated how this activity was assisted by functional connectivity which allowed individuals to navigate through landscapes, and recommended connectivity-focussed conservation strategies to promote colonisations for the silver-spotted skipper butterfly. For example, protected areas provide 'stepping stone' habitats that may facilitate the range expansions of species (Thomas *et al.*, 2012). In my general discussion chapter, I consider connectivity issues further and what sorts of techniques, such as connecting habitat patches ('stepping stones' or 'corridors'), can best help species move through the landscape (Hodgson *et al.*, 2012, 2016).

The ability to shift across fragmented landscapes is influenced by species traits (Angert *et al.*, 2011; Reif & Flousek, 2012) such as habitat specificity. Habitat generalists generally have a greater ability to adjust to environmental change and are therefore more likely to track climate change than specialists, assuming their resources are widely available (Warren *et al.*, 2001; Hill *et al.*, 2002). Specialists have a smaller pool of resources that they can utilise, so these species are more likely to be threatened by habitat loss, unless they specialise on a particularly widespread habitat, or on human-modified environments. Accessing suitable habitat in fragmented landscapes is a key challenge for species. In this thesis, I examine how species traits and their landscapes interact to influence rates of range shift. While there are many studies examining habitat influences on species' persistence and range shifts, these studies are often restricted to a few species, and use specific resources (e.g. hostplants) to define habitats. In Chapter 3, I calculate detailed habitat associations and specialism scores for a wide range of species to explore the influence of habitat and species traits on rates of range shift.

## 1.6 Monitoring species' responses to climate change

To examine species' responses to climate change in this thesis, I use distribution data which are collected as species' presence records at a given time and location. Established in 1964, the UK Biological Records Centre (BRC) holds distribution records for many different taxonomic groups. Recording schemes are primarily volunteer-run organisations that collect these records. Over 80 schemes share their data with the BRC, making it a valuable source of biogeographical data containing millions of records, in some instances dating back from the 16<sup>th</sup> century (Roy *et al.*, 2014). BRC data are the foundation of this thesis, accompanied by two other data sources. The British Trust for Ornithology (BTO) has gathered distribution data for UK birds since 1933, and I include these data in Chapter 2 to increase the number of taxonomic groups studied. In Chapter 4, I compare patterns in abundance and distribution data, and use abundance records from the UK Butterfly Monitoring scheme (UKBMS), which runs weekly transect walks to monitor butterfly populations across the UK. Abundance data are important to ecological studies, but are not nearly as widely available (compared to distributional data) among different taxa. In this section, I discuss how abundance data are used to measure responses to climate change and how distribution data may be used in similar ways when abundance data are lacking (1.6.1). Then, I discuss the biases in distribution records during data collection, and how these biases can be addressed (section 1.6.2).

#### 1.6.1 Population responses to climate change

In order to measure responses to climate change, suitable data must be available, and here I consider the opportunities distribution data provide to measure population variability. I have previously discussed the sensitivity of species' population abundance to climate change, because species rely on suitable weather conditions to sustain their fecundity, dispersal and resource use. Changing these conditions may have positive and/or negative impacts on species population growth and variability (Vázquez *et al.*, 2017). This makes abundance data a valuable resource for monitoring climate change responses. Abundance is often monitored at fixed locations to enable comparability over time. For example, volunteers collect abundance data for butterflies in the UK by making counts along fixed transect routes, recording numbers once a week for 26 weeks in a year, when the adult butterflies will be flying, and when weather conditions are suitable. The UKBMS uses these data to produce research outputs, such as broad assessments of UK butterfly status (Fox *et al.*, 2015) and statistical metrics (indicators) to demonstrate fluctuations in population numbers (Brereton *et al.*, 2011). Changes in abundance give ecologists and conservationists an early warning that a species may expand its range, or that it may be at risk (Ehrlen & Morris, 2015), as populations can decline gradually over time under unsuitable conditions, prior to extinction. Distribution records do not do this: a species is either observed as present at a site, or not observed. Despite the value of abundance data, the majority of species in the UK (and in the world) do not have detailed abundance data. In order to monitor changes in species' abundances and assess impacts of environmental change on populations, ecologists are examining the potential for distribution data to fill in the abundance data gap.

Because abundance and distribution are related, and distribution data are readily available for many taxonomic groups, these data are increasingly employed to estimate metrics of species' population changes. Distribution data have been used to create composite trends of occupancy and abundance (Pagel *et al.*, 2014) or to assess population trends by measuring changes in occupancy (Maes *et al.*, 2015). In this thesis, I describe these uses further in Chapter 4. Distribution records have not commonly been used to measure interannual changes in species' populations, a metric used to explore population-level responses to environmental change. I address this knowledge gap by investigating the potential for year-to-year changes in distribution records to act as a proxy for year-to-year changes in abundance, and discuss the applications of this proxy. This is important because understanding how species populations vary under climate change and over time helps

ecologists comprehend patterns in species' population dynamics and to determine species responses to climate change.

#### 1.6.2 Biases in distribution records

Distribution data in the UK are a long-term, widespread and ubiquitous source of ecological information, which I use in this thesis to create metrics of range shift, habitat associations and population variability. However, in the collection of these data, species are sampled unevenly due to biases in the behaviour and distribution of recorders. This phenomenon is sometimes referred to as the 'recorder effort problem' (Prendergast *et al.*, 1993; Hill, 2012). Four main biases have been identified in species' records (Isaac *et al.*, 2014) that I discuss below: 1) temporal biases in recording effort, 2) spatial biases in recording, 3) irregular recording effort per site visit, and 4) uneven detectability of the taxa being studied. There are a wealth of studies in the literature, which aim to address these biases, so that they do not adversely influence studies of distribution change.

Temporal biases arise when the intensity of recording is inconsistent over time. Methods of identifying species have improved, for example, smartphones allow users to identify and/or submit species records quickly. More people have become involved in recording and distribution datasets have rapidly increased in size (Tulloch *et al.*, 2013). For example, macromoths experienced a sevenfold increase in records over four decades (see Chapter 2). As a result, comparison of species' occupancy over time is not straightforward, and increased records of species over time may not be indicative of more individuals or of expanding ranges.

Spatial bias is the manifestation of highly variable sampling coverage (observed in Britain and globally, see Boakes *et al.* 2010, and Amano *et al.* 2016). This bias is driven by accessibility: volunteers tend to record in short-distance, familiar areas, such as the places they live or close-by (Isaac & Pocock, 2015). Because of this, recording effort has been noted to be intensified around human infrastructure such as roads and cities, particularly where large numbers of casual participants are involved in schemes (Geldmann *et al.*, 2016). This means that while improvements in transport have helped recorders access different parts of the country, and GPS technologies facilitate the accurate recording of locations, these transport links may create intensification of recording, while less accessible and less urban areas remain unrecorded. Additionally, recorders can demonstrate spatial bias by focusing their attention on areas where rare or interesting species have been reported.

Another source of bias is irregular recording effort per site visit. The number of species recorded during a site visit depends on how many species are actually present, and the amount of effort used to find those species. Also, the number of individuals of a species that are present at a site depends on the interaction between population dynamics and resource availability, e.g., how many offspring are produced, immigration and emigration levels, emergence periods of species (their phenology), and how many individuals the site can sustain. By visiting a site, recorders collect observations of a sample of the total species richness at the site, rarely attempt to record all species at a site, but rather record on an adhoc basis or record a specific species. Therefore, the number of species recorded at a site will vary between visits and between different recorders due to irregular recording effort and different protocols.

Detectability is the fourth source of bias; different species are not equally easy to locate *in situ* and therefore some species require more effort to be detected. Large, colourful species are easier to detect than cryptic or small species. One visit to a site is unlikely to detect all species present: species accumulation curves demonstrate how many site visits are required for the species richness to plateau (Graham *et al.*, 2015). Recording range shifts becomes challenging if the presence of a species can go unnoticed (Lahoz-Monfort *et al.*, 2014), particularly at the edges of a species' range, where numbers of individuals are lower.

There are also differences in recording effort and detectability between different taxonomic groups. Well-recorded groups can have millions of records, where others only have a few thousands (Isaac & Pocock, 2015). Recording schemes have different methods for collecting data, which will produce different patterns in numbers and locations of records (Geldmann *et al.*, 2016). For example, grasshopper species can be identified by their calls; moth recorders use light traps to lure species to a location; aquatic molluscs are sampled by netting. These differences should be taken into consideration when assessing differences in species' responses to environmental change.

Statistical methods are necessary to account for temporal and spatial heterogeneity in sampling effort within and between taxa: without these methods, estimates of range shift may be under- or over-estimated (Kujala *et al.*, 2013). Various techniques have been developed to deal with the bias associated with the recorder effort problem. The Hickling method (Hickling *et al.*, 2005, 2006) uses thresholds to determine the extent of species' ranges. This is done by comparing the number of species recorded in a location in two time periods and selecting those locations where a sufficient number of species was recorded,

i.e. where a sufficient amount of recording effort was applied, in both time periods. The Hickling methods have been improved upon in this thesis, to incorporate issues of spatial bias (Mason *et al.*, 2017). FRESCALO (FREquency SCAling LOcal) is a recent method developed for dealing with detectability problems (Hill, 2012). This method estimates the likelihood of a species' presence given the level of recording effort a grid cell has undergone. The level of recording effort is estimated from the number of locally relevant 'benchmark' species recorded at the site in question. FRESCALO has widely used to develop occupancy patterns and trends (Fox *et al.*, 2014; Woodcock *et al.*, 2014; Dyer *et al.*, 2017). In these methods, key issues are avoiding false negatives or positives (measuring species' presence or not when the opposite is true), and to maximise the data which can be analysed. In this thesis, I apply a methodology that also considers local species richness to account for recording effort differences in distribution data in each of my data chapters, and I discuss the future for recording schemes in the General Discussion (Chapter 5).

### 1.7 Thesis structure

Following this introduction, (**Chapter 1**), this thesis is constructed around three data chapters:

**In Chapter 2** (*Geographical range margins of a wide range of taxonomic groups continue to shift polewards*), I quantify range margin shifts of southerly-distributed species over time. I calculate range shift as the change in the location of the northern range margin (in km per decade) for 21 taxonomic groups (1599 species), over two intervals. I expand upon the previous study by Hickling *et al.* (2006) by including more recent data, more taxonomic groups, and an improved method to deal with spatial and temporal variation in recorder effort. I explore variation in rates of range shift over time for four taxonomic groups (butterflies, moths, dragonflies and birds), and present evidence that Lepidoptera have shifted their ranges fastest over time. I conclude that range shifts vary both within and between taxonomic groups, and that the rates at which ranges shift may not be consistent over time.

**In Chapter 3** (*The importance of habitat for climate-driven range shifts across multiple taxa*), I examine the role of specialism and habitat availability on rate of range shift for multiple taxonomic groups. Range shifts, specialism scores and a metric of habitat availability are calculated for species from 14 taxonomic groups. I quantify intra and intertaxon variation within and between groups, and use mixed models to test the relationships

between range shifts, specialism and habitat availability. I show that habitat availability is more strongly linked to variation in range shifts (explaining up to 36% of the variation) than is specialism. Habitat availability (an interaction with specialism and the landscape) is an important part of determining rate of range shift, and is likely to play an important role in predicting species' responses to future climate scenarios.

**Chapter 4** (*Population variability of species can be deduced from opportunistic citizen science records: a case study using British butterflies*), assesses the potential for distribution data to be used as a proxy for abundance data, by quantifying relationships between yearto-year changes in distribution and abundance. I focus on butterflies as a study taxon, and I explore the importance of biogeographical attributes derived from distribution datasets (frequency of records, spatial aggregation of species, mean inter-annual changes in numbers of records, and spatial scale) on the strength of distribution-abundance relationships. I conclude that distribution data can provide information on year-to-year changes in abundance, for some species, but most importantly that mean year-to-year changes in distribution records are comparable to mean year-to-year changes in abundance for all butterfly species. Thus, distribution records do show potential to be used as proxies for metrics of abundance in some circumstances, for example in calculating population stability, which could be important to assessments of species' extinction risk.

**Chapter 5** discusses the findings of Chapters 2-4 in the context of the wider scientific literature and the implications of my results for conservation ecology. I also consider limitations of the data, and suggest future avenues of research. I conclude that 1) there is substantial variation in range shifts both within and between high level taxa, but the majority of variation in range shifts is found within taxonomic groups (rather than between groups); 2) a significant portion of this variation is explained by species' habitat specificity within a landscape context; and 3) distribution records have potential to act as proxies for abundance metrics, where abundance data are lacking.

# Chapter 2

# Geographical range margins of a wide range of taxonomic groups continue to shift polewards

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## 2.1 Abstract

Many species are extending their leading-edge (cool) range margins polewards in response to recent climate change. Here, we investigated range margin changes at the northern (cool) range margins of 1599 southerly-distributed species from 21 animal groups in Britain over the past four decades of climate change, updating previous work. Depending on data availability, range margin changes were examined over two time intervals during the past four decades. For four groups (birds, butterflies, macromoths, and dragonflies and damselflies), there were sufficient data to examine range margin changes over both time intervals. We found that most taxa shifted their northern range margins polewards and this finding was not greatly influenced by changes in recorder effort. The mean northwards range margin change in the first time interval was 24 km decade<sup>-1</sup> (n=13 taxonomic groups), and in the second interval was 18 km decade<sup>-1</sup> (n=16 taxonomic groups), during periods when the British climate warmed by  $0.21^{\circ}$ C and  $0.28^{\circ}$ C per decade, respectively. For the four taxa examined over both intervals, there was evidence for higher rate of range margin change in the more recent time interval in the two Lepidoptera groups. Our analyses confirm continued range margin shift polewards in a wide range of taxonomic groups.

### 2.2 Introduction

In recent years, ecological responses to climate change have been observed in global fauna and flora as species have responded and adapted to new environmental conditions (Parmesan 2006; IPCC 2014a). Species responses encompass genetic, physiological, phenological and biogeographical changes, and these responses by species may have implications for ecosystem functioning and structure (Bellard *et al.* 2012). One commonly observed response to climate change in a wide range of terrestrial and aquatic ecosystems is the polewards extension of species' distributions (Parmesan & Yohe 2003; Poloczanska *et al.* 2013).

Climate influences the distribution of species, often acting as a limiting factor on the extent and location of species' range margins (Hill & Preston 2015). Historical data have demonstrated how species' distributions have changed over time (Hill *et al.* 2002), extending their ranges at leading-edge 'cool' margins when climates become more favourable for these species (Chen *et al.* 2011a). Some species have shifted their ranges at rates reflecting local rates of climate warming (Parmesan *et al.* 1999; Chen *et al.* 2011a), whereas other species have lagged behind climate changes (Menéndez *et al.* 2006; Devictor *et al.* 2008; Valladares *et al.* 2014). Considering the wide variety of habitats, pre-warming ranges, life histories, resource requirements, dispersal behaviours and opportunities available to different taxonomic groups, the expectation has been for responses to climate change to vary between taxonomic groups (Angert *et al.* 2011). Indeed, studies have reported large inter- and intra-specific variation in the responses of taxonomic groups to climate change (Thomas *et al.* 2004; Hickling *et al.* 2006; Rapacciuolo *et al.* 2014). For example, butterflies have demonstrated idiosyncratic responses to climate change (Mair *et al.* 2012), with inter-specific variation partly explained by trends in abundance and habitat availability (Mair *et al.* 2014). The availability of large data sets for a wide range of taxonomic groups in Britain held by the UK National Biodiversity Network and other organisations, provides an excellent opportunity to explore the responses of different taxonomic groups to recent climate change.

Many species reach their leading-edge 'cool' range margins in Britain, and hence might be expected to shift their range northwards under recent climate warming. There are some single-taxon studies that have examined range changes in Britain (Hill *et al.* 2002; Hickling *et al.* 2005), but not all taxonomic groups may respond in the same way to climate warming. Hickling *et al*. (2006) studied range margin changes in 16 taxa that reach a

leading-edge range margin in Britain, and here we update and build upon this earlier study by analysing 21 taxonomic groups, containing 1599 species monitored over four decades of climate warming. We also examine range margin changes over two time intervals, thereby investigating changes in response rates over time, as well as being able to compare range margin changes across more taxonomic groups than previously examined.

### 2.3 Materials and methods

#### 2.3.1 Species data sets

We analysed British data gathered mainly by volunteer naturalists through recording schemes (see acknowledgements) overseen by the UK Biological Records Centre (www.brc.ac.uk), British Trust for Ornithology (BTO, www.bto.org) and Butterfly Conservation (www.butterfly-conservation.org). We categorised each observation (recorded presence) of individual species according to its location (Ordnance Survey 10km x 10km grid square; hereafter termed 'hectad') and the time period it was recorded in (see below). Most observations were for a specific day, but some recording schemes collate observations into date ranges spanning several years. In this study, we excluded observations with date ranges that fell outside our time periods (see below). Species were grouped into taxonomic groups, determined primarily by the recording schemes that collated records for that group. A total of 21 taxonomic groups had sufficient data for range margin changes to be calculated for at least one interval (the groups accepted or rejected for study are listed in Table A2.1). Four taxonomic groups (birds, butterflies, macromoths, and dragonflies and damselflies) had sufficient data for range margin changes to be calculated for both intervals.

Our analysis focussed on southerly-distributed species that reach a northern (leading-edge) range margin in GB. The study area was the British mainland, including islands connected to the mainland according to the contiguous distribution of hectads (2566 hectads in total). Hence, near-shore islands were included, but off-shore islands were not. Montane species (defined as species with a mean elevation ≥200m across their British range) were excluded from the analyses because latitudinal range changes by these species would be confounded by elevational shifts. We also excluded ubiquitous species (defined as those occurring in more than 90% of the study area), as well as species with a northern range margin in the first time period less than 100km from the north coast of mainland GB, because these species would have little opportunity for polewards range shifts. Species were also excluded if they were listed in the GB Non-native Species Information Portal (Roy *et al.*

2014b), because range changes by introduced species are likely to involve human-assisted dispersal and range filling unrelated to climate change. We also excluded observations where the identification of the species was uncertain (e.g. record listed as several possible species). Species listed with a sub-species trinomial were grouped to the species level (e.g. for the Dingy skipper butterfly, *Erynnis tages* subsp*. tages* was grouped with *Erynnis tages*), and different subspecies of the same species were grouped together.

