Stat 415 – Ecological Ordination – Fall 2011

Homework 2 answers

1) Continuation of Echinacea lipophyllic metabolites data set

a) mean within same species: 0.494, mean between species: 0.801

If you got 0.384 for within species, you included the 0’s on the diagonal with your mean. That isn’t appropriate.

b)



c) I would expect to reject the null hypothesis of no difference. The distances between pairs within the same species tend to be much smaller than those between pairs from different species.

d) No. A t-test assumes all observations are independent. Distances are not independent.

e) The Mantel r = 0.519, p = 0.001, Very strong evidence of at least one difference between species.

f) F = 6.89, p = 0.001, Very strong evidence of at least one difference between species.

g) Pur (E. purpurea) and Ten (E. tennessiensis) seem to differ most from the rest (see plot on next page)



h) betadisper(), F = 1.58, p = 0.16

2) Continuation of the Missouri Fish analysis

a) F = 2.55, p = 0.005, strong evidence of a difference in species composition between the three sites.

b) F = 3.38, p = 0.01, evidence of a difference in species composition between main and chute habitats.

c) F = 3.38 (same as before), p = 0.00998 (slightly different). The second analysis uses a different set of permutations.

My R code:

# My R code for HW 2

# Problem 1) more Echinacea lipophyllic metabolite analyses

# code below assumes lipo and lipo.m already created

lipo$spp <- substring(lipo$access,1,3)

lipo$spp.f <- as.factor(lipo$spp)

library(vegan)

lipo.canb <- vegdist(lipo.m, method='canb')

lipo.canbd <- as.matrix(lipo.canb)

lipo.DN <- outer(lipo$spp, lipo$spp, '!=')

# FALSE is same spp, TRUE is diff spp

# zeros on diagonal considered 'same spp', set to missing

diag(lipo.DN) <- NA

tapply(lipo.canbd,lipo.DN,mean, na.rm=T)

boxplot(split(lipo.canbd,lipo.DN), names=c('Within','Between'))

title("Canberra distance on Echinceae metabolites")

mantel(lipo.canb,lipo.DN)

adonis(lipo.canb ~ spp.f, data=lipo)

dimnames(lipo.m)[[1]] <- lipo$spp

lipo.mds <- metaMDS(lipo.m, 'canb', autotransform=F,expand=F, k=2)

plot(lipo.mds, display='sites', type='t')

ordihull(lipo.mds, lipo$spp)

lipo.bd <- betadisper(lipo.canb,lipo$spp)

anova(lipo.bd)

# problem 2: Missouri fish analysis

# code below assumes that fish, fish.m, fishenv, and fish.bray

# alread constructed and variables converted to factors.

# Uses Bray-Curtis distance (not specifically stated in the problem, but that is my default distance)

adonis(fish.bray~gear+habitat+site, data=fishenv)

adonis(fish.bray~gear+site+habitat, data=fishenv)