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###DISSIMILARITY MATRICES + MANTEL CORRELATION----------------------
##import data
spe <- read.delim("forest_JMK_species.txt", header=T, row.names=1)

#standardize to presence/absence data
#library(vegan)
spe.pa <- decostand(spe, "pa")
spe.pa[1:10,1:10]



#calculate dissimilarity matrices
beta.j <- vegdist(spe.pa, method = "jaccard")
head(beta.j)
class(beta.j)

#convert to matrix
beta.j.mat <- as.matrix(beta.j)
beta.j.mat[1:5,1:5]

betadiver(help=TRUE)
beta.b <- betadiver(spe.pa, method = "sim")

#calculate environmental and geographical distances
coord <- forest[, c("X",  "Y")]
geodist <- dist(coord, method = "euclidean")
envdist <- dist(env.tab.s, method = "euclidean")

#mantel correlation
m.geo <- mantel(beta.b, geodist, permutations=499)
m.env <- mantel(beta.b, envdist, permutations=499)

#plot relationship
plot(geodist, beta.b)
plot(envdist, beta.b)
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plot.data <- cbind(envdist, beta.b)

plot(plot.data, col = densCols(plot.data, colramp =
colorRampPalette(c("gray90", "gray10"))))
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