#### 2.3.2 Time periods of analysis

With the exception of birds, data were collated into three time periods (1966-1975; 1986- 1995; 2001-2010), defining the northern range margin of each species in a given period. Range margin changes were analysed over two time intervals corresponding to range margin changes between the first and second periods (interval 1, 1966-1975 to 1986-1995) and between the second and third periods (interval 2, 1986-1995 to 2001-2010). We imposed gaps between time periods to provide opportunities over which range margin changes could occur. Bird data were analysed over slightly different time periods and intervals (interval 1, 1968-72 to 1988-1991; interval 2, 1988-1991 to 2008-2011) corresponding to bird atlas recording periods (Sharrock 1976; Gibbons, Reid & Chapman 1993; Balmer *et al.* 2014). We standardised the time periods as far as possible across the different taxonomic groups to ensure all species were studied over similar periods, and hence experienced similar climatic changes. A preliminary analysis using the slightly different time periods analysed by Hickling *et al*. (2006) produced qualitatively similar results to the standardised dates used in this study.

### 2.3.3 Controlling for variation in recorder effort

The intensity of recorder effort in GB has varied over time and space, as well as within and between taxonomic groups. Thus for each time interval and taxonomic group we controlled for variation in recording effort by selecting hectads with a minimum threshold of recording effort based on observed local species richness relative to the regional species richness pool. First, for each focal hectad, We identified the nearest 100 hectads (sufficient for the regional pool size of species to asymptote) where at least one species from that taxonomic group was recorded in both time periods (i.e. 1966-1975 and 1986-1995 for analyses of interval 1, or 1986-1995 and 2001-2010 for analyses of interval 2; or equivalents for birds). Second, the species richness of these neighbouring hectads was calculated from the total number of unique species recorded in both time periods. Focal hectads were included in analyses according to the level of recording effort they experienced, and hectads were
termed 'recorded', 'well-recorded' and 'heavily-recorded' as follows. 'Recorded' hectads contained at least one species in both time periods, 'well-recorded' hectads contained at least 10% of the species richness of the surrounding hectads in both time periods, and 'heavily-recorded' hectads contained at least 25% of the species richness of the surrounding hectads in both time periods. This method for accounting for recorder effort was broadly similar to that used by Hickling *et al*. (2006) except that we used local species richness rather than the richness of all species in Britain when selecting hectads for inclusion. This new method is likely to be more sensitive in accounting for recorder effort, because it takes better account of underlying spatial variation in species richness across Britain.



**Figure 2.1.** Locations of northern range margins calculated for different thresholds of recording effort control in each of three time periods of study (1966-75, 1986-95 and 2001- 10) for the small skipper butterfly (*Thymelicus sylvestris*). This exemplar species was selected for illustration because it has extended its range northwards in recent years. Maps show species presence in well-recorded and heavily-recorded grid squares (10 km x 10 km), and (apparent) absence (hollow squares) where butterflies were observed, but not *Thymelicus sylvestris*. Labelled lines indicate range margin locations from analyses of welland heavily-recorded hectads in each time period.

Our analyses of range margin changes were repeated for each of the three levels of recorder effort control. For the four taxonomic groups (birds, butterflies, macromoths, and dragonflies and damselflies) studied over both time intervals, northern range margins were calculated in a second analysis (see methods below) that used a subset of well-recorded and heavily-recorded hectads from both intervals that were common to all three time periods. Figure 2.1 shows how analysing well-recorded or heavily-recorded squares affected the calculation of the range margin location for an exemplar butterfly species, *Thymelicus sylvestris*. Compared with the other taxa studied, recorder effort variation is far less in birds than other taxonomic groups. For example, macromoths experienced a more than sixfold increase in the number of observations over the study period (294,951 and 1,474,592 unique year-location observations of species in GB hectads during time periods 1 and 3 respectively), such that hectads were more likely to have been intensively surveyed in the later time periods. By contrast, bird data are collated systematically for each atlas and so there is less change in the number of records of birds over time. Figure 2.2 shows the locations of well-recorded and heavily-recorded hectads for birds, butterflies, dragonflies and damselflies, and macromoths.



Distribution of well-recorded and heavily-recorded hectads across both time intervals, for the four taxonomic groups analysed in Figure 2.4. Sample sizes for well-recorded hectads are 2561, 1729, 477 and 414 for birds, butterflies, macromoths and dragonflies and damselflies respectively. Sample sizes for heavily-recorded hectads are 2500, 1218, 205 and 119 for the respective group

# 2.3.4 Minimum data requirements for taxonomic groups and species

Each taxonomic group was selected for study if it occupied at least 20 well-recorded hectads during interval 1 or interval 2, and contained more than one species for which range margin changes could be calculated. Taxonomic groups without their own formal recording scheme (which apply various quality control measures, e.g. to avoid misidentifications) were rejected. Those taxonomic groups which had data from multiple sources (and hence no uniform quality control measures) were also rejected. Criteria for selecting taxonomic groups analysed over both intervals were stricter, given the more statistically challenging task of trying to identify not only range margin changes but also whether rates had changed over time. Thus taxonomic groups needed at least 20 heavilyrecorded hectads which were common to all three time periods to qualify for inclusion, and also had to contain five or more species for which a range margin could be calculated (see below) based on heavily-recorded hectads. These criteria resulted in four taxonomic groups being studied (birds, butterflies, macromoths, and dragonflies and damselflies).

For each time period, the range margin of each species was calculated for each level of recording effort control. We excluded species from a time period if they were observed in fewer than 20 hectads, for a given level of recording effort control, because estimates for the locations of range margins would be subject to high recording error. Once northern range margins were calculated (see methods below), species which had fewer than 10 hectads of the necessary level of recording effort within 100km to the north and to the south of their range margin in the first time period were excluded. This excluded species whose estimates of potential range margin changes northwards or southwards would be biased by poor recording effort.

### 2.3.5 Calculating northern range margin changes

The locations of northern range margins were calculated in each of the three time periods. For each species that was included, the location of its northern range margin was computed as the mean northing (in km north, from the Ordnance Survey GB grid) of the species' 10 most northerly occupied hectads in that time period. For each taxonomic group and time interval, mean rate of change (plus 95% confidence intervals) in northern range margin was then calculated as the distance moved in km decade<sup>-1</sup> (based on the number of years between the mid-points of each time period), with positive rate values indicating northward shifts, and negative values indicating southward shifts. These analyses were

carried out for each of the three levels of recording effort. We used ANOVA and onesample t-tests to examine differences in rates of range margin change among the taxonomic groups in each time interval, and whether rates of range margin change were significantly different from zero.

We examined if rates of range margin change differed between time intervals 1 and 2 in the four selected taxonomic groups (birds, butterflies, macromoths and dragonflies and damselflies). We generated linear mixed models using *lme4* package in R (Bates *et al.* 2013) with rate of range margin change (km decade<sup>-1</sup>) as the response variable, time interval and taxonomic group as explanatory variables and species identity as a random effect. We fitted models with all possible combinations of explanatory variables and their interaction term and examined the goodness of fit of each model using Akaike information criterion (AIC) values, and models where ΔAIC was < 2 were assumed to be equally good at explaining the data (Burnham & Anderson 2002). Additionally, rates of range margin change in the two time intervals in each taxon were compared using paired t-tests, and one-sample t tests were used to examine if rates of range margin change in each interval were significantly different from zero. All statistical analyses were performed in R, v3.0.2 (R Core Team 2013).

### 2.3.6 Temperature variation across the study period

Mean seasonal temperature data from the Hadley Centre Central England Temperature (HadCET) series were downloaded from the UK Met Office [\(www.metoffice.gov.uk/hadobs\)](http://www.metoffice.gov.uk/hadobs). Over the study period (1966-2010), annual mean temperature was computed from the mean value of each of the four seasons (i.e. annual temperature was measured from December through to the following November). Descriptive analyses were undertaken to describe changes in temperature over the years included in interval 1 (1966-95) and interval 2 (1986-2010), and between these two intervals. We used regression analysis to examine changes in mean seasonal and annual temperatures within each time interval, and ANCOVA to determine if there was a difference in the rate of temperature change between the two time intervals.

### 2.4 Results

### 2.4.1 Northern range margin changes

Here, we focus primarily on describing the results for well-recorded hectads because we consider this level of recorder effort control to be the best compromise between robustness of data analysis and retaining large numbers of species and taxonomic groups in our analyses; although we also report full statistical results for the other two levels of recording effort control in appendices (Tables A2.2, A2.3). The locations of the northern range margins of all species during each time period are provided in Tables A2.4 (interval 1) and A2.5 (interval 2). Generally, most taxonomic groups shifted northwards for all levels of recording effort for which they could be analysed (Figure 2.3). The mean overall rate of range margin change, calculated from each taxonomic groups' mean rate of range margin change, was 24.1 km decade<sup>-1</sup> (standard error [SE] = 5.5; n = 13 taxa) in time interval 1 and 18.0 km decade<sup>-1</sup> in interval 2 (SE = 4.0; n = 16 taxa).

Eight of the 13 groups in interval 1 (butterflies, centipedes, dragonflies and damselflies, hoverflies, macromoths, millipedes, spiders, woodlice) and seven of the 16 groups in interval 2 (aquatic bugs, bees, butterflies, dragonflies and damselflies, hoverflies, macromoths, wasps) significantly extended their range margins northwards, for wellrecorded hectads (Figure 2.3, Table A2.3). Qualitatively similar results were obtained for the other levels of recording (Figure 2.3); ten of the 13 groups analysed in interval 1, and eight out of 16 taxa in interval 2, showed significant northwards shifts for one or more levels of recording effort (Figure 2.3; Table A2.3). Despite most taxa shifting their range margins northwards in both time intervals, three taxa (ground beetles, hoverflies, solderflies and allies) demonstrated significant southwards retractions in interval 2, although the significance of the change depended on levels of recorder effort control (Figure 2.3, Table A2.2, A2.3). For taxonomic groups which occurred in both time periods (i.e. panels B and D in Figure 2.3), their rates of range margin change are not directly comparable between the two intervals because different sets of hectads and species were used to calculate rate of range margin change in each interval. Taxonomic groups differed in their rates of range margin change, and this was evident in both time intervals (ANOVA, interval 1, F<sub>12, 560</sub> = 4.41, p < 0.001; interval 2, F<sub>15, 868</sub> = 9.64, p < 0.001), and this finding was insensitive to the level of recorder effort control (Table A2.2). Mean annual temperature generally increased in Britain during the study period (on average by 0.21°C decade<sup>-1</sup> during interval 1 and 0.28°C decade<sup>-1</sup> during interval 2), with mean spring (March-May)

temperature increasing significantly during interval 1, and mean autumn (September - November) temperatures increasing significantly in interval 2 (Table A2.6).



Recording effort Recorded Well recorded Heavily recorded

**Figure 2.3.** Mean rates of northern range margin changes of species in 21 taxonomic groups over interval 1 (upper panels) and interval 2 (lower panels); for each level of recording effort control. Panels A and C show range margin changes for taxonomic groups studied over one time interval only (13 taxa) and panels B and D show taxa studied in both intervals (8 taxa). Error bars represent 95% confidence intervals of the mean. Asterisks above bars indicate range changes that were significantly different from zero (one-sample t-test). In panels A-C, the bars are ordered along the x-axis by magnitude of range margin changes according to analyses of well-recorded hectads; panel D is ordered according to panel B's order. The number of species per taxonomic group varied among groups, recording effort control levels and intervals (see Table A2.3). Heavily-recorded bars are absent for some taxa because this level of analysis was not possible. For taxonomic groups studied in both

intervals, there were different species compositions in each interval and different sets of recorded, well-recorded and heavily-recorded grid squares. Thus differences in rates of range change between time intervals may be a result of differences in the species included and locations recorded, and so comparisons should be made with caution. Taxonomic group names accompanied by a dagger symbol indicate that the group contains allied species (See Table A2.1).

#### 2.4.2 Changes in rates of range margin change over time

We examined if rates of range margin change were similar in the two time intervals for four taxonomic groups (birds, butterflies, macromoths, and dragonflies and damselflies) with sufficient data to analyse the same hectads across all three time periods. The estimates of rates of range margin change from this subset of hectads generated comparable estimates to those from the larger set of hectads used to calculate rates of change separately for intervals 1 and 2 (Figure A2.1). All four taxonomic groups shifted northwards in both intervals (Figure 2.4), and macromoths and butterflies showed significantly faster rates of range margin change in interval 2 compared with interval 1 (Table A2.7; macromoths paired t-test,  $t_{131}$  = -5.77, p = <0.001; butterflies  $t_{34}$  =-2.26, p = 0.03). The locations of the northern range margins of all species during all three time periods are provided in Table A2.8.

The most parsimonious statistical model of rate of range margin change for these four groups included the interaction term between taxonomic group and interval (Table 2.1). The interaction occurred primarily because macromoths tripled their rates of polewards range margin change between intervals 1 and 2 (interval 1 = 11.4km decade<sup>-1</sup>, interval 2 = 31.2km decade<sup>-1</sup>) and rates for butterflies nearly doubled (interval 1 = 18.3km decade<sup>-1</sup>, interval 2 = 30.3km decade<sup>-1</sup>). However, rates of rates of range margin change of birds and dragonflies and damselflies did not significantly differ over time (Table A2.7). This conclusion was not dependent on the inclusion of any single taxonomic group, and serial omission of each group (and of all Lepidoptera, i.e. butterflies and macromoths) consistently found that a mixed model with the interaction term between taxon and interval had the lowest AIC value (i.e. was the best model; Table A2.9). This apparently faster rate of range margin change in Lepidoptera in interval 2 was evident despite the fact that the rate of temperature warming was similar between interval 1 (1966 to 1995) and interval 2 (1986 to 2010; Table A2.10) for most measures of temperature. However, mean autumn temperature increased significantly between interval 1 and 2 (Table A2.10).



 $(km$  decade<sup>-1</sup>)

**Figure 2.4.** Comparison of rates of northern range margin change for four taxonomic groups across two time intervals (see main text for time interval dates). Taxonomic groups are as follows: birds (31 species), butterflies (35 species), dragonflies and damselflies (7 species) and macromoths (132 species). These estimates of rate of range margin change differ slightly from those in Figure 2.3, because only those hectads that were well-recorded in all three time periods were included. Asterisks indicate groups where range margin changes differed over time (two-tailed paired t-test, P≤0.05, see Table A2.7). 'Dragonflies' represents all Odonata, including damselflies.

**Table 2.1.** Linear mixed effects models for rate of northern range margin change (response variable, in km decade<sup>-1</sup>) in well-recorded hectads, between two time intervals (spanning 1966-2010), for the four most heavily-recorded taxonomic groups (N = 205 species in total). All models included species identity as a random factor. For fixed effects, the most complex model included time interval and species group as predictor variables, as well as the interaction term. Shown for each model is the difference in AIC (ΔAIC) from the most parsimonious model (model 5). The four right hand columns provide information on the individual coefficients expressed as the difference relative to the intercept term.



## 2.5 Discussion

We analysed rates of range margin change in 1599 southerly-distributed species from 21 animal groups in two time intervals. Overall, the majority of taxonomic groups in our study shifted their range margins northwards in both time intervals (23.2km decade<sup>-1</sup> in interval 1, 18.0km decade<sup>-1</sup> in interval 2), supporting the findings of Hickling *et al.* (2006). Rates of range margin change varied between taxonomic groups and, for some groups, over time. For the four groups with sufficient data to undertake robust analyses of whether these rates have changed over time, there was evidence that recent rates of range margin change have been faster for macromoths and butterflies. These findings were relatively insensitive to recorder effort control, although increasingly strict recorder effort control reduced the number of hectads that could be analysed.

## 2.5.1 Controlling for variation in recorder effort

Variation in levels of recording effort across spatial and temporal scales can present problems to ecologists wishing to quantify range shifts (Tingley & Beissinger 2009; Isaac *et al.* 2014). Our results showed that the majority of taxa studied have shifted their range margins northwards for all levels of recording effort that we considered. However, there were some taxonomic groups where the shift in the northern range margin was qualitatively different according to the level of recorder effort control. For example, northern range margins of hoverflies apparently retracted southwards in interval 2 if recorded and well-recorded grid squares were analysed, but extended northwards according to analysis of heavily-recorded squares (Figure 2.3D). As the control for recorder effort became stricter, the number of hectads included was reduced, and so the number of species included was also reduced. Hence 137 and 131 species of hoverfly were included in analyses of 'recorded' and 'well-recorded' hectads respectively, but only 21 species for heavily-recorded hectads. If recorded and well-recorded hectads were assessed for just these 21 species, the recorded range margin shift (9km decade<sup>-1</sup> southwards) was smaller than when all available species were analysed, and the well-recorded range margin shift changed to a northwards direction (8km decade<sup>-1</sup> northwards). Thus, the reported range margin changes are a function of both the hectads included in the analyses as well as the identity of species included. Using the most thoroughly surveyed (heavily-recorded) subset of data, the observed trend was for 13 out of 14 measured changes (taxon by interval combinations) to show a northwards margin shift (Figure 2.3), and the overall data showed significant northwards trends across all taxa in both periods for all three levels of recording

effort (Table A2.2). Thus, our qualitative findings appear robust to variation in recorder effort (at least for the three control methods assessed), although the quantified rate of change depends on the level of recorder effort control.

