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library(vegan)

##Read in data file, samples in rows, taxa in columns
rhm.data <- read.table (file = "RHM_data.txt", header=TRUE,
row.names=1)
##Read in sample info file, with formation and lithology for each
sample
rhm.info <- read.table (file = "RHM_info.txt", header=TRUE,
row.names=1)

##dataset details
dim(rhm.data)
sum(rhm.data)

##SAMPLE DATA FOR TABLE 5.1
results <- data.frame(rhm.info$Lithology, rowSums(rhm.data),
specnumber(rhm.data), t(rarefy(rhm.data, sample = 300, se =
TRUE))), diversity(rhm.data, index =
"invsimpson")/specnumber(rhm.data))
colnames(results) <- c("Lithology", "N", "S", "R300", "St. dev",
"E1/D")
write.table(results, "Table5.1.txt", sep = "\t", row.names = T,
col.names = T)

##INDIVIDUAL-BASED RAREFACTION CURVES
##Compute one rarefaction curve per sample
ind.rare.AC13 <- rarefy(rhm.data[1,], sample =
c(1:sum(rhm.data[1,])), se = TRUE)
ind.rare.AC12 <- rarefy(rhm.data[2,], sample =
c(1:sum(rhm.data[2,])), se = TRUE)
ind.rare.AC11A <- rarefy(rhm.data[3,], sample =
c(1:sum(rhm.data[3,])), se = TRUE)
ind.rare.AC009 <- rarefy(rhm.data[4,], sample =
c(1:sum(rhm.data[4,])), se = TRUE)
ind.rare.AC008 <- rarefy(rhm.data[5,], sample =
c(1:sum(rhm.data[5,])), se = TRUE)
ind.rare.AC006 <- rarefy(rhm.data[6,], sample =
c(1:sum(rhm.data[6,])), se = TRUE)
ind.rare.AC004 <- rarefy(rhm.data[7,], sample =
c(1:sum(rhm.data[7,])), se = TRUE)
ind.rare.AC002 <- rarefy(rhm.data[8,], sample =
c(1:sum(rhm.data[8,])), se = TRUE)

##Figure 5.2
plot(c(1:sum(rhm.data[1,])), ind.rare.AC13[1,], xlim = c(0,
1400), ylim = c(0, 50), xlab = "Number of specimens", ylab =
"Expected richness", type = "l", las = 1)
lines(c(1:sum(rhm.data[2,])), ind.rare.AC12[1,])
lines(c(1:sum(rhm.data[3,])), ind.rare.AC11A[1,])
lines(c(1:sum(rhm.data[4,])), ind.rare.AC009[1,])
lines(c(1:sum(rhm.data[5,])), ind.rare.AC008[1,])

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lines(c(1:sum(rhm.data[6,])), ind.rare.AC006[1,])
lines(c(1:sum(rhm.data[7,])), ind.rare.AC004[1,])
lines(c(1:sum(rhm.data[8,])), ind.rare.AC002[1,])

##RANK/ABUNDANCE PLOT
##Compute relative abundances for each sample, convert to
percentage, and plot as ranked abundances on a log scale
rhm.stand <- decostand(rhm.data, method = "total")
rhm.stand.percent <- rhm.stand*100

stand.AC13 <- rhm.stand.percent[1,]
stand.AC12 <- rhm.stand.percent[2,]
stand.AC11A <- rhm.stand.percent[3,]
stand.AC009 <- rhm.stand.percent[4,]
stand.AC008 <- rhm.stand.percent[5,]
stand.AC006 <- rhm.stand.percent[6,]
stand.AC004 <- rhm.stand.percent[7,]
stand.AC002 <- rhm.stand.percent[8,]

##Figure 5.3
plot(rev(sort(stand.AC009[stand.AC009>0])), type = "l", log =
"y", xlim = c(0, 50), yaxp = c(0.1, 2, 3), las = 1, xlab = "Taxa
in rank order of abundance", ylab = "Percentage of grains counted")
lines(rev(sort(stand.AC13[stand.AC13>0])), type = "l")
lines(rev(sort(stand.AC12[stand.AC12>0])), type = "l")
lines(rev(sort(stand.AC11A[stand.AC11A>0])), type = "l")
lines(rev(sort(stand.AC008[stand.AC008>0])), type = "l")
lines(rev(sort(stand.AC006[stand.AC006>0])), type = "l")
lines(rev(sort(stand.AC004[stand.AC004>0])), type = "l")
lines(rev(sort(stand.AC002[stand.AC002>0])), type = "l")

##SAMPLE-BASED RAREFACTION CURVES
##Compute sample-based rarefaction curves for lignite and clastic
samples. Use method = "exact" to get expected richness (y axis on
graph), and method = "rarefaction" to get average number of
individuals per sample (x axis on graph) (from $inindividuals
output for "rarefaction" method - spelling is correct!)

samp.rare.lig <- specaccum(rhm.data[rhm.info$Lithology ==
"Lignite",], method = "exact")
samp.rare.lig.ind <- specaccum(rhm.data[rhm.info$Lithology ==
"Lignite",], method = "rarefaction")

samp.rare.clast <- specaccum(rhm.data[rhm.info$Lithology ==
"Clastic",], method = "exact")
samp.rare.clast.ind <- specaccum(rhm.data[rhm.info$Lithology ==
"Clastic",], method = "rarefaction")

##Figure 5.4
plot(c(0, samp.rare.lig.ind$inindividuals), c(0,
samp.rare.lig$richness), type = "l", las = 1, xlim = c(0, 3500),

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ylim = c(0, 70), xlab = "Number of specimens (based on mean number
of specimens per sample)", ylab = "Expected richness")
lines(c(0, samp.rare.lig.ind$invididuals), c(0,
samp.rare.lig$richness)+1.96*c(0, samp.rare.lig$sd), lty = 2)
lines(c(0, samp.rare.lig.ind$invididuals), c(0,
samp.rare.lig$richness)-1.96*c(0, samp.rare.lig$sd), lty = 2)
lines(c(0, samp.rare.clast.ind$invididuals), c(0,
samp.rare.clast$richness))
lines(c(0, samp.rare.clast.ind$invididuals), c(0,
samp.rare.clast$richness)+1.96*c(0, samp.rare.clast$sd), lty =
2)
lines(c(0, samp.rare.clast.ind$invididuals), c(0,
samp.rare.clast$richness)-1.96*c(0, samp.rare.clast$sd), lty =
2)

##NMDS
##NMDS for non-unique taxa. Function call includes square root
transformation and Wisconsin standardisation
nm.ds.rhm <- metaMDS(rhm.data[,specnumber(rhm.data, MARGIN = 2) >
1])

##Preliminary plots with labels
plot(nm.ds.rhm, display = "sites", type = "t", las = 1, xlab = "NMDS
axis 1", ylab = "NMDS axis 2")
plot(nm.ds.rhm, display = "species", type = "t", las = 1, xlab =
"NMDS axis 1", ylab = "NMDS axis 2")

##Figure 5.5
plot(nm.ds.rhm, display = "sites", type = "n", las = 1, xlab = "NMDS
axis 1", ylab = "NMDS axis 2", shrink = FALSE)
points(nm.ds.rhm, display = "sites", choices = c(1,2), type="p",
pch = 2, cex = 1.5, rhm.info$Lithology == "Lignite", shrink = FALSE)
points(nm.ds.rhm, display = "sites", choices = c(1,2), type="p",
pch = 1, cex = 1.5, rhm.info$Lithology == "Clastic", shrink = FALSE)
points(nm.ds.rhm, display = "species", choices = c(1,2), type="p",
pch = 3, shrink = FALSE)

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