**Appendix E: R-code used for rarefaction of data**

# sample code for rarefaction of dataset

# Set the working directory to documents 2020 analyses

setwd("~/Raw Counts")

# load diversity dataset

RAW <- read.csv(raw data.csv')

#Install packages: vegan (with a lowercase v)

install.packages('vegan')

library('vegan')

#install fossil package too

install.packages('fossil')

library('fossil')

# Reformat the data set

# Make a matrix organised by changed over sample

RAWmatrix <- create.matrix(RAW, tax.name = "sample", locality = "species", abund = TRUE, abund.col = "abundance")

# Can only rarefy to the size of the smallest sample, if smaller than it is not changed

DMSrarefy <- rarefy(DMSRmatrix, 200)

# rarefaction curve for each row of the input data, evaluated using the interval of step sample size always including 1, and total sample size, if sample = TRUE a vertical line is drawn at sample (250) with horizontal lines for rarefied

# species richness

rarecurve(RAWmatrix, step=1, 200, xlab = "Sample Size", ylab = "Species", label = TRUE)

# rareslope will calculate the slope of rarecurve (derivative of rarefy) at given sample size

S <-specnumber(RAWmatrix) # observed number of species

(raremax <- min(rowSums(RAWmatrix)))

Srare <- rarefy(RAWmatrix,raremax)

plot(S, Srare, xlab = "Observed No. of Species", ylab = "Rarefied No. of Species")

abline(0,1)

# write data into CSVs

write.csv(RAWrrarefy, "DMSrrarefy200.csv")

write.csv(RAWrarefy, "DMSrarefy200.csv")

write.csv(RAWdrarefy, "DMSdrarefy200.csv")