Our approach to filtering data for analysis represents an assessment of the sensitivity of our conclusions to variation in recording effort, rather than a true measure of 'control' for recording effort, given that the true recorder effort is unknown. We adopted the same general approach as Hill (2012), and assumed that any species that might potentially be recorded in a particular location (hectad) would be drawn from the pool of species found in the surrounding region (which we defined here as the nearest 100 hectads with any records for the taxon). The distribution of species richness in Britain does not change greatly from one hectad to the next (Fox *et al.* 2011; Balmer *et al.* 2014), and so the percentage of the regional species pool recorded as present in a hectad represents a first approximation for the relative level of recording effort. However, the percentage of species actually recorded in a hectad depends on the actual number of species present (which itself depends on local environmental conditions), as well as on the level of recording that has taken place. Hence we adopted an approach whereby we used thresholds (>0%, 10%, 25% of the regional species pool) rather than a continuous metric of species recorded.

Recorder effort has changed over time and the number of records of species in Britain has increased rapidly. However, if increased recording effort through time is primarily responsible for generating the erroneous impression of range margin changes, we would expect the recorded rate of range margin changes of common species to be less rapid than the rate of range margin changes of all species taken together, because rare species are more likely to go unnoticed during lower intensity surveys (Bates *et al.* 2014). In fact, we found few differences when we repeated our analyses to include only common species (defined as the top 50% of species ranked by number of presences in heavily recorded hectads). Analysing only common species, the estimated rate of range margin change decreased for common birds (despite little or no increase in recording effort), was largely unaffected for macromoths (which showed the greatest increase in recording effort), and increased for butterflies (Figure A2.2). If sampling effort was having an important influence, we would also expect higher levels of recording effort to generate markedly reduced estimates of range margin change, which we did not observe. Poor recorder effort may be an issue in interval 1, but analysis of well-recorded and heavily-recorded hectads in interval 2 produced higher estimates of northwards range margin change than data from recorded

hectads, suggesting that northwards range margin changes are not primarily artefacts of recorder effort changes, at least since 1986-95. Examination of the rate of range margin changes of individual species (e.g. Figure 2.1) and differences in the distribution changes of northern and southern species also indicate that the polewards range margin shifts we report here are real (Warren *et al.* 2001; Hickling *et al.* 2005; Fox *et al.* 2013, 2014; Cham *et al.* 2014).

#### 2.5.2 Variation over time and between taxonomic groups

Our results suggest that some taxa differed in their rates of range margin change over time, and that Lepidoptera apparently spread northwards more rapidly in the more recent time period, during a period when autumn temperatures significantly increased. The faster rate of range margin change more recently in Lepidoptera does not obviously align with any major morphological, habitat-use or other features of this group, and trait-based analyses have rarely explained very much of the variation in rates of range shift among species within taxonomic groups (Angert *et al.* 2011). Species may vary in their sensitivity to different aspects of climate, and responses of species may also reflect the amount of warming as well as habitat availability (Hill *et al.* 2001), which may contribute to these differences among taxa. We only compared four taxonomic groups, two of which were Lepidoptera, which is too few to draw any firm conclusions. In addition, the considerable variation that is exhibited between species within individual taxonomic groups (Chen *et al.* 2011a) and over time (Mair *et al.* 2012) suggests that there may be no simple explanation for variation among taxa in their responses to climate change.

Climate change is driving many species to extend their ranges northwards (Chen *et al.* 2011a) and the majority of taxonomic groups studied here supported that finding. However we found variation in rates of range margin change amongst the animal taxa studied. Taxa may vary in their response to temperature at different time of the year, and to different aspects of climate (Araújo, Thuiller & Pearson, 2006; Jiguet, Brotons & Devictor, 2011; Schweiger *et al.*, 2012). Taxa may also vary in the extent to which they occupy their climate niche (Sunday, Bates & Dulvy, 2012), and hence non-climatic constraints could account for differences in the rate of range margin changes we observe between groups. For example, Fox *et al.* (2013) suggested that the range extension of footman moths in Britain could be related to increased availability of larval hosts (algae and lichens), which in turn could be benefitting from changes in air quality and nutrient availability, as well as climate change (Morecroft *et al.* 2009; Pescott *et al.* 2015). In addition, evolutionary changes in dispersal

ability and ecological changes in habitat associations may contribute to variation in rates of range change (Thomas *et al.*, 2001; Hill, Griffiths & Thomas, 2011; Pateman *et al.*, 2012). However, whilst resource and habitat availability are important for individual species, it is not clear whether they and many other range-determining factors (e.g. natural enemies, competing species) are important causes of the differences that we have observed between broader taxonomic groups.

### 2.5.3 Conclusion

Our study provides further support that the majority of taxonomic groups have shifted their leading-edge margins northwards. We also have evidence that rates of range margin change vary over time and between taxonomic groups, just as they vary between species within each taxonomic group. Hence conservation planning and habitat management strategies should be aware that rates of species' range changes in response to environmental change are highly variable. Our analyses have benefitted from the extensive data sets that exist for a large number of taxa in Britain, recording changes in distributions over the past four decades. Such recording schemes are vital for understanding biodiversity changes in human-dominated landscapes. Establishing robust monitoring systems that build on those that already exist will increase our capacity to detect, understand, and manage these changes (Pescott 2015).

# Chapter 3

# Habitat explains variation in climate-driven range shifts across multiple taxa

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Please find Supplementary Methods to accompany the text on page 51.

# 3.1 Abstract

It is not understood why individual species vary so greatly in the rates at which their ranges are shifting in response to climate warming. Using 40 years of distribution data, for 347 species from 14 invertebrate taxa in Britain, we show that habitat availability explains up to half of the variation in range boundary shifts. Habitat availability depends on habitat specificity of species, whether species are specialised on rare or widespread habitats, and the mixture of habitats in any given landscape. Hence, interactions between species' attributes and the environment are important determinants of variation in range shifts. Understanding this variation across multiple taxa leads us to conclude that betterconnected landscapes could facilitate polewards shifts for the subset of species that are habitat constrained, whereas other species will successfully track the climate without intervention, or face barriers that cannot be circumvented.

# 3.2 Introduction and Methods

On average, species are shifting polewards and to higher elevations in response to climate warming, but there is extremely large variation in the rates at which the range boundaries of individual species are moving (Parmesan & Yohe, 2003; Lenoir *et al.*, 2010; Crimmins *et al.*, 2011). This variation could arise from species-specific climatic or habitat requirements, population growth rates, dispersal or biotic interactions (Hill *et al.*, 2001; Warren *et al.*, 2001; Mair *et al.*, 2014; Carroll *et al.*, 2015; Liang *et al.*, 2017). Yet, none of these factors has been shown to explain a large proportion of the between-species variation across multiple taxonomic groups (Angert *et al.*, 2011; MacLean & Beissinger, 2017). Here, we evaluate the degree to which species-specific habitat associations underlie the observed variation in range shifts. Our results help explain why responses to climate change appear individualistic, and provide insight into how we might facilitate species' responses to climate change.

We examined 347 non-migratory, native invertebrate species in mainland Britain, drawn from 14 taxonomic groups: aquatic bugs, bees, butterflies, dragonflies and damselflies, grasshoppers and allies, ground beetles, hoverflies, macromoths, non-marine molluscs, shieldbugs and allies, soldierflies and allies, spiders, wasps, and woodlice (Table A3.1). Each species reaches its northern (poleward) range margin in Britain and might, therefore, be expected to shift northwards during a period of sustained regional warming. We measured range shifts (latitudinal changes in the ten-northernmost occupied 10-km squares) between 1976-1990 and 2001-2015. The median observed range shift was 33 km (1.3 km  $y<sup>-1</sup>$ , mean = 1.8 km  $y^{-1}$ ) indicating significant poleward expansions (Wilcoxon signed rank,  $P < 10^{-30}$ , N = 347) in response to 0.8 °C of regional warming over the same time period (Hollis & McCarthy, 2017). There was considerable variation among species (Figure 3.1); one in five species retracted its range margin southward, and the interquartile range spanned twice the median shift (Table A3.2). Nearly all (91%) of this variation between species occurred within, rather than among, taxonomic groups ( $R^2$  = 0.09 in a linear model of range shift *vs*. taxonomic group). The lack of a strong 'group effect' suggests that major trait differences among groups cannot be responsible for the variation in range shifts. In contrast, individualistic attributes of species and/or location-specific constraints, such as habitat factors, could still make strong contributions.





Hence, we quantified habitat associations, habitat specialisation and habitat availability (in range-margin landscapes) for the 347 species. We developed logistic regression models to quantify habitat associations, using 100-m resolution presence-absence records of study species in 18 satellite-derived habitat classes (Morton *et al.*, 2011). Species' specialisation indices (SSIs) were defined as the coefficient of variation (SD/mean) in the probability of occurrence across the 18 habitat classes (Julliard *et al.*, 2006), and ranged from SSI = 0.36 for the Gatekeeper butterfly *Pyronia tithonus*, a generalist present at varying densities in 17 of the 18 habitat classes, to SSI = 3.22 for the woodlouse *Ligidium hypnorum*, a broadleaved-woodland specialist. We estimated habitat availability by projecting probabilities of occurrence on to the land cover map at 25-m resolution, and averaging over the range-margin landscape (50-km buffer around the northernmost 10-km squares occupied by the species in 1976-1990). Habitat availability ranged from 0.4% for the heathland-associated Small Grass Emerald moth *Chlorissa viridata*, to over half of the landscape (56%) for *P. tithonus* butterfly. Again, this variation was mainly a feature of differences between individual species (93% for specialisation, 85% for habitat availability), rather than between taxonomic groups (tables A3.3- A3.4). Habitat specialisation and availability are inevitably related to one another, but they are not interchangeable (Figure 3.2): availability depends on whether a species is specialised on common or rare habitats, and on the absolute (rather than relative) probabilities of occurrence within those habitat classes. For more methods details, please refer to the Supplementary Methods on page 51.

### 3.3 Results and Discussion

Generalist species expanded northwards faster than specialists (Pearson correlation coefficient [*r*] of range shift *vs*. SSI = -0.22, *P* < 10-4 , *N* = 347). In a linear mixed-effects model, with taxonomic group as the grouping variable, the marginal  $R^2$  (fixed SSI effect,  $R^2_{\{\ m\}}$ ) was 0.04 and the conditional  $R^2$  (fixed and group effects,  $R^2$ <sub>c</sub>) was 0.13. The explanatory power of SSI was weak compared to the random effect of taxonomic group (Table A3.6). This echoes previous studies in which generalists (and species with traits potentially linked to generalism) have been found to track climate significantly better than specialists but where effect sizes are small, inconsistent in time and/or space, or not consistent between taxonomic groups (Angert *et al.*, 2011; MacLean & Beissinger, 2017). In contrast, we found that  $log<sub>10</sub>$ -habitat availability was more strongly correlated with range shifts ( $r = 0.38$ ,  $P <$ 10<sup>-12</sup>) and, in a mixed model, explained four times more variation ( $R<sup>2</sup><sub>m</sub>$  = 0.17,  $R<sup>2</sup><sub>c</sub>$  = 0.21). Habitat availability rather than specialism *per se* provides a stronger explanation for the observed variation in range shifts (*cf*. SSI model: ΔAIC = 35, ΔcAIC = 35; Table A3.6).





Individual species also differ in the threshold amount of habitat required for metapopulations to persist or expand at the range margin (Hanski, 1999); on average, species have less habitat available in range-margin landscapes than in their distribution cores (Figure 3.3, D, H and L; species with less *vs*. more habitat at the margin,  $\chi^2$  = 10.03, 1 df, *P* < 0.002, *N* = 347). We discovered that species with below-average habitat availability at the range margin (relative to availability in the entire range) have failed to expand northwards (dashed lines in Figure 3.3, C, G and K), most likely because those landscapes fall below their species-specific habitat requirements (dashed lines in Figure 3.3, D, H and L). Habitat availability (as a main effect) and our metric of relative range-margin habitat availability (as an interaction) provided the most parsimonious explanation of species' range shifts (*cf*. habitat model with random slopes for each group separately: ΔAIC = 8,  $\Delta$ CAIC = 4; Table A3.6). The explanatory power of this model is likely to be driven by the combined effects of increased breeding success in landscapes with greater habitat availability, and more successful dispersal in landscapes where the distances between habitats patches are reduced (Wilson *et al.*, 2009; Hodgson *et al.*, 2012).

The distribution data for our study species come from citizen-science schemes, and so recorder effort varies among taxa (e.g., 20 million macromoth records were available, compared with 30 thousand records for shieldbugs and allies). Therefore, we tested the sensitivity of our findings to recording effort (we also analysed macromoths separately because light trapping may attract individuals from adjacent habitat types).



**Figure 3.3.** Models of species' range-margin shift as a function of habitat specialisation and  $log<sub>10</sub>$ -habitat availability at the range margin, for 14 taxonomic groups (indicated by different coloured points). (A-D) Butterflies, dragonflies and damselflies, grasshoppers and allies, and hoverflies. (E-H) Macromoths. (I-L) Nine taxonomic groups with lower levels of recording (Table A3.1). In the first two columns, different coloured lines show the random effect of taxonomic group (Table A3.6). In the third column, group-specific slopes are not shown but rather the effect of habitat is varied (as an interaction term) by the relative habitat availability at the range margin as compared to the whole range (calculated as a percentage of the range-wide average). Dashed and solid black lines illustrate the interaction term using two exemplars: below-average habitat in range-margin landscapes (dashed, 80% of a species' range-wide average) and above-average habitat in range-margin landscapes (solid, 120%). In the fourth column (D, H and L), the frequencies of different range-margin habitat availability are displayed in histograms for each set of taxonomic groups, with the same dashed and solid lines used as in the previous column.

The habitat interaction model explained over a third of the variation in range shifts for the best-recorded groups ( $R_{m}^{2}$  = 0.36, Figure 3.3C), 19% of the variation for macromoths ( $R^{2}$  = 0.19, Figure 3.3G), and 9% for nine groups with reduced levels of recording ( $R^2$ <sub>m</sub> = 0.09, Figure 3.3K). More generally, we found that the greater the level of biological recording (i.e., ranking groups by geographic coverage of recording across both time periods), the more variation in range shifts could be explained by habitat factors (*r* = 0.97, *P* < 10<sup>-6</sup>, *N* = 10). Extrapolating to assume universal geographic recording for all study taxa implies that habitat availability could explain up to half of the variation in species' range shifts (Figure 3.4). This is extremely high, given that there are additional sources of variation in the data: satellite-derived habitat classes do not provide a full species-eye view of 'habitat', land cover may change over time (although minimal for our study region/period), species' habitat associations may vary geographically, and evolutionary changes in resource use can take place during range expansion (Thomas *et al.*, 2001; Oliver *et al.*, 2009, 2012; Hanski & Mononen, 2011; Pateman *et al.*, 2012, 2016; Weiss-Lehman *et al.*, 2017). The remaining variation between species may be explained by species-specific sensitivities to different elements of the climate, and hence their exposure to climate change (Palmer *et al.*, 2017), other phylogenetic variation which has not yet been tested, and perhaps also by the accidental or deliberate transportation of individuals to otherwise unreachable locations (Auffret *et al.*, 2014).



**Figure 3.4.** Variation explained by habitat in range-shift models, as a function of the geographic coverage of citizen-science biological recording. Recording level is the number of 10-km squares where at least 25% of the regional species richness was recorded in both time periods (up to a maximum of 2566 in Britain). Vertical lines extend from marginal  $R^2$ (grey circles, fixed effects of habitat) to conditional  $R^2$  (black dots, random intercept conditional on taxonomic group). The fixed effects are log10-habitat availability at the range margin, interacting with margin habitat as a percentage of the range-wide average. Each pair of points was generated over 10,000 randomised draws of 30 species from any three qualifying groups, with the pool of groups decreasing from left to right as fewer met the required level of recording. The higher the recording level, the greater the explanatory power of habitat, up to a possible 49% (dashed lines, assuming complete geographic recording for all study taxa).

# 3.4 Conclusions

We conclude that range boundary dynamics vary greatly among species, and that up to half of this variation depends on the interplay between species' habitat associations and the landscapes they encounter during range expansion. This has important consequences for facilitating species' responses to climate change: (i) a subset of species will successfully track climate polewards without intervention, because their species-specific habitat requirements are already exceeded in range-margin landscapes; (ii) some species may be assisted by the provision of better-connected landscapes that contain high quality habitats for these species; whereas (iii) location-specific natural or human-related barriers may make it impractical to achieve sufficient connectivity for others (Hoegh-Guldberg *et al.*, 2008; Robillard *et al.*, 2015). Landscape management and restoration strategies need to target habitats required by species in the second category, because these are the interventions that can increase the rates at which species' distributions are able to spread polewards.

# 3.5 Supplementary Methods

We conducted all statistical analyses and created figures using R version 3.3.3 (R Core Team, 2017). In additional to base R functions, we used several contributed packages, detailed in Table A3.7.

### 3.5.1 Study region and observed warming

The study region encompassed 2566 Ordnance Survey 10 km × 10 km grid squares (hectads) covering the British mainland plus any near-shore islands connected to the mainland by the contiguous spread of hectads. We calculated annual mean temperatures for the study region using gridded data from the UK Meteorological Office (Hollis & McCarthy, 2017). During the first recording period (1976-1990), the mean temperature was 8.5 °C, increasing to 9.3 °C during the second recording period (2001-2015). The level of warming was therefore 0.8 °C (0.03 °C  $y^{-1}$ ) across the 25-year interval between the midpoints of the two recording periods.

### 3.5.2 Species occurrence records

Great Britain has one of the highest concentrations of volunteer naturalist biological recorders (citizen scientists) in the world (Sutherland *et al.*, 2015), supported by various recording schemes and societies, whose data are housed by the UK Biological Records Centre (BRC, http://www.brc.ac.uk).

