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setwd("D:/Data/aktuell/BESS/R_FoodWeb/specialisation")
require(bipartite)
# REQUIRES BIPARTITE VERSION 1.11 (or higher)!! (before the species names are
inconsistent and BC/CC incorrect)

#----- example network -----
exa <- matrix(0, 8,11)
exa[1,] <- c(100, 20, 20, 0,0,0,0,0,0,0)
exa[1:4,11] <- c(94,3,2,1) # as contrast to A
exa[1:5,2] <- c(22,21,20,19,18)
exa[2,4] <- 20
exa[6,5] <- 20
exa[1,6] <- 1
exa[3,7] <- 1
exa[7,8] <- 1
exa[c(5,8),9] <- 1
exa[1:5,10] <- 1
exa <- exa[,c(1,5,8,4,7,3,6,9,11,2,10)]
rownames(exa) <- letters[1:8]
colnames(exa) <- paste("S", c("1c", "2i", "2r", "3i", "3r", "4i", "4r", "5r", "6c", "7c", "7r"), sep="")

exa
# plot network:
windows(height=6, width=12)
quartz(height=3, width=6)
par(mfrow=c(1,2), mar=c(0,0,0,0))
plotweb(exa>0)
plotweb(exa)
require(sna)
gplot(exa>0, gmode="twomode", vertex.cex=2) # plot as binary graph!
gplot(as.one.mode(exa, weighted=F, project="higher")) # plot only the pollinator-projection

# calculate indices for this network
indices <- specieslevel(exa, index="ALLBUTD")$"higher trophic level"[-4]
write.table(round(indices[,c(1,2,5,6,7,3,4,9,10,11)], 3), file="exampleweb_indices.txt", sep="\t")
indices.red <- indices[, -c(2,8,10)]

#----- run null models for example web -----
# visualise the p-mat of the null model:
pweb <- tcrossprod(rowSums(exa), colSums(exa)/sum(exa))
dimnames(pweb) <- dimnames(exa)
visweb(exa, type="none")
visweb(round(pweb*10000), type="none")

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# generate null models and calculate their index values:
exanulls <- nullmodel(exa)
ex1 <- exanulls[[1]];dimnames(ex1) <- dimnames(pweb)
visweb(ex1, type="none")
# this will take some minutes:
exanull.res <- lapply(exanulls, function(x) specieslevel(x, index="ALLBUTD")$"higher trophic
level"[-c(2,4,9,11)])
save(exanull.res, file="exanulls.res.Rdata")

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# calculate z-scores:
z.mat <- matrix(0, 11, 8)
colnames(z.mat) <- colnames(indices)[-c(2,8,10)]
rownames(z.mat) <- colnames(exa)
for (i in 1:8){
  mean.n <- apply(sapply(exanull.res, function(x) x[,i]), 1, mean, na.rm=T)
  sd.n <- apply(sapply(exanull.res, function(x) x[,i]), 1, sd, na.rm=T)
  z <- (indices.red[,i] - mean.n)/ifelse(sd.n==0, 1, sd.n) # sd is 0 when null model values are
constant (i.e. mean.n==index);then the z-score should be 0
  z.mat[,i] <- z
}
z.mat
write.table(round(z.mat[,c(1,4,5,6,2,3,7,8)], 2), file="exampleweb_z.scores.txt", sep="\t")

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# calculate ROBUST z-scores:
z.rob.mat <- matrix(0, 11, 8)
colnames(z.rob.mat) <- colnames(indices)[-c(2,8,10)]
rownames(z.rob.mat) <- colnames(exa)
for (i in 1:8){
  median.n <- apply(sapply(exanull.res, function(x) x[,i]), 1, median, na.rm=T)
  IQR.