We considered all animal groups held in the BRC database, and included any group that contained at least five species meeting our inclusion criteria, and for which range-margin shifts and habitat associations could be calculated (see sections below). We identified 14 taxonomic groups with sufficient data for inclusion: aquatic bugs, bees, butterflies, dragonflies and damselflies, grasshoppers and allies, ground beetles, hoverflies, macromoths, non-marine molluscs, shieldbugs and allies, soldierflies and allies, spiders, wasps, and woodlice. These are all invertebrate groups, and therefore share some commonality, but they are also diverse in many respects. They include carnivores, herbivores and omnivores, aquatic and terrestrial taxa, groups that disperse in the soil, by walking, by ballooning and by active flight, and span orders of magnitude in body mass.

Each of these groups was covered by a formal recording scheme (Table A3.1). The data were mainly collected by citizen scientist recorders, before being collated and cleaned by experts in the group/region to filter out possible errors. We retained the taxonomic

distinctions and groupings used by these recording schemes (e.g. butterflies and macromoths were treated as separate groups, whereas dragonflies and damselflies were aggregated). It should be noted that any 'group effect' may reflect differences in the recording schemes as well as the effects of taxonomic group *per se*.

Each biological record represents a unique location × date observation of species presence. We removed records with ambiguous taxonomy (*sensu lato*, *sensu auct*, naming multiple species or identified only to genus). Species listed with a sub-species trinomial, with the label *sensu stricto*, with variants or different morphs were aggregated at the species level. When analysing range shifts, we used all records with at least hectad-level spatial accuracy that could be unambiguously assigned to one of the two recording periods (1976-1990 and 2001-2015). For habitat associations, we used day-specific records accurate to 100-m resolution (for the 347 species included in the final analysis, 74% of records had this level of precision).

### 3.5.3 Criteria for species inclusion

We selected non-migratory species that reach their northern (cool) range boundaries in southern/lowland Britain. We defined these species as having 90% of their 1976-1990 distribution in the warmest 50% of the study region (using gridded temperature data from the UK Meteorological Office (Hollis & McCarthy, 2017), averaged over the same time window). Since these species have historically been concentrated in the warmer half of Britain, it is reasonable to postulate that they might be favoured by climate warming. As non-migrants, any expansion should represent the establishment of new, persistent populations, which ought to be evident in the distribution record from the second recording period (2001-2015).

We excluded species classified as non-native, alien-native hybrid, unknown origin, and those that are dependent on non-native species, as defined by the BRC and the GB Nonnative Species Information Portal (Roy *et al.*, 2014). We also excluded vagrants and species thought to be extinct from the study region, including species that have been reintroduced following extinction (e.g. Large Blue butterfly *Maculinea arion*). Many such species are not at equilibrium with the climate (e.g. following (re)introduction), and so recent changes in their distributions cannot be reliably linked with changes in temperature. Other exclusions were made only if species' distribution data were insufficient for range-shift or habitat calculations.

### 3.5.4 Range-shift calculations

To calculate range shifts, we first controlled for changes in recorder effort over time (1976- 1990 to 2001-2015). We restricted distribution data to hectads for which at least 10% of the regional species pool for a group was recorded present in both recording periods (Hickling *et al.*, 2006). For each group × hectad, we defined the regional species pool as the total number of species recorded in the nearest 100 hectads (Mason *et al.*, 2015), using all species in the database for a given taxonomic group (i.e. regardless of the above inclusion criteria).

For all species occupying at least 20 such hectads in both recording periods, we calculated northern (cool) range margins as the mean latitude of the ten-northernmost occupied hectads. We checked that species had sufficient area to expand or retreat from their 1976- 1990 range margins: we excluded any species with fewer than ten hectads reaching the 10% criterion within 100 km to the north, and ten such hectads within 100 km to the south of the range margin (Mason *et al.*, 2015). For the remaining species, we defined range shifts as the latitudinal change (km) in range margins between 1976-1990 and 2001-2015. We converted latitudinal changes to annual rates (km  $y^{-1}$ ) by dividing by the interval between the midpoints of the two recording periods (25 years). Results are summarised by group in Table A3.2, and are reported for individual species in Table A3.8.

#### 3.5.5 Habitat classes

To identify habitat classes, we used a 25-m land cover map for Great Britain (LCM2007). This map was created by the NERC Centre for Ecology and Hydrology (Morton *et al.*, 2011), using combined summer and winter satellite data (Landsat-TM5, IRS-LISS3, SPOT-4 and SPOT-5 sensors, pixel size of 20-30 m), enhanced with extensive cartographical information (e.g. Ordnance Survey data, soil types, agricultural census boundaries and urban extents). The classification was trained and validated using a large network of habitat surveys and ground reference points, producing an overall accuracy of 83%. Out of 23 habitat classes identified in LCM2007, we discarded one (saltwater), retained 14 as originally mapped, and created four aggregate classes from the remaining eight: 'heather' and 'heather grassland' became 'dwarf shrub heath'; 'supra-littoral rock' and 'littoral rock' became 'coastal rock'; 'supra-littoral sediment' and 'littoral sediment' became 'coastal sediment'; 'suburban' and 'urban' became 'built-up and gardens'. This resulted in a total of 18 habitat classes (Table A3.9).

Habitat, as we use the term here (we could alternatively have referred to ecotype or biotype), reflects a combination of the physiognomy of the vegetation and land management, and does not imply any particular mechanism of association; i.e. we take a resource-based view of habitat (Dennis, 2010), recognising that a species occupies particular habitat classes because certain resources (e.g., host plants, prey, mutualists), structural elements (e.g., that enable spider webs to be built), or micro-environments (e.g., sheltered microclimates) are present somewhere within that class, and/or because negative influences (e.g., natural enemies, disruptive land management) are absent. For example, hedgerow species can be positively associated with arable and improved grassland (albeit at low frequencies), which is a true reflection of where many of these species live, given that field boundaries are demarcated by hedgerows, and that such linear features are nested within the grain size of satellite imagery.

### 3.5.6 Habitat associations

We identified habitat associations using logistic regression of species presence or absence (binary response) overlaid on the 18 habitat classes (categorical predictor). The regression equation for each species was used to estimate its probability of occurrence in each habitat class, under the assumption of equal availability of all habitat classes (i.e., as close as is possible to a 'species characteristic'). We defined levels of habitat specialisation to be the coefficient of variation across these 18 probabilities (13), producing a species' specialisation index (SSI) which, for our dataset, ranged from SSI = 0.36 (generalist) to SSI = 3.22 (highly specialised). Results are summarised by group in Table A3.3, and are reported for individual species in Table A3.8.

Given the finer grain of the land-cover map (25 m), compared with species records (100 m), individual species records could potentially be associated with up to 16 different habitat classes. To reduce the number of false positive associations, we removed mixed pixels at 100-m resolution (so that each species record was associated with exactly one habitat class). We further restricted the spatial extent for analysis to a 50-km buffer around presence records for the target species, excluding landscapes that were occupied during only one recording period. We did this to reduce the number of absences that might be caused by unsuitable climate or dispersal limitation (i.e., a pixel contains suitable habitat for a species, but lies outside its climate niche or dispersal radius in one or both recording periods).

We took all recorded presences to be 'true' for the purposes of modelling, and included in the final analysis all species with at least 50 such records (mean = 787, median = 197, maximum = 44 580). Inferring absence data from presence-only datasets is inherently more difficult. Further to the spatial filters described above, we applied the following criteria to minimise the number of false absences in the models. First, we only included as potential absences those pixels that had been visited by recorders of the same recording scheme (as deduced from records of other species within the same recording scheme). Second, we filtered absences according to time of year, for example to avoid treating late summer data as absences if the target species' flight period is in spring. We did this by fitting a smooth phenology curve to the frequency of records for the target species, as a function of the Julian day of observation. Any potential absences with record dates in the tails of this distribution (lower or upper 10% area under the curve) were excluded.

The remaining absences were from pixels visited under the same recording scheme as the target species, in landscapes where (or near where) the target species occurred and within the appropriate phenological time window(s). The absences still varied in reliability, however, because some qualifying pixels had only been visited once, whereas others had been visited multiple times. Third, therefore, we weighted absence data by the probability of recording the target species if it was present, given the number times (t) the absence pixel was visited:

$$
\frac{1}{n} \sum_{s=1..n} (1 - p_s)^t
$$

That is, one minus the probability of failing to detect the species on every occasion, where the ps are probabilities of detection across n known presence sites for the target species (these were calculated as the number of times the species was recorded in pixel s divided by the number of times s was visited).

### 3.5.7 Habitat availability

We obtained spatial estimates of habitat availability by projecting each species' regression model back on the land cover map at 25-m resolution (so that all pixels, including mixed pixels at the 1-ha scale, were included), using the same 50-km buffer as we used for model calibration. Range-wide habitat availability for each study species was calculated as the mean value across all of these pixels, indicative of the amount of habitat typically accessible to a species across its British distribution.

Habitat availability at the range margin was defined as the mean value across all land cover pixels in a 50-km buffer around the ten (or more) northernmost hectads that were used to define the range margin in the first recording period (1976-1990); i.e. landscapes across which the species had potential to expand (or retract) over time. Habitat availability for individual species at the range margin ranged from 0.4% (very little of the landscape could be colonised) to 56% of the landscape (ample opportunity for expansion, given suitable climate; Table A3.4 and Table A3.8).

To assess the relative suitability of the range-margin landscape, compared to what a species experiences on average across its range, we divided the mean habitat availability in rangemargin landscapes by the range-wide average. Significantly more species had reduced habitat availability in their range-margin landscapes  $(\chi^2 = 10.03, 1$  df,  $P < 0.002, N = 347)$ . The size of the effect was small on average, but correlated positively with higher levels of recording (*r* = 0.54, *P* < 0.05; reduction in margin habitat *vs*. number of hectads where at least 25% of the regional species richness was recorded in both time periods).

### 3.5.8 Models of range shift

We modelled range shifts (km y<sup>-1</sup>) as linear functions of habitat specialisation, and log<sub>10</sub>transformed habitat availability at the range margin. Habitat specialisation and  $log<sub>10</sub>$ -habitat availability are highly correlated (*r* = -0.70; see Figure 3.1B), and so we did not include both predictors in the same model. Rather, we tested the hypothesis that habitat availability provides a stronger explanation for the observed variation in species' range shifts, compared to specialisation.

To account for phylogenetic relatedness and methodological differences in recording between taxonomic groups (i.e. across recording schemes), we used linear mixed-effects models fitted via maximum likelihood (Bates *et al.*, 2014), with taxonomic group specified as a random intercept term. We included random slopes of the predictor variable, with respect to taxonomic group identity, if this lowered the conditional AIC (Greven & Kneib, 2010) when all 347 species were included in the model, considering both a correlated or uncorrelated random slope and intercept for the random effect grouping variable.

For all random effects structures, habitat availability was a stronger predictor of range shifts than was specialisation (Table A3.6). For range shifts modelled against specialisation, the top model included a random intercept term but not random slopes (model 1); for range shifts against habitat availability, the top model included (uncorrelated) random

intercept and random slope terms (model 2). Next, we extended model 2 by including an interaction between  $log_{10}$ -habitat availability, and margin habitat as a percentage of the range-wide average. This model had lower AIC and cAIC, compared with single-predictor models. The top model included the interaction term plus random intercept with respect to group (model 3).

### 3.5.9 Sensitivity to recording level

We ranked the 14 taxonomic groups by descending geographic coverage of citizen-science recording, defined by the number of hectads where there has been sufficient recording for at least 25% of the regional species richness (considering the nearest 100 hectads) to have been sampled in both time periods (Table A3.1). In Figure 3.3 of the main text, we plotted models 1-3 separately for: (i) four groups with the highest levels of recording, minus macromoths; (ii) macromoths; and (iii) nine groups with lower levels of recording. We plotted macromoths separately because, unlike other groups, moth recording used attractant methods (light traps at night) so that the areas sampled – and thus habitat associations – were more uncertain.

The proportion of variation in range shift that could be explained was higher for taxonomic groups with higher recording coverage. The slopes of the relationships were, however, similar (Figure 3.3 and Table A3.6), demonstrating that the patterns we report are qualitatively robust to recorder effort. In Figure 3.4, we systematically varied the threshold of recording coverage, above which species are included in the model. For example, when the recording threshold is very low, all groups are eligible for inclusion; when the threshold is very high, only the best-recorded groups are included. For consistency across different levels of group inclusion, each pair of points ( $R_{\text{m}}^2$  and  $R_{\text{c}}^2$ ) in Figure 3.4 was generated by averaging over 10,000 randomised draws of 30 species from three qualifying groups. This analysis revealed a log-linear relationship between the geographic coverage of citizenscience recording, and the proportion of variation in range shifts that could be explained. Extrapolating the fitted line to assume complete geographic coverage (2566 hectads) for all groups in the study, we infer that approximately half (49%) of the variation in range shift could be explained by habitat availability.

# Chapter 4

# Population variability of species can be deduced from opportunistic citizen science records: a case study using British butterflies.

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# Abstract

Abundance data are the foundation for many ecological and conservation projects, but are only available for a few taxonomic groups. In contrast, distribution records (georeferenced presence records) are more widely available. Here we examine whether year-to-year changes in numbers of distribution records, collated over a large spatial scale, can provide a measure of species' population variability, and hence act as a metric of abundance changes. We used 33 British butterfly species to test this possibility, using distribution and abundance data (transect counts) from 1976-2012. Comparing across species, we found a strong correlation between mean year-to-year changes in total number of distribution records and mean year-to-year change in abundance (N = 33 species;  $R^2$  = 0.66). This suggests that annual distribution data can be used to identify species with low versus high population variability. For individual species, there was considerable variation in the strength of relationships between year-to-year changes in total number of distribution records and abundance. Between-year changes in abundance can be identified from distribution records most accurately for species whose populations are most variable (i.e. have high annual variation in numbers of records). We conclude that year-to-year changes in distribution records can indicate overall population variability within a taxon, and are a reasonable proxy for year-to-year changes in abundance for some types of species. This finding opens up more opportunities to inform ecological and conservation studies about population variability, based on the wealth of citizen science distribution records that are available for other taxa.

### 4.2 Introduction

The long term monitoring of population dynamics is an important aspect of ecology, and allows examination of factors driving species' abundance trends, such as the effects of weather (Roy *et al.* 2001), habitat availability and land use (Lemoine *et al.* 2007), disease (Daszak, Cunningham & Hyatt 2003), and human impacts (Lewis & Vandewoude 2015). Monitoring abundance trends of species thus helps to identify species at risk, develop conservation strategies to halt population declines (Brown, Mehlman & Stevens 1995), and identify increasing populations of pests to implement control strategies (Petrovskii, Petrovskaya & Bearup 2014). Measuring population variability is essential to explore the influence of environmental factors, such as climatic cycles or food availability, on population dynamics (van Schaik & van Noordwijk 1985; Lynam, Hay & Brierley 2004). In addition, population variability may be an important determinant of the likelihood that populations will survive in habitat fragments, and variability may indicate the sensitivity of populations to climatic fluctuations (Pimm, Jones & Diamond 1998; Vucetich *et al.* 2000; Oliver *et al.* 2012). However, collecting abundance data may be time-consuming and expensive, and thus many taxonomic groups lack information on abundance trends and population dynamics. By contrast, many more species have large datasets of distribution records (i.e. unique records of the presence of species at a given location and date). Such data are available for a wide range of taxonomic groups, tend to cover wide areas, span many years, and are often collected as part of 'citizen science' projects (Devictor, Whittaker & Beltrame 2010; Pocock *et al.* 2015).

It is well known that there is a positive relationship between species' abundances and distributions (Brown 1984; Gaston *et al.* 2000) and very abundant species tend to have larger ranges (Holt *et al.* 1997). Abundance-distribution relationships are general patterns in ecology, but there are many forms of the relationship (Gaston 1996), and these relationships are not necessarily linear (Hartley 1998). In spite of this complexity, strong relationships have been found between distribution and abundance, which are evident over time, large spatial scales and different taxonomic groups (Zuckerberg, Porter & Corwin 2009; Roney, Kuparinen & Hutchings 2015). These relationships allow occupancy changes (changes in the likelihood of a species' presence) to be used to estimate population trends (Tempel & Gutiérrez 2013), broad biodiversity changes to be assessed across multiple taxonomic groups (Oliver *et al.* 2015a), and long-term trends in the frequency of species' occurrences to be modelled (Pearce & Boyce 2006). These long-term occurrence trends have been shown to be reasonable proxies for abundance trends for both birds (Kamp *et al.*

2016) and butterflies (Warren *et al.* 2001; Oliver *et al.* 2015a). However, there is little information on the capacity of distribution data to describe other aspects of population dynamics, such as population variability, which is an important factor affecting extinction risk (Inchausti & Halley 2003; Mace *et al.* 2008).

A challenge for ecologists is deriving an accurate measure of population variability when standardised abundance estimates are lacking. The positive associations between distribution size and abundance suggest that distribution records could potentially be used in analyses inferring species' population dynamics, by acting as proxies for abundance data. If there are strong and predictable relationships between year-to-year changes in abundance and year-to-year changes in distribution records, then distribution records could provide a useful metric for ecologists to study the factors affecting population variability in a much wider range of taxa than is currently possible.

In this study, we examine the relationships between abundance and distribution to assess whether year-to-year changes in the number of distribution records are strongly related to year-to-year changes in abundance. We study British butterflies because there are longterm and fine-scale data on both distribution and abundance, allowing robust testing of these relationships. We predict that year-to-year changes in abundance will be strongly positively related to year-to-year changes in distribution records, because increasing numbers of individuals would be expected to result in an increased likelihood of a species being recorded. In addition, as a population increases in size, density-dependent dispersal would be expected to result in individuals moving away from areas of high population density, thereby increasing the number of sites where species can be observed (Gaston *et al.* 2000).

Within this broad topic, we examine three issues. The first is whether it is possible to identify species with higher or lower population variability using distribution data – a between-species comparison. We do this by calculating average between-year changes in the numbers of distribution records over time, and comparing these estimates with measures of variability that are based on fixed-transect population count data. Secondly, we assess whether distribution records can be used as proxies for inter-annual changes in abundance in each species separately – a within-species analysis. Finally, we identify the characteristics of species for which distribution data provide a proxy for abundance, concentrating on three attributes that can be deduced from the distribution records themselves (i.e. not requiring additional ecological or population dynamic data, which are
lacking for many taxa). We selected these metrics because they are likely to be linked to our statistical capacity to detect year-to-year variation in abundance from distribution records: (1) the total number of distribution records for a species, (2) how aggregated these records are in space (using a metric of 'fractal dimension' of distribution records), and (3) the average size of the year-to-year changes in distribution records (i.e. how much annual variation there is in distribution records for a species). We refer to these metrics as 'biogeographical attributes', but recognise that they are also influenced by variation in recording intensity across species and over time. We also examine the effect of the spatial scale of the study area on the relationship between year-to-year changes in distribution records and year-to-year changes in abundance, by comparing data analysed at national (UK study area, 302,800 km<sup>2</sup>) and regional (county study area, 440 km<sup>2</sup>) levels, given that population fluctuations may be synchronous in their dynamics at one spatial scale but not others (Sutcliffe, Thomas & Moss 1996).

## 4.3 Materials and methods

### 4.3.1 Study species

We studied 33 species of British butterfly (See Table 4.1), including northern and southern species, and resident and migrant species, over the period 1976 to 2012. This study period was selected to maximise the geographic coverage of data, the length of the time-series of data analysed, and the number of species analysed. We excluded species without 37 years of abundance and distribution data. Species that were subject to targeted, intensive surveying effort during certain years of the study period were also excluded (*Hesperia comma*; Thomas & Jones, 1993, *Boloria euphrosyne*; Brereton, 1998, and *Satyrium walbum*; Thomas, 2010), because large differences in the level of recording effort between years could bias results.

### 4.3.2 Distribution records

We computed year-to-year changes in distribution records based on data collected by volunteers for the Butterflies for the New Millennium (BNM) recording scheme, surveying sites in the study area (see below) on an opportunistic basis using unstructured sampling (Fox *et al.* 2015). A distribution record is an observation (recorded presence) of an individual species at a location on a particular date. Recording efforts are generally unstructured (there are no fixed or assigned times, places or methods for recording) and opportunistic, with little to no guidance given to recorders as to how, when and where to

record, meaning that recording is influenced heavily by recorder behaviour (Boakes et al., 2010; Isaac & Pocock, 2015). Recorder behaviour can vary due to encouragement to record in under-represented regions for the purposes of atlas creation or other targeted survey efforts. Despite these attempts to encourage, spatial and temporal variation in opportunistic recording effort remains high. Due to increased recruitment of recorders over time numbers of distribution records have increased (see Figure A4.2), which is why we detrended the data prior to analysis. The spatial and temporal resolution of BNM distribution records varies; we excluded records with spatial resolution coarser than a 10 km x 10 km grid square or with date ranges which fell outside the study period. The study area was the UK, Isle of Man and Channel Islands (3028 hectads in total). We analysed a total of 5,873,182 distribution records from 1976 to 2012, after all filtering processes (see below). The majority of distribution records are independent of abundance data (UK Butterfly Monitoring Scheme (UKBMS) transect), but the distribution dataset did contain some records sourced from transects. Therefore, distribution records were excluded if they occurred within the 1 km grid cell that contained a UKBMS transect (based on the centroid of the digitised transect route). This led to 1604 1km cells being excluded; approximately 5.3% of the UK land area and 26.2% (2,089,886) of records. Year-to-year changes in  $log<sub>10</sub>$ distribution records were calculated for each study species over the 37-year study period by subtracting the number of distribution records (log<sub>10</sub>-transformed) in year *t-1* from the number of records in year *t*.

#### 4.3.3 Abundance data

We analysed abundance data from the UKBMS national collated index (www.ukbms.org). The UKBMS calculates their index from counts from weekly transect walks along fixed routes undertaken during the recording period (April-September) every year since 1976 (see http://www.ukbms.org/Methods.aspx for full details). Counts are taken from sites in Great Britain and Northern Ireland (1854 transect sites in total). Counts for missing weeks are estimated by the UKBMS by considering the area of a GAM curve fitted to observed weekly count data throughout the year (Rothery & Roy 2001). The UKBMS national collated index from 1976-2012 is created using a log-linear model, with a transect site and year effect (Brereton *et al.* 2011), as shown below:

$$
\log_{10}(c_{ij}) = x_i + y_j
$$

Where c is the expected count for site *i* in year *j*, and where x*<sup>i</sup>* and y*<sup>j</sup>* give the means for the *i*th site and the *j*th year. The index is then scaled to a mean of 2, for the purposes of comparing abundance trends across species. This produces a  $log<sub>10</sub>$ -transformed abundance index, which we used in our calculation of population variability. We computed year-toyear changes in  $log_{10}$  abundance by subtracting the abundance index value ( $log_{10}$ transformed) for year *t-1* from the value for year *t*.

### 4.3.4 Accounting for phylogeny

The butterfly species studied here are phylogenetically related, and this must be taken into account when analysing species together in models. All multi-species analyses conducted in this study accounted for the non-independence of species using phylogenetically-informed linear models with estimated Pagel's λ, using the *pgls* function of the caper package in R (Pagel, 1999; Orme et al., 2013), and a recently-published butterfly phylogeny (please see Brooks *et al.* 2016 for full details of how the phylogeny was constructed). These models are interpreted by lambda P values (distinct from the P values produced by the model estimates) indicating the difference between the phylogenetic correlation  $\lambda$  value (estimated using maximum likelihood) and the upper and lower bounds: 1 (indicating phylogenetic dependence) and 0 (indicating phylogenetic independence). In all our analyses, the phylogenetic correlation was not significantly different from the lower bound, indicating that there was little evidence of phylogenetic signal in our models.

## 4.3.5 Examining relationships between abundance and distribution records

First, we explored whether mean yearly changes in  $log_{10}$  distribution records (as above) were correlated with mean yearly changes in  $log_{10}$  abundance (as above) over the 37-year study period, in a multi-species analysis with a control for phylogenetic independence (see section above). In both cases (distribution-record and abundance changes), we calculated the average absolute magnitude of the year-to-year changes, rather than directional changes (positive or negative). This analysis tests whether species with high population variability (on transects) also have high variability in terms of numbers of distribution records.

Secondly, we examined each species separately. We calculated the strength of the relationships between year-to-year changes in  $log_{10}$  distribution records and changes in  $\log_{10}$ abundance using R<sup>2</sup> values from least squares regressions. This relationship is

hereafter termed the inter-annual distribution-abundance relationship and, for each study species, it reflects the extent to which yearly changes in  $log_{10}$  numbers of distribution records can be used to predict population size changes (from transect data). We analysed year-to-year changes rather than absolute numbers each year to de-trend the data, and to remove any temporal trends in recording effort.

Thirdly, we examined the influence of three independent biogeographical attributes on these inter-annual distribution-abundance relationships to identify species for which distribution records were adequate proxies for population change. These attributes were: total number of distribution records; fractal dimension of a species' range; and overall variability in distribution records. We computed the total number of distribution records collected at any spatial resolution (10 m to 10 km grid) for a species during the study period (1976-2012). Fractal dimension is a metric of how 'well-filled' a species' range is, based on the proportion of 10km grid cells with records within each occupied 100km grid cell (Wilson *et al.* 2004). For each species, we calculated the total area of all occupied 10 km and 100 km grid cells, and regressed these values against the length of the grid cells (10 km and 100 km respectively; all values  $log_{10}$  transformed). The slope of the regression gives a measure (fractal dimension) of how 'well-filled' a species range is at 10km scale, where a slope of 0 indicates a completely-filled range, and a slope of 2 indicates a minimally-filled range (see Figure A4.1 for two exemplar species; *Thymelicus sylvestris,* with the most well-filled range and *Hipparchia semele* with the most minimally-filled range). For overall variability in distribution records we used the mean year-to-year change in  $log_{10}$  distribution records over the study period.

A phylogenetic multivariate regression was then fitted with the three biogeographical attributes as explanatory variables and the  $R^2$  value of each species' inter-annual distribution-abundance relationship as the response variable. We fitted a fourth term to the model, the quadratic term of mean year-to-year change in  $log_{10}$  distribution records, to account for its apparent non-linear relationship with goodness-of-fit ( $R^2$ ) values when relationships were visually inspected by plotting the data. We tested a full model, then removed non-significant terms using a stepwise deletion approach.

Autoecological information may be limited for other taxonomic groups, but the biogeographical attributes tested in this paper can be easily derived from distribution datasets for many different taxa. Because butterflies do have detailed autoecological information, we tested the influence of dispersal ability on the inter-annual distribution-

abundance relationship in PGLS models, using two metrics: dispersal rankings based on expert opinion (Cowley et al., 2001) and a mobility score calculated from indices of ecological information (Dennis et al., 2004). We found no significant relationship between dispersal ability and the strength of the inter-annual distribution-abundance relationship (see Supplementary Table 4.2).

## 4.3.6 Comparison of national and regional inter-annual distribution-abundance relationships

To investigate whether the goodness of fit of the inter-annual distribution-abundance relationships varied with spatial scale, we repeated our analysis of this relationship at a regional level, for the county of Dorset. We compared  $r^2$  values from national and regional inter-annual distribution-abundance relationships for a sub-set of 23 butterfly species for the period 1983-2009 (maximum time period containing abundance data for species in Dorset). Dorset was selected because of its extensive history of surveying butterflies (Robertson, Woodburn & Hill 1988; Thomas *et al.* 2001).

### 4.4 Results

## 4.4.1 Relationship between variability in abundance and distribution records across species

Across the 33 study species, there was a strong positive relationship between the mean year-to-year changes in  $log_{10}$  distribution records and mean year-to-year changes in  $log_{10}$ abundance (Figure 4.1a, PGLS,  $\lambda$  = 0, R<sup>2</sup>: 0.95, F<sub>1,31</sub> = 623.8, P = <0.001), even when two outlier species were removed (Figure 4.1b, λ = 0.059, PGLS,  $R^2$ : 0.66, F<sub>1,29</sub> = 55.35, P = <0.001). Thus, species that show high variability in abundance also have high variability in distribution records, and there was little evidence for any phylogenetic signal (i.e. results were not significantly different between models based on estimated  $λ$ , and where  $λ$  was set to 0).



Figure 4.1. Regressions of the mean year-to-year change in log<sub>10</sub> distribution records against the mean year-to-year change in  $log_{10}$  abundance: a) including all 33 species, with two outlier species labelled as follows: *Celastrina argiolus* (1) and *Vanessa cardui* (2); and b) for 31 species, excluding these outlier species.

## 4.4.2 Measuring inter-annual distribution-abundance relationships within species

For each of our 33 study species, the relationships between year-to-year changes in  $log<sub>10</sub>$ distribution records and year-to-year changes in  $log<sub>10</sub>$  abundance produced an overall mean  $R^2$  value of 0.36, indicating that year-to year changes in distribution records of UK butterflies provide a moderate proxy for year-to-year abundance changes. Eight butterfly species had  $R^2 > 0.5$ , showing that distribution records were particularly informative in approximately 25% of study species. However, there was considerable variation among species, with  $r^2$  values varying between 0.03 and 0.92 (Table 4.1). Figure 4.2 highlights two exemplar species, where the relationship was strong (Holly blue, *Celastrina argiolus,*  $R^2$  = 0.85) and one where the relationship was very weak (Marbled White, *Melanargia galathea,*   $R^2 = 0.16$ ).

**Table 4.1.** Goodness of fit of the inter-annual distribution-abundance relationships for 33 butterflies. Latin names with an asterisk (\*) indicate migratory species. Presented are the Pearson's R<sup>2</sup> values of the relationship between year-to-year log<sub>10</sub> change in abundance and year-to-year log<sub>10</sub> change in total number of distribution records. We checked r values and found them to all be positive, indicating that the relationships below were always positive. Biogeographical attribute values are also included for each species: total number of distribution records ( $\Sigma$ D), mean absolute year-to-year change in log<sub>10</sub> distribution records, fractal dimension (Fractal D).





**Figure 4.2.** Inter-annual distribution-abundance relationships for two exemplar species. Plots show year-to-year changes in  $log_{10}$  distribution records and year-to-year change in log<sup>10</sup> abundance for *Celastrina argiolus* (a, c; left panels) and *Melanargia galathea* (b, d; right panels). Panels a and b show regressions (each point represents the change between a given pair of years), and panels c and d plot the same data together in a time series (solid lines indicate year-to-year changes in  $log_{10}$  abundance, dashed line year-to-year changes in log<sub>10</sub> distribution records).

### 4.4.3 Influence of biogeographical attributes

The  $R^2$  value for each species' inter-annual distribution-abundance relationship (i.e. relationships between year-to year changes in  $log<sub>10</sub>$  distribution records and year-to-year changes in  $log_{10}$  abundance; as in Figure 4.2) was then analysed in relation to the biogeographical attributes of each species, which are provided in Table 4.1. We tested all these variables in a full model (PGLS,  $\lambda$  = 0,  $R^2$  = 0.64, F<sub>4,28</sub> = 12.58, AIC = -30.43, P = <0.001; Table 4.2a). Only mean absolute year-to-year changes in distribution records and its quadratic term significantly influenced inter-annual distribution-abundance relationships: total number of distribution records and fractal dimension did not, and were consequently dropped during model simplification. The best and most parsimonious model (PGLS,  $λ = 0$ ,  $R^2$  = 0.63, F<sub>2,30</sub> = 26.02, AIC = -33.70, P = <0.001; Table 4.2b) revealed that the strength of the relationship (R<sup>2</sup> value) increased with overall variability in distribution records (Figure 4.3). Thus, the results show that species with greater fluctuations in distribution records over time had stronger inter-annual distribution-abundance relationships (although the effect of variability in records was non-linear and asymptoted at roughly 0.8; Figure 4.3). Two species (*Celastrina argiolus* and *Vanessa cardui*) potentially had strong effects on the analyses (Figure 4.3c), but excluding these two species did not alter our conclusions (Table A4.1).

Table 4.2a and 4.2b. The influence of species attributes on the goodness of fit (R<sup>2</sup> value) of the inter-annual distribution-abundance relationships, which is the response variable. Table 4.2a shows the first, full model with the following explanatory variables: mean absolute year- to-year change in distribution records, total number of species records, and fractal dimension. The model summary statistics were:  $\lambda$  = 0, R<sup>2</sup> = 0.64, F<sub>4,28</sub> = 12.58, AIC = -30.43, P = <0.001. Table 4.2b shows the best model with only one explanatory variable: mean absolute year-to-year change in distribution records. Model summary statistics: λ = 0, R<sup>2</sup> = 0.63, F<sub>2,30</sub> = 26.02, AIC = -33.70, P = <0.001. In both models, the quadratic term of the mean absolute year-to-year change in distribution records was included to account for the non-linear nature of the relationship, and model results with estimated λ were not significantly different from a model with λ set to 0 (Fig. 3).





**Figure 4.3.** Inter-annual distribution-abundance relationship and three biogeographical attributes of the species: a) total number of distribution records (PGLS,  $\lambda$  = 0.907, R<sup>2</sup> = <0.01  $F_{1,31}$  = 0.09, P = 0.76); b) fractal dimension (PGLS, λ = 0.928, R<sup>2</sup> = 0.02, F<sub>1,31</sub> = 0.61, P = 0.44), and c) mean absolute year-to-year change in log<sub>10</sub> distribution records (PGLS,  $\lambda$  = 0, R<sup>2</sup> = 0.63, F<sub>2,30</sub> = 26.02, P = <0.001). Each dot represents a species; the numbered data points on panel (c) are *Celastrina argiolus* (1) and *Vanessa cardui* (2).

## 4.4.4 Comparison of national and regional inter-annual distribution-abundance relationships

The strength of inter-annual distribution-abundance relationships computed for species at a regional level (Dorset) were strongly positively correlated with those computed at the national level, PGLS, λ = 0.562, R<sup>2</sup> = 0.53, F<sub>1,21</sub> = 23.25, P = <0.001; Figure 4.4). This is despite the fact that the average value of the inter-annual distribution-abundance relationships was higher at the national level (Mean, National = 0.41 Regional = 0.19; SD, National = 0.24 Regional = 0.24). Therefore, we conclude that any differences in population synchrony between national and regional scales had little influence on the strength of inter-annual distribution-abundance relationships for butterfly species.



**Figure 4.4.** National inter-annual distribution-abundance relationship regressed against a regional inter-annual distribution-abundance relationship (region = county of Dorset) calculated for 23 butterfly species, indicated by the solid black line. The dashed line indicates the 1:1 line.

### 4.5 Discussion

We found that citizen-collected distribution data can be used to extract information about population variability, in the absence of bespoke abundance monitoring programmes. In particular, mean year-to-year changes in distribution records were positively related to mean year-to-year changes in abundance (with outlier species removed,  $R^2$  value: 0.66; Figure 4.1). Thus, we were able to identify species with low and high between-year population variability quite accurately, using distribution data. This result supports the ability of unstructured citizen science data to reflect population-dynamic patterns found in long-term abundance data, and hence citizen science data may be useful in multi-species studies for which it is necessary have an overall measure of population variability (Robertson *et al.* 2015; Gandiwa *et al.* 2016) where abundance data are lacking. The ability to recognise species with the highest levels of population variability may help identify species that are at greatest risk of stochastic extinction following habitat fragmentation (Pimm, Jones & Diamond 1998; Vucetich *et al.* 2000; Oliver *et al.* 2012), and the most variable species may potentially be the most responsive to yearly variation in climatic conditions (Maclean *et al.* 2008; Howard *et al.* 2015) and to parasitoids or other natural enemies (Robertson *et al.* 2015). The findings from these analyses imply that information from citizen science data can provide useful input to landscape-scale conservation planning and to climate-change risk assessments.

When we considered each species in turn, there was considerable variation in the strength of relationships between year-to-year changes in distribution records and abundance among the study species; although these associations were always positive, averaging an  $R^2$  of 0.36 across all species (Table 4.1). These relationships suggest that there is also some potential to use the distribution records of individual species to infer their population dynamics in greater detail (rather than as one metric for overall variability of the time-series). However, this is only feasible for some species: only eight out of 33 species having 'strong' relationships (R<sup>2</sup> > 0.5) between year-to-year abundance and distribution changes. Thus it should not be presumed that distribution records can be used as a substitute for population data in the assessment of inter-annual change for all species.

### 4.5.1 Inferring abundance change from distribution data

Many species are declining or facing range retractions (Hayhow *et al.* 2016), and it is important to monitor their population trends. Species with highly variable population dynamics tend to be at high risk of extinction (Pimm, Jones & Diamond 1998; Vucetich *et al.* 2000; Oliver *et al.* 2012) and thus our measure of variability in distribution records has ecological value, with the potential to assist conservation assessments by helping to identify species at risk of extinction or habitats in need of management (Meyer *et al.* 2015; Sánchez-Hernández, Cobo & Amundsen 2015). Our multi-species analysis (Figure 4.1) indicates that it is possible to derive robust estimates of population variability using distribution data alone.

Despite the promising results, there are two caveats that we should highlight. In this study, we examined only one taxonomic group with a high level of recording effort by citizen scientists. We also included only species with data in every year of the study period, excluding rare/less well-studied species. The value of other distribution datasets with lower recording effort may not be so informative. Kamp et al. (2016) found that reducing the number of distribution records resulted in poorer abundance trend estimates for Danish birds. Even without reducing the sample size, population trends were misclassified for 50% of the species they considered. Thus, using distribution data to infer population changes may require quite mature citizen science schemes, with substantial numbers of distribution records. Given that butterflies are a data-rich taxonomic group in the UK it is unknown whether other groups will have sufficient data to replicate these results. Datasets which may have sufficient data for this method are butterflies in other countries, or other taxa in the UK, for which standardised abundance monitoring schemes are lacking, e.g. dragonflies.

The second caveat is that more detailed population-dynamic interpretations of distribution data only seem possible for some species. Our finding that citizen science distribution data explain an average of only 34% of the year-to-year variation in abundance is unlikely to be sufficient to build meaningful models for examining the sensitivity of populations to environmental drivers, such as specific climate variables. For example, Malinowska *et al.* (2014) were unable to detect impacts of extreme weather events on populations of ectothermic species from distribution records, despite evidence of these impacts from population data (e.g. Oliver *et al.*, 2015b). In addition, while we have removed species which have unusually high levels of recording effort due to species-specific surveys, not all species are necessary reliably

monitored by UKBMS, which could result in poor year-to-year distribution-abundance relationships. For example, the purple hairstreak butterfly (*Favonius quercus*) occurs in tree canopies, and is therefore difficult to monitor from ground-based surveys. Other species may suffer from limited recording for other reasons, such as occurring in restricted locations or not being identified correctly due to confusion with other morphologically similar species.

### 4.5.2 Biogeographical attributes

Despite the above caveats, we conclude that year-to-year changes in distribution records represented an adequate proxy for abundance change in species with large fluctuations in their occurrence from year to year (Figure 4.3, Table 4.1). Species with large year-to-year fluctuations in their occurrences, such as migrants, may offer the greatest statistical power to deduce population changes from distribution data. Even though two migrant species and the holly blue butterfly *Celastrina argiolus* demonstrate the strongest inter-annual distributionabundance relationships, the mean year-to-year change in distribution records was also an important variable in predicting the strength of the year-to-year distribution-abundance relationship for other species. Therefore, mean year-to-year change in distribution records may help to identify non-butterfly species where citizen science distribution data could be used as a 'replacement' for direct population data. We found that total numbers of records and fractal dimension did not significantly influence the inter-annual distribution-abundance relationship. The most parsimonious explanation for this is that these variables are not important, and that our hypotheses, that the statistical capacity to detect year-to-year variation in abundance from distribution records was linked to the total number of distribution records, and fractal dimension, were wrong. We had predicted that a large total number of records would mean greater statistical power to find the inter-annual distribution-abundance relationship. The lack of a significant relationship between the inter-annual distribution-abundance relationship and total number of distribution records could be because patterns of year-to-year change in distribution records can be similar those in abundance even when numbers of observations are low. Recorder behaviour may have biased our results, as recorders may not record widespread common species on an ad hoc basis instead favouring notable records (e.g. rare species), this contrasts the abundance data that were collected following a structured survey design where all species seen are recorded. This could lead to mismatch in abundance and distribution patterns even for inter-annual changes, as recording effort varies temporally. Finally, the

lowest total number of distribution records in this study was quite high (see Table 4.1), therefore the concerns with low sample size were not an issue here. However, the issue may be important to other more poorly recorded taxonomic groups.

Fractal dimension of species' distribution also did not impact the inter-annual distributionabundance relationship. This might be because even if a range is fragmented, distribution recorders and transect volunteers still find and document species in those locations. In addition, if a species is known to be fragmented (which usually indicates rareness or being at risk of extinction), there may be a recording bias towards it (Isaac & Pocock 2015), which results in good information for that species. Therefore, species with a high fractal dimension may still have a positive inter-annual distribution-abundance relationship. However, it should be noted that species which are very poorly studied, and therefore likely rare and in fragmented habitats, were not been included due to the selection criteria. The study species also had ranges which were relatively well-filled, with fractal dimension scores ranging from 0.257 to 0.716 (maximum possible value is 2). It is possible that fractal dimension is an important factor for highly fragmented species, and there may have been insufficient variation in this attribute to be important to the inter-annual distribution-abundance relationship. Similarly we found no relationship between the inter-annual distribution-abundance relationship and dispersal for butterflies (Table A4.2). If these variables lack significant explanatory power even for a well-studied taxon, then this suggests that they will have limited use for identifying species in other taxa for which our method may be appropriate.

## 4.5.3 Population synchrony and inter-annual distributionabundance relationships

The success of year-to-year changes in distribution records mirroring abundance changes in migratory species suggests that population synchrony over large areas may play a role, and so we examined the impact of scale on the inter-annual distribution-abundance relationship by comparing national and county-level analyses. Weak relationships at the national level may occur if species' population dynamics are asynchronous, such that abundances and distributions may be closely linked locally, but a 'good year' in one region might occur when it is a 'bad year' in another region, obscuring any overall pattern at a national scale. However, when we repeated the national-scale analysis for a much smaller region (the county of Dorset), the results were similar: goodness of fit scores across species for the inter-annual distribution-

abundance relationship for Dorset were correlated with those for the same species at the national level (Figure 4.4). The majority of species had lower  $R^2$  values for the regional analyses, probably due to reduced data quantity. The spatial scales at which abundance and distribution changes are linked deserve more attention, but our preliminary conclusion is that reducing the extent of the study region considered does not improve the inter-annual distributionabundance relationship.

#### 4.5.4 Conclusions

The key finding that (mean year-to-year changes in) citizen-collected distribution data can provide useful information on population variability suggests that it may be possible to expand these methods to other taxonomic groups, or to populations of butterflies in countries that do not have standardised population monitoring schemes. Such measures of variability can inform habitat, landscape and regional conservation decision-making. The use of distribution data for more detailed analyses of inter-annual population change is only likely to be possible, however, for species that have highly variable numbers of records between years. For these species, it may be possible to analyse year-to-year population changes across much longer time periods than are covered by transect data and hence identify how populations are influenced by the effects of specific weather variables, density dependence, and any other process that operates at a large geographic and temporal scale. Further investigation is required, however, in the feasibility of extending these methods to other taxonomic groups without abundance data (e.g. grasshoppers, dragonflies).

## Chapter 5

## General Discussion

## 5.1 Synthesis

The overall aim of my thesis was to explore species' responses to climate change, quantifying rates of range shifts for multiple taxonomic groups and testing the influence of species' attributes and landscapes on these shifts. I did this by utilising British species' occurrence records and land cover maps derived from satellite and cartographic data. My results demonstrated that species are, on average, shifting their ranges northwards, and habitat specialism and the availability of suitable habitats influences the rate of species' range expansion. Quantifying species' habitat availability can help conservationists determine appropriate actions to facilitate range shifts. In addition, I investigated the potential for distribution data to be used as a proxy for abundance patterns. Environmental changes affect species' populations, making it valuable to find ways to make deductions about changes to species' populations in circumstances when abundance data are lacking. I found that the mean year-to-year change in distribution records and the mean year-to-year change in abundance matched well across all species, suggesting that distribution records may be applied to ecological studies in place of abundance change metrics. Below, I briefly review the content and results of each of my chapters, before discussing my results and their implications for ecology, conservation and species monitoring.

**Chapter 1** is a General Introduction to my thesis, and provides an overview of the impacts of climate change on biodiversity, explaining the need to understand how species are responding to climate change, and clarifying how citizen science data facilitate the exploration of patterns in species' range shifts.

In **Chapter 2**, I investigated the variation in rates of range shifting among 21 taxa, using citizen science data to measure changes in northern leading-edge range boundaries from 1966 to 2010. For the analyses, I examined range shifts across two intervals: interval 1 was 1966 to 1995, and interval 2 was 1986 to 2010. In this chapter, I investigated variation in range shifting rates among taxa and over time. I found that taxonomic groups studied experienced a mean

northwards range shift of 24 km decade<sup>-1</sup> over interval 1 (13 taxa), and 18 km decade<sup>-1</sup> over interval 2 (16 taxa). At least half of the taxonomic groups studied underwent significant northwards shifts for at least one level of recording effort. The different levels of recorder effort were: 'recorded', for which range shift calculations incorporated data for all cells where at least one species was recorded in both time periods of one interval; 'well recorded', which included all cells where at least 10% of a regional species richness was recorded in both time periods; and 'heavily recorded', with cells including 25% of a regional species richness. There were significant differences in rates of range shifting among taxonomic groups at every level of recording effort (P<0.05), and confidence intervals indicate high levels of variation in range shifts within groups. I also investigated changes in the rate of range shift over time for four taxa (dragonflies and damselflies, birds, butterflies and macromoths), and found that the Lepidoptera appeared to have accelerated their range expansions over interval 2. I concluded that species are responding to environmental change through range shifts, that there is variation in rates of shift within and between taxa, and that these rates may not be constant over time.

In **Chapter 3**, I tested the influence of habitat and traits on rates of range shifting for 347 species (from 14 taxa) over four decades (1976-1990 to 2001-2015). I investigated the relative importance of habitat specialism (a single score indicating how strongly a species was associated with 18 habitat classes) and habitat availability (the probability of species being observed in those habitats) on range shift, measured as the distance in kilometres that a species' northern range margin moved per year. I used species-specific values for all metrics. Using linear regression, I found that there appears to be more variation in range shifts among species within taxonomic groups (91%) than between taxonomic groups (9%). I tested the hypothesis that habitat availability provides a stronger explanation for the observed variation in species' range shifts, compared to specialisation. Both specialism (4%) and habitat availability (17%) significantly explained variation in rates of range shifting (linear mixed-effects model, P<0.01). Next, I included an interaction term in my linear model that compared habitat availability across the whole range with availability at the northern margin for each species. Those species with less habitat availability at the margin were less likely to shift their northern range margins polewards. The amount of variation explained by the covariates depended on the level of recording effort (defined as the number of heavily recorded grid cells, as described in Chapter 2 and above). For well-recorded groups, covariates explained 36% of variation in

rates of range shifting. If all 2566 hectads in the study region had been heavily recorded for all taxa groups, I estimated that the influence of habitat and traits could explain up to half of the variation in species' range shifts. I concluded that variation in species' range shifts is driven substantially by the habitat availability of species, which is the interplay between species' level of specialisation, the types of habitats species are specialised to, and the accessibility of habitat within the landscape. By increasing connectivity and the amount of habitat in the landscape for species with low habitat availability, conservationists can facilitate range expansions that may not otherwise occur (see 'Conservation Management' section below).

In **Chapter 4**, I examined the potential of distribution data to act as a proxy for changes in species' abundance. Using 33 British butterflies in both between- and within-species analyses, I explored whether there were relationships between inter-annual changes in abundance and inter-annual changes in distribution records. A multi-species analysis demonstrated that the relationship between mean year-to-year changes in abundance and mean year-to-year changes in numbers of distribution records was positive and strong (PGLS,  $R^2$ = 0.95,  $F_{1,31}$ = 623.8, P = <0.001). This relationship was maintained when two outlier species were removed from the analysis (PGLS,  $R^2$ = 0.66, F<sub>1,29</sub> = 55.35, P = <0.001). Next, I performed a species-specific analysis of the relationship between year-to-year changes in abundance and year-to-year changes in distribution records. My findings demonstrated that the strength of the relationship varied among species (min R<sup>2</sup>= 0.03 for *Boloria selene*, max R<sup>2</sup>= 0.92 for *Vanessa cardui*, mean R<sup>2</sup>= 0.36), implying that using distribution data to monitor inter-annual population changes is limited to certain types of species. I investigated species-specific biogeography attributes that could explain variation in  $R^2$  values. I found that species that had large mean year-to-year changes in distribution records showed strong inter-annual abundance-distribution relationships ( $R^2 > 0.5$ ). In other words, it is feasible to use year-to-year changes in distribution records to estimate abundance changes for species such as *Vanessa cardui* and *Celastrina argiolus*, which have high levels of inter-annual population variability. I concluded that distribution records have potential to be used to measure population variability and long-term changes in year-to-year abundance.

In my data chapters, I found that variation in species' range shifts is influenced by the species' traits and habitat availability. However, much of this variation remains unexplained. I also found that distribution data has potential to be used as a proxy for abundance patterns, which

is important because abundance data is lacking for many species. In the remainder of this chapter, I discuss the implications of these findings, their relationship to the wider literature, constraints of my studies and future opportunities for research. I then discuss the overall contribution of my findings for conservation of species under climate change, the future for citizen science recording schemes, and my final conclusions.

## 5.2 Exploring variation in range shifts

The results indicate that many species from a wide variety of taxonomic groups are shifting the leading-edges of their ranges polewards in response to climate change. This finding provides further evidence to support the evidence in the current literature, which shows species are shifting polewards (Parmesan & Yohe, 2003; Chen *et al.*, 2011a; Lenoir & Svenning, 2015). I quantified variation in range shifts within and between taxonomic groups in this thesis, and I discuss this below.

One of my primary goals was to explore variation in range shifts within and between taxonomic groups, and I found that, while there are significant differences in mean range shifts among different taxonomic groups (Chapter 2), linear regressions revealed that there is more variation within groups than between groups (Chapter 3). This is new evidence; previous studies that have assessed rates of range shifting have not previously analysed this variation. Chen *et al.* (2011a) examined rates of shift between different taxonomic groups and concluded that groups showed similar averages, but contained species with variable rates of range shift, and did not explicitly test variation within- and between-groups. My findings indicate that closelyrelated species within a single taxon may not necessarily have similar responses to climate change. In an ecological context, this conclusion is perhaps unsurprising as single taxonomic groups contain species with a variety of niches, life histories, reproductive strategies, habitat specialisations, and climate sensitivities, and therefore would be expected to vary in their rates of range shift. My results indicate that species within taxonomic groups should be investigated individually to quantify specific responses to climate change. Variation in range shift within taxonomic groups may be driven by a few species, where most species are responding in a similar manner, but a few make large retractions or expansions, which has been observed in grasshoppers and crickets (Beckmann *et al.*, 2015). Therefore, average range shifts should be taken as general observations about groups of species, and these average shifts may not be indicative of rates of individual species' range shifts.

Another discovery of my research is that some taxonomic groups appear to be increasing their rates of range shifting over time. For example, butterflies and macromoths shifted their northern range margins faster in interval 2, compared to interval 1 (Chapter 2). Past changes in rates of range shift have been measured over coarse spatial and temporal scales (Jackson *et al.*, 2000; Davis & Shaw, 2001), and few studies have considered changes in rates of range shifts over recent time scales. One example is the work of Mair *et al.* (2012), who measured range shifts in British butterflies from 1970 to 2009. They noted that species had faster rates of shifting in the second time interval (1.29 km yr $^{\text{-}1}$  on average; 1995-1999 to 2005-2009) than the first (-0.17 km yr<sup>-1</sup> on average, 1970-1982 to 1995-1999), despite a smaller increase in warming in the second time period (0.03 °C yr<sup>-1</sup> vs. 0.01 °C yr<sup>-1</sup>). In my study, I did not observe a statistically significant change in mean annual temperature between intervals. It is possible that the statistically significant increase in autumn (September, October, November) temperatures over interval 2 (0.46 °C decade<sup>-1</sup>) contributed to increases in rates of range shift in Lepidoptera, given that this was when most warming was detected (Chapter 2, Figure 2.4, Table A2.6). Warm autumn temperatures may delay insect diapause, allowing individuals to remain active for longer periods, potentially dispersing further. However, in spite of the many ecological processes that occur in autumn, the impacts of changing autumn temperatures on species is relatively unknown (Gallinat *et al.*, 2015), and warrants further study.

In Chapters 2 and 3, I examined rates of range shift and found that while the majority of species are shifting northward, some species have not shifted far or have retracted their ranges southwards (e.g. 20% of species' range margins retracted southwards in Chapter 3). This is consistent with other studies; slower rates or lags in response to climate change have been noted in a variety of taxa including birds (Devictor *et al.*, 2008), fish (Comte & Grenouillet, 2013) and butterflies (Devictor *et al.*, 2012). Invertebrates, which most of my study species were, tend to have rapid generation times and high fecundities, giving them an advantage in tracking climate change. However, some invertebrate species may be delayed in responding immediately to climate change due to limited dispersal capabilities, or there may be physical barriers such as mountains or coastlines, or regions of intensive agriculture, that prevent them from doing so (Parmesan & Yohe, 2003). Retractions at leading-edge range margins are a result of local extinctions, and for warm-adapted species in the UK, indicate that unfavourable climatic conditions (Thomas *et al.*, 2006) or other, non-climatic factors such as habitat loss are probably influencing species occupancy of these sites. Habitat, species' traits, climate and biotic

interactions have all been suggested as being important to range shifts, and hence I discuss them in the following sections.

### 5.3 Habitat and trait drivers of range shift variation

In Chapter 3, I found that habitat availability, which arises from the interplay with species' attributes and the environment, affected rates of range shifting in multiple taxonomic groups. Whilst habitat is commonly assumed to be important to species' range shifts, this idea is rarely directly tested among different taxa, and those tests that do exist often use methodological simplification, such as expert opinion (Warren *et al.*, 2001). One of my key findings was that species' attributes (habitat specialism) did not explain much variation in range shifting when studied alone (only ~4% across 347 species). In contrast, but when habitat associations were combined with a landscape context (i.e. the amount and distribution of suitable habitat), the explanatory power was much higher (up to 36%, and as much as 49% under an assumption of extensive recording). Thus, I conclude that whilst species' attributes may be influential to rates of range shift, it is the context of the landscape where species are found that determines the impacts of species' traits on range shifting, as species can only utilise habitat that is accessible to them. These results are of general importance, both for the fundamental ecological understanding of species' range dynamics, and to identify effective habitat management and restoration strategies, which can facilitate range expansions of species for which habitat availability is limiting (for example, Great Crested Newts experiencing southwards retractions, which is likely caused by the absence of suitable breeding ponds, see Rannap et al., 2009). In this next section, I discuss the impacts of habitat availability and species' traits on variation in range shifting, and then discuss other potential drivers of variation in range shifting in the next section.

The impacts of species' traits on rates of range shifting have been investigated many times in recent years. In a key study, Angert *et al.* (2011) tested the influence of different species' traits (e.g. dispersal rates, physiology and habitat specialism) on rates of range shifting for four taxonomic groups (mammals, birds, dragonflies and alpine plants). They found only weak associations between traits and rates of shift, with only 3-6% of range shift variation explained by traits. Because there are many species' attributes, and different methods to measure them, understanding the role of species' characteristics on range shifts is not a simple task. MacLean & Beissinger (2017) published a recent review and meta-analysis of trait studies across multiple

taxa, including more species than Angert *et al.*, and analysed the effect sizes of different traits on variation in range shifts. Habitat breadth (the number of habitats a species occupies) in some studies had significant positive impacts, so that generalists moved further than specialists. However, an important point noted by these authors is that effect sizes of habitat specificity varied across studies, and they suggested that this may be due to differences in the methods used to calculate specialism metrics. Coverage and quantity of data available may also contribute to differences in trait effect sizes, as my findings in Chapter 3 indicated that recording effort influenced the amount of variation explained by my models. While habitat specialism does appear to be important does appear to be an important influence on range shifts, many traits remain untested or have insufficient evidence to determine whether they impact range expansion (MacLean & Beissinger, 2017).

As part of my analysis on the influence of habitat availability on species' rates of range expansion, I used a metric which assessed specialism based on a species distribution modelling (SDM) approach (Julliard *et al.*, 2006). By using a logistic regression with a detailed, fine-scaled land cover map and long-term species presence data, I determined the likelihood of species' presences in different habitats. The species' specialism index (SSI) was the coefficient of variation calculated from these likelihoods. This methodology for quantifying habitat associations of species can potentially be applied to any species that has sufficient occurrence data (at least 50 occurrence records found in 100m cells containing one land use or habitat type), and where habitat data are present. Previous methods of measuring habitat specialisation of species have relied on expert opinion (Reif *et al.*, 2010), or on creating composite scores of ecological values (Oliver *et al.*, 2009), or on counting the number of habitats where a species is present (MacLean & Beissinger, 2017). Measuring habitat specificity objectively is difficult and many methods of calculation do not allow ecologists to compare across different taxa (Lawton, 1993; McGeoch & Latombe, 2016). The method I use addresses some of these issues, by providing a way of investigating species' habitat associations that is quantitative, comparable across taxa, and does not require in-depth ecological knowledge of species.

In my investigation on the impacts of habitat availability on range shift, I found that habitat availability at the northern range margin (relative to the whole range) had a significant effect on rates of range shift. In the UK, the quantity of upland and montane habitat increases with

latitude, and southern species that are specialised to lowland habitats may be less likely to have as much suitable habitat in the north of the country. Habitat generalists, utilising many habitats, and habitat specialists, that utilise montane and upland habitat, will be able to expand through these areas (excepting any non-habitat barriers). Therefore, habitat availability at the leading-edge margin, as determined by species' specialism, may be a critical barrier to British species' ability to track climate and expand their ranges. This has implications for conservation efforts, which can implement techniques to assist species to overcome problems caused by low habitat availability, which I discuss further below in Section 5.4.

## 5.4 Climate change and other drivers of range shifting

Habitat and species' specialism explained up to 36% of variation in range shifts (Chapter 3), yet much of the variation in rates of range shifting remained unexplained. Range shifts were examined as a response to climate change, however the degree to which climate drives variation in range shifts for multiple taxonomic groups (as opposed to other drivers such as habitat and species' traits) is largely unknown. A lack of abundance data or detailed understanding of population trends for most species meant that investigating species' sensitivity to climate, as a driver of range shift variation, was not possible in my thesis. I found that range shifts, as well as habitat specialism and availability, are species-specific. This implies that the degree to which climate impacts species' rates of range shift may also be individualistic, an idea which is supported in the literature (Davis and Shaw, 2001, Parmesan *et al.* 2006), who suggest that past and present range shifts may be linked to species' climatic tolerances. The majority of studies focus on single dimensions of climate i.e. mean temperature changes, although species are likely to respond to several different aspects of the climate, such as rainfall and seasonal temperatures. Variability and declines in species' populations as a response to climatic extremes have also been shown to be highly individualistic (Palmer *et al.*, 2017), which is why proxy metrics for population variability would be beneficial to ecologists wishing to assess species' status under climate change. I discuss my attempts to produce a proxy measure of abundance changes below (section 5.6.1)

Because different environmental processes impact species' responses to climate change, there is much uncertainty around the extent to which these factors interact. Many biotic factors influence range shifts, such as interspecific competition, population dynamics and predation (Van der Putten *et al.*, 2010). Mair *et al.* (2014) found that the importance of habitat availability

(measured as the proportion of a butterfly's breeding habitat in the landscape) was moderated by species' population trends. Population growth was a key predictor of range margin shift, because stable and increasing population produce individuals which can disperse and establish further populations. This suggests that habitat creation and restoration to improve availability will not help declining species unless these conservation practices also have positive effects on population trends. Abundance trend data were not available for most of my study species, and so I could not test the importance of population trends on range shifting in my study, but further research could investigate whether habitat availability as measured in this thesis also interacts with abundance to influence range expansion.

### 5.5 Conservation management

Under climate change, species may respond to altered environmental conditions by exhibiting phenotypic plasticity, adapting *in situ*, moving to environments that are more suitable, or by going extinct. My findings suggest that while some species are able to shift their ranges to track climate change, other species are shifting their ranges at a slower rate or not at all. The failure of species to shift their ranges in response to environmental change may result in local or, eventually, global extinction. Therefore, conservation strategies can be implemented to facilitate range shifting for these at-risk species. Several techniques are available to do this, by tackling different constraints that limit dispersal and the colonisation of new habitats. These include the role of protected areas, habitat connectivity, and human movement of species (through reintroductions and translocations). I will introduce each of these techniques and their advantages and disadvantages.

### 5.5.1 Protected areas and connectivity

This thesis demonstrates that habitat availability is important for species' range shifts, and so conservation could aim to maintain the quantity and quality of suitable habitat, which will act to both provide breeding habitats for species to establish populations, and suitable habitats which will help species move through landscapes (Thomas & Gillingham, 2015). Protected areas (PAs) are a longstanding method for conserving species where a specific area of land is afforded special status, forbidding certain human activities in it and/or promoting beneficial management. Over 18% of land in the European Union is protected under the Natura 2000 network (European Environment Agency, 2015), and the UK has many types of PA, depending on the conservation need. These areas are designated by governmental and public bodies, and

include National Nature Reserves, Sites of Special Scientific Interest, and Special Areas of Conservation.

As species are shifting their ranges under climate change, there has been concern that species currently protected by PAs, would shift outside of these regions, reducing conservation protection of vulnerable species and therefore the conservation value of PAs. Thomas and Gillingham (2015) reviewed the impacts of protected areas for species under climate change and found that while some species shifted their ranges out of protected areas, others persisted or colonised PAs as they shifted polewards. Thus, one benefit of PAs is that they may act as breeding sites for colonising species, and hence help facilitate range shifts (Thomas *et al.*, 2012). PAs have also been referred to as 'landing mats' and 'stepping stones' due to their role in allowing species to establish populations and move polewards beyond PA borders (Thomas & Gillingham, 2015). In addition, PAs support retracting species, which have showed increased persistence within protected regions (Gillingham *et al.*, 2015). PAs benefit species and their range shifts by maintaining the amount of available habitat in the landscape through management and protection, and conservation efforts should maintain these areas for species.

Protected areas can also provide connectivity benefits, which are key management strategies for facilitating species' range shifts (Saura *et al.*, 2014). As the climate changes, functional connectivity is important for many southern species in the UK, so they can disperse across landscapes and colonise climatically-suitable habitats. Enhancing habitat connectivity is done through the (re)creation and maintenance of new or existing habitat. Computer modelling studies have been used to assess how species will move through landscapes (Hodgson *et al.*, 2012), identifying colonisation routes through different landscape structures (Hodgson *et al.*, 2016a) and suitable sites to create and restore habitats. Being able to identify how species move through landscapes, and therefore which habitat patches, corridors and conservation techniques are associated with high levels of dispersal and range expansion is a vital tool for conservationists to implement evidence-based management for range shifting species (Baguette *et al.*, 2013). Connectivity measures can be variable in their success, for example, wildlife road tunnels, designed to allow species such as great crested newt (*Triturus cristatus*) to transverse underneath, are often not utilised by individuals (Matos et al., 2017). These results suggest that careful monitoring is required to check the success rate of connectivity measures, with reassessment of conservation strategies based on the latest evidence.

### 5.5.2 Reintroductions and translocations

My results demonstrate that species with less habitat availability at their northern range margins will be less likely to shift northwards into newly climatically suitable areas. Creating new habitat or linking habitats together is not always feasible, and so conservationists transport species to new areas, bypassing barriers to species' dispersal that prevent recolonisations. Reintroduction is the practice of moving individuals of a species to establish a new population, in a location where the species was previously present but became locally extinct. Translocation involves the same actions, but species are moved to locations where they are not know to have existed previously, but where conditions are now suitable.

Reintroductions are undertaken in order to rebuild populations where they are known to have been established in the past. The motivations for doing so may be to protect species from extinction, return ecosystems to a 'traditional' state, or to reap ecosystem service benefits from the reintroduction. A case study is the reintroduction of the large blue butterfly (*Maculinea arion*) to England, after total extinction in the UK in 1979 (Thomas, 1995). The large blue is an endangered species, with a globally declining population. The extinction of this species in Britain is thought to have been driven by changes in agricultural practises, coupled with specific needs to support a complex life cycle. Reintroductions have taken place at several locations, and the butterfly has been successfully re-established in England, 33 years after the first reintroduction in 1984. This example demonstrates that reintroductions can benefit endangered species that have become locally extinct. However, if climate change makes an environment unsuitable for a species, then there is no logic in reintroduction (Seddon, 2010), as re-establishment sites must meet the species' requirements for long-term persistence. Conservationists must consider not only how suitable a potential habitat is now, but also how suitable it will be in the future as the climate continues to change. In 2013, the IUCN released guidelines on releasing species to indigenous and non-indigenous habitats, emphasising that for reintroductions, the causes of extinction must be removed or sufficiently reduced before any action is taken (IUCN/SSC, 2013). This is why translocations should be preferred in cases where climate-driven extinctions occur (Thomas, 2011): species can be moved outside their indigenous ranges, and ecosystems which lose species of important functional groups can acquire different non-indigenous species which fulfil those roles. Certain types of habitat are becoming climatically unsuitable for the species which traditionally dwelt there, such as

montane habitat (Hoegh-Guldberg *et al.*, 2008). Species have been noted to shift to higher elevations under climate change (Hickling *et al.*, 2006; Chen *et al.*, 2011b), and translocations to higher regions outside of species' indigenous ranges (if possible) may be the only option for conservation beyond committing species to extinction. Translocations can assist species that have barriers to dispersal (e.g. physical barriers such as mountains, or threats to population growth such as disease, competition or predation) and are restricted to isolated habitats. Where habitat has become unsuitable, careful management and restoration can make conditions suitable for reintroductions. In order to help species respond to climate change, these activities are likely to become a vital part of conservation management.

Human movement of species has many benefits but it also comes with risks. Dealing with the logistics of capturing individuals, moving them, monitoring their progress, costs time and money, and can have legal constraints, especially if these actions occur over country borders (Hoegh-Guldberg *et al.*, 2008). Many introduction attempts fail, which can reduce species' populations; all such projects require careful planning and management (IUCN/SSC, 2013). When species are introduced to new areas, there is always uncertainty of how species will fit in the pre-existing ecological networks. A famously disastrous example is the release of the cane toad *Bufo marinus* into Australia to act as biocontrol for beetles that fed upon sugar cane crops, whereupon the toads became invasive pests. To prevent similar problems occurring, conservation actions that involve moving species must be carefully planned.

To summarise, there are effective conservation strategies available to assist species under climate change. Conservation management practices tend to be undertaken by conservation charities or government agencies which either target taxonomic groups (e.g. in the UK the charity Butterfly Conservation) or geographic areas (e.g. National Park Authorities and Wildlife Trusts). These groups need to manage habitats to support the general ecological requirements of species according to their rates of range shift, helping maintain breeding habitats to support populations, improving connectivity to facilitate range expansions, and moving species to establish populations in suitable locations when necessary and appropriate.

## 5.6 Recording species: applications and future prospects

Throughout this thesis, I stress the importance of measuring biogeographical responses to climate change across multiple taxonomic groups. My results endorse the value of citizen science data for measuring these responses, using these data to estimate range shifting rates, and factors affecting range shifts, including habitat availability. Data derived from citizen science schemes can address many ecological questions. In this thesis, I have focussed on occurrence data from citizen science schemes, but other sorts of data can be derived from voluntary mass participation activities such as Zooniverse, where members of the public extract scientific information from images, e.g. population sizes from pictures of penguin colonies (Simpson *et al.*, 2014). Here I discuss how I have used occurrence records to estimate population trends and my thoughts on the future of recording for ecological research.

### 5.6.1 Measuring population variability

In my thesis, I decided to take a different approach in Chapter 4, and explored the potential for distribution data to act as a proxy for abundance data, as abundance is a valuable metric that can be used to measure species' responses to environmental change. By doing this, I provided new evidence that population variability information could be obtained from distribution data for some British butterfly species, particularly species with highly-fluctuating populations. Interannual fluctuations in population are often linked to weather variation, with climate change causing positive or negative impacts depending on species' climatic tolerances. Martay *et al.* (2016) used inter-annual variation in abundance to assess the impacts of climate change on mammal, bird, aphid, and Lepidoptera species, and concluded that climate change is causing population declines in many species, while promoting increase in other species. McCain *et al.* (2016) carried out simulations to test the impacts of population variability on estimates of population trends and range shifts. They found that when abundances were low, but highly variable, there was a 50% chance of detecting local extinctions where none occurred, and moderate to high variability in abundance produced a bias towards detecting false range expansions and contractions. This means that population variability influences detections of range shifts and other responses to climate change. To accurately measure these responses, ecologists need to develop methods to estimate these abundance patterns for species without detailed population data.

There are several avenues for further research after my exploration of a potential abundance proxy; firstly, whether other groups with abundance data (macromoths and birds) demonstrate similar relationships between abundance and distribution metrics, as my research as only examined butterflies. The second question would be whether this abundance and distribution relationship is observed in other groups, most of which have no abundance data. This is an interesting and important question because taxonomic groups that are lacking in detailed abundance information would benefit most from an accurate proxy metric, providing new data on how the populations of those species change and respond to changes in their environment, particularly climate change. To explore this question, I would investigate the how reducing the level of recording intensity would impact the relationship between year-to-year changes in abundance and numbers of distribution records. My study was focussed on a taxonomic group (butterflies) with widespread intensive recording effort, however this level of recording effort is not common across all taxonomic groups (Chapter 2, Figure 2.2). Using the butterfly distribution data, subsampling methods would be applied to test how recording intensity (and variation in recording effort in time and space) affects the capability of occurrence records to measure population variability. These additional investigations further explore the potential for citizen science data to provide metrics of population dynamics.

### 5.6.2 Future of recording

As the trajectory of climate change and habitat loss, and consequently their impacts, are set to continue (Frishkoff *et al.*, 2016), and ecologists should explore methods for encouraging widespread species monitoring, to provide data to examine these impacts. One of the main concerns for recording species' responses to climate change is encouraging the monitoring of a wide array of species, so that ecologists can observe responses in different types of species in different environments. While I have demonstrated the heterogeneity of responses across multiple species and groups in this thesis, the majority of species that are included belong to invertebrate families. Invertebrates are only one part of biodiversity, though a large one. It is important that other taxa such as mammals, fish, plants, fungi and others are studied to examine how these species are responding to climate change. Some groups are not included in this thesis because I focused upon groups with the best data availability. For example, Hickling *et al.* (2006) included fish in their analyses, but data from this scheme were insufficient for my study. The National Amphibian and Reptile Recording Scheme (NARRS) has experienced a

decline in recording effort in recent years, although work has been done to engage more volunteers in herptile recording activities. It is important that schemes are maintained because many taxonomic groups suffer from a recording deficit. Groups like bryophytes, fungi and reptiles each contribute roughly 1% to the Global Biodiversity Information Facility (GBIF) records dataset, whereas birds make up over 50% (Chandler *et al.*, 2017). These numbers do not reflect the true global biodiversity of these groups, of which bryophytes (0.0008%), reptiles (0.0004%), and birds (0.0005%) comprise only a small proportion, and fungi contain a larger share (5.2%, all percentages calculated from Chapman, 2009). To get a full picture of ecosystem-wide responses to climate change, we need to encourage recording of species across the tree of life, and one of the problems that ecologists face is how to encourage recording of cryptic and uncharismatic species, which may be of ecological importance.

Species monitoring benefits from new technologies, as many improvements are made to assist and speed up the recording process. This includes apps that help the identification of species, geolocation on smart devices which pinpoint the location to fine-scale accuracy, and internet connections which allows instant submission of records. Apps also allow rapid responses to the detection of invasive species, for example, the Asian Hornet Watch app was created in response to a sighting of an Asian hornet in Gloucestershire in 2015, to help people distinguish between European and Asian hornets. The iGrasshopper app uses acoustic identification to detect species by their calls, with no visual identification required. eDNA and barcoding techniques can be used to classify species by their genetic material. Drones flying on fixed routes can survey sites for species (Hodgson *et al.*, 2016b), and this has been accomplished for bat surveys in Oxfordshire. Hence spatial and temporal coverage of species records has greatly increased, improving ecologists' ability to monitor species and their responses to climate change.

## 5.7 Conclusion

By examining species' responses to climate change, my study has highlighted the variation in range shifts that is present within and between taxonomic groups. For the first time, within and between group variation has been compared and my findings demonstrate that differences in range shifts are larger within taxonomic groups than between groups, supporting previous work which has inferred this result (Chen *et al.*, 2011a). While the causes of this variation are uncertain, my research points to a substantial proportion (up to a third) being explained by species' traits that affect habitat use and habitat availability. My findings have broad implications for conservation management, which can identify species that cannot access suitable habitats, and take steps to facilitate range expansion or support population sizes. My investigations were only possible due to the enormous amount of data held in citizen science schemes, and in this thesis I also demonstrated how occurrence records derived from such schemes have the potential to show patterns of population variability where abundance data are lacking. The creation and maintenance of these schemes should be encouraged, so that a greater variety of species' responses to climate change can be explored in future.

# Appendix Chapter 2

*In Chapter 2's appendices, group names with asterisks (\*) indicate that those groups contain allied species, i.e. species which are phylogenetically related, such as dragonflies and damselflies.*

**Table A2.1.** List of taxonomic groups considered for analysis: the number of species (not all of which qualify for analysis) and observations (records) across all time periods for all species for each taxonomic group that was analysed. Taxonomic groups were either accepted or rejected for analysis in interval 1, interval 2 or over both intervals according to whether they met the selection criteria (see methods in main text).



Groups rejected from all analyses were: auchenorrhyncha, click beetles, craneflies, fleas, gelechiid moths, jewelled beetles, lacewings, long horned beetles, mayflies, non-marine molluscs, plantbugs and allies, plume moths, predaceous diving beetles, soldier beetles\*, ticks, and water scavenger beetles

**Table A2.2.** Overall mean rate of range margin changes (and SEs) across taxonomic groups, calculated for interval 1 and interval 2, and for each level of recording effort control. Means were calculated by taking the average of the mean rate of range margin change of all taxonomic groups included. With the number of groups is the number of those (in parentheses) which are significantly expanding northwards (see Table A2.3). Total numbers of species included in each estimate are shown. The ANOVAs compare mean rate of range margin changes across the groups, for each level of recording effort control in each interval; significant results indicate that taxonomic groups differ in northwards range shifts.


**Table A2.3.** Summary table and statistics for Figure 3: mean rate of range shift and 95% confidence interval (CI) for each taxonomic group, for each interval, and for each level of recording effort. Numbers of hectads (No. hectads), the number of species per group (No. spp), and results of one-sample t-tests to assess whether shifts for each group differ from zero (significant p values in bold) are also given.





**Table A2.4.** Northern range margin locations (in metres, on the GB Ordnance Survey Grid) during interval 1 of all species included in Figure 3, for each time period, T1 (1966-75) or T2 (1986-1995), and for each level of recording effort control (Recorded, Well Recorded or Heavily Recorded). For bird species, the time period years are 1968-72 for T1 and 1988-1991 for T2. Margin values which are denoted as 'C' indicate confidential data. Note that for species which also qualify for analysis in interval 2, the calculation of range margin locations for 1986-1995 in interval 2 (in Table A2.5) will differ from values for 1986-1995 in interval 1 due to a different set of hectads being analysed.



































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**Table A2.5.** Northern range margin locations (in metres, on the GB Ordnance Survey Grid) during interval 2 of all species included in Figure 3, for each time period T2 (1986-1995) or T3 (2001-2010) and for each level of recording effort control (Recorded, Well Recorded or Heavily Recorded). For bird species, the time period years are 1988-1991 for T2 and 2007-2011 for T3. Margin values which are denoted as 'C' indicate confidential data. Note that for species which also qualify for analysis in interval 1, the calculation of range margin locations for 1986-1995 in interval 1 (in Table A2.4) will differ from values for 1986-1995 in interval 2 due to a different set of hectads being analysed. Ground beetles are denoted by 'G beetles'.




























































**Table A2.6.** Seasonal and annual temperature trends across the study period (1966-2010). P values in bold denote a significant change in the temperature measurement over each interval period. Seasons are defined by three month bins: Winter (December, January, February; assigned to the year represented by January and February); Spring (March, April, May); Summer (June, July, August); Autumn (September, October, November). The annual temperature of year T is, thus, the average temperature taken across December of year T-1 and January through November of year T.



**Table A2.7**. Summary table and statistics for Figure 4 (taxonomic groups studied over both intervals). Mean rates of range margin change were compared between the two intervals using paired t-tests (species as pairs; shifts that are significantly different from zero are given in bold).

|                    | Level of         | Number  |     | Interval 1                   |        | Interval 2                   |        | paired t test |         |         |
|--------------------|------------------|---------|-----|------------------------------|--------|------------------------------|--------|---------------|---------|---------|
| <b>Taxonomic</b>   | recording effort | οf      | No. | Mean range shift             |        | Mean range shift             |        |               |         |         |
| group              | control          | hectads | spp | $(km$ decade <sup>-1</sup> ) | 95% CI | $(km$ decade <sup>-1</sup> ) | 95% CI | df            |         | p value |
| <b>Birds</b>       | Well recorded    | 2561    | 31  | 7.7                          | 15.8   | 6.3                          | 21.6   | 30            | 0.12    | 0.908   |
| <b>Birds</b>       | Heavily recorded | 2500    | 31  | 6.7                          | 16.3   | 6.5                          | 20.8   | 30            | 0.02    | 0.983   |
| <b>Butterflies</b> | Well recorded    | 1729    | 35  | 18.3                         | 8.0    | 30.3                         | 10.7   | 34            | $-2.26$ | 0.030   |
| <b>Butterflies</b> | Heavily recorded | 1218    | 35  | 16.9                         | 8.2    | 28.0                         | 9.5    | 34            | $-2.26$ | 0.031   |
| Dragonflies*       | Well recorded    | 414     | 7   | 32.0                         | 13.3   | 43.3                         | 23.8   | 6             | $-1.32$ | 0.236   |
| Dragonflies*       | Heavily recorded | 119     | 7   | 25.1                         | 7.5    | 37.4                         | 23.8   | 6             | $-1.00$ | 0.356   |
| <b>Macromoths</b>  | Well recorded    | 477     | 132 | 11.4                         | 4.4    | 31.2                         | 6.5    | 131           | $-5.77$ | < 0.001 |
| <b>Macromoths</b>  | Heavily recorded | 205     | 132 | 9.4                          | 3.3    | 26.1                         | 5.6    | 131           | $-5.41$ | < 0.002 |

**Table A2.8.** Northings (in metres, on the GB Ordnance Survey Grid) of all 205 species included in Figure 4, with their northern range margin locations for each time period, for well-recorded and heavily-recorded cells that were common to all three time periods (T1: 1966-75, T2: 1986- 95, T3: 2001-2010). Note that for bird species, the time period years are 1968-72, 1988-1991, and 2007-2011.











**Table A2.9.** Results of linear mixed effects models for the rate of range margin change between two intervals spanning 1966-2010 (response variable is change in northern range margin in km per decade), for well-recorded and heavily-recorded hectads. Numbers in cells show differences in Akaike information criterion (ΔAIC) values between the best model (shown as 0.0) in each column and the other models. Comparisons with all four taxonomic groups included ('All groups'), models excluding each taxon in turn (columns 6-9), and models excluding both butterflies and macromoths ('Without Lepidoptera'), all found that the best model was always the one that included an interval\*group interaction term (these models also included group and interval as fixed effects). The numbers of species given in each column (in parentheses) are the numbers of species remaining in the analysis after the specified taxonomic group(s) had been excluded.



**Table A2.10.** Results of ANCOVAs of seasonal and annual temperatures in each interval. Seasons are defined by three month bins: Winter (December, January, February); Spring (March, April, May); Summer (June, July, August); Autumn (September, October, November); annual as December year t-1 through to November year t. Intervals are as follows: Interval 1: 1966-1995, Interval 2: 1986- 2010, all years inclusive. There was no significant change in the rate of seasonal or annual temperature change between the two intervals, except for mean autumn temperature, which significantly increased between intervals.





Figure A2.1. Comparison of mean rates of range margin change calculated for four taxonomic groups when the hectads selected for analysis are common to two time periods in a single interval or the subset of hectads common to intervals 1 and 2.



Figure A2.2. Comparison of mean rates of range margin change for common species in three taxonomic groups across two intervals (as in Figure 2.4).

## Appendix Chapter 3

**Table A3.1.** (see next page) Details of citizen-science recording schemes. Data were obtained on 02 June 2017 from the UK Biological Records Centre (https://www.brc.ac.uk/theme/datasets), and represent *ad hoc* point observations at or near breeding sites (but see Remarks). Recording level is the number of 10-km grid squares (out of a possible 2566 in the study area) where at least 10% or 25% of the regional species pool was sampled in both recording periods (1976-1990 and 2001-2015).



**Table A3.2.** Descriptive statistics for species' range shifts (km  $y<sup>-1</sup>$ ), detailed by taxonomic group. Positive values indicate northward (poleward) expansion, negative values indicate southward retreat, measured over a 25-year period (1976-1990 to 2001-2015). Range shifts varied significantly between taxonomic groups  $(F_{13, 333} = 2.503, P = 0.003)$ , with group explaining 9% of the variation in linear regression.



**Table A3.3.** Descriptive statistics for species' specialisation indices (SSIs), detailed by taxonomic group. Low values indicate a generalist, and high values indicate a high level of habitat specialisation. Specialisation varied significantly between taxonomic groups ( $F_{13, 333}$  = 1.919, *P* = 0.027), with group explaining 7% of the variation in linear regression.


**Table A3.4.** Descriptive statistics for habitat availability at the range margin (%), detailed by taxonomic group. Values in parentheses are on the  $log_{10}$  scale used in models of range shift. Log<sub>10</sub>-habitat availability varied significantly between taxonomic groups ( $F_{13, 333}$  = 4.443,  $P$  <  $10^{-6}$ ), with group explaining 15% of the variation.

| Taxonomic group             | Median |        | Mean |        | <b>SD</b> |        | Min |           | Max  |        |
|-----------------------------|--------|--------|------|--------|-----------|--------|-----|-----------|------|--------|
| Aquatic bugs                | 7.1    | (0.85) | 11.9 | (0.99) | 8.3       | (0.28) | 4.6 | (0.66)    | 26.8 | (1.43) |
| <b>Bees</b>                 | 7.5    | (0.88) | 9.2  | (0.90) | 5.5       | (0.23) | 3.6 | (0.56)    | 23.5 | (1.37) |
| <b>Butterflies</b>          | 7.5    | (0.87) | 12.8 | (0.91) | 13.7      | (0.43) | 1.3 | (0.11)    | 55.7 | (1.75) |
| Dragonflies and damselflies | 13.4   | (1.13) | 16.3 | (1.12) | 10.9      | (0.33) | 3.6 | (0.56)    | 36.4 | (1.56) |
| Grasshoppers and allies     | 5.3    | (0.71) | 10.4 | (0.81) | 9.4       | (0.47) | 1.5 | (0.17)    | 28.7 | (1.46) |
| Ground beetles              | 5.5    | (0.74) | 5.8  | (0.74) | 2.1       | (0.14) | 3.4 | (0.53)    | 10.7 | (1.03) |
| <b>Hoverflies</b>           | 3.5    | (0.54) | 4.5  | (0.58) | 3.4       | (0.26) | 1.4 | (0.14)    | 15.5 | (1.19) |
| <b>Macromoths</b>           | 7.8    | (0.89) | 9.5  | (0.84) | 7.1       | (0.38) | 0.4 | $(-0.41)$ | 35.4 | (1.55) |
| Non-marine molluscs         | 8.1    | (0.91) | 11.2 | (0.98) | 6.8       | (0.28) | 4.6 | (0.66)    | 21.6 | (1.33) |
| Shieldbugs and allies       | 12.6   | (1.02) | 14.0 | (1.03) | 10.2      | (0.37) | 4.3 | (0.64)    | 26.4 | (1.42) |
| Soldierflies and allies     | 4.6    | (0.67) | 6.0  | (0.72) | 3.3       | (0.22) | 2.3 | (0.35)    | 15.5 | (1.19) |
| <b>Spiders</b>              | 3.6    | (0.55) | 4.6  | (0.56) | 3.5       | (0.30) | 1.1 | (0.04)    | 15.4 | (1.19) |
| Wasps                       | 7.2    | (0.86) | 8.7  | (0.85) | 6.1       | (0.29) | 2.5 | (0.40)    | 22.3 | (1.35) |
| Woodlice                    | 3.4    | (0.53) | 3.6  | (0.52) | 1.6       | (0.19) | 1.9 | (0.28)    | 5.9  | (0.77) |
| All groups                  | 6.2    | (0.79) | 8.7  | (0.81) | 7.3       | (0.35) | 0.4 | $(-0.41)$ | 55.7 | (1.75) |

**Table A3.5.** Descriptive statistics for habitat availability at the range margin, as a percentage of the range-wide average, detailed by taxonomic group. Low values indicate habitat-poor margins relative to the average across a species' range; high values indicate habitat-rich margins. This variable did not vary significantly between taxonomic groups (*F*13,  $333 = 0.859$ ,  $P = 0.598$ ), with group explaining 3% of the variation.





\*\*\*, *P* < 0.001; \*\*, *P* < 0.01; \*, *P* < 0.05 (t-tests using Satterthwaite approximation)

**Table A3.6.** Linear mixed-effects models of range shift (km y<sup>-1</sup>) *vs*. habitat specialisation (SSI),  $log<sub>10</sub>$ -habitat availability at the range margin (HA), and margin habitat relative to the range-wide average for a species (HR). We fitted models using the R function 'lmer' via maximum likelihood, with all predictors centred and scaled. The grouping variable for random effects was taxonomic group. For each set of fixed effects, we tested models with a random intercept only, and models with both random slope and intercept terms (with either uncorrelated (||) or correlated (|) random effects). In each case, coloured text identifies the top model (lowest conditional AIC), as reported in the main text and applied to the subsets of groups in Figure 3.3.

**Table A3.7.** R packages used in the analysis (in addition to base R).



Table A3.8 Study results summarised for 347 species: range shifts, specialisation index scores, habitat availability at the margin and at the margin vs across the whole range. Range shifts in the polewards range margin are given in km per year. The specialisation index is the coefficient of variation across 18 habitat classes. Habitat availability at the margin is the mean species' probability of occurrence in a 50km buffer around the margin. Margin vs range-wide habitat availability is the division of margin habitat availability by the range-wide habitat availability.























**Table A3.9** Summaries of habitat associations for 352 species. The columns below show species' probability of occurrence values for 18 habitat classes derived from the Land Cover Map 2007. Four categories are the result of combining narrower categories: Heather and Heather Grassland became Dwarf Shrub Heath [1]; Supra-littoral Rock and Littoral Rock became Coastal Rock [2]; Supra-littoral Sediment and Littoral Sediment became Coastal Sediment [3]; Suburban and Urban became Built-up and Gardens [4].





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 $\overline{\phantom{a}}$ 



Macromoths











' molluscs











## Appendix Chapter 4

**Table A4.1.** Results of the best model explaining the inter-annual distribution-abundance relationship. Two outlying species, *Celastrina argiolus* and *Vanessa cardui* were excluded from this analysis. One biogeographical attribute was included as an explanatory variable: mean absolute year-to- year change in distribution records. PGLS model results:  $\lambda$  = 0.049,  $R^2$  = 0.43, F<sub>1,28</sub> = 20.86, AIC = -31.11, P = < 0.001.



**Table A4.2.** Results of two models examining the relationship between dispersal ability and the inter-annual distribution-abundance relationship. The explanatory variable in Model 1 is a dispersal ranking from Cowley et al. (2001), PGLS model results:  $\lambda$  = 0.904, R<sup>2</sup> = 0.13, F<sub>1,26</sub> = 3.776, AIC= -17.52, P = 0.063; and the explanatory variable in Model 2 is a dispersal score from (Dennis *et al.* 2004) PGLS model results: λ = 0.874, R<sup>2</sup> = 0.08, F<sub>1.26</sub> = 2.119, AIC = -15.78,  $P = 0.157$ .





**Figure A4.1.** The ranges of a) the small skipper butterfly, *Thymelicus sylvestris*, a species with a well-filled range (fractal dimension: 0.257), and b) the Grayling butterfly, *Hipparchia semele*, a species with the most minimally filled range of the 33 species studied (fractal dimension: 0.716).



**Figure A4.2.** The annual total number of distribution records for all 33 study butterfly species across the study period 1972–2012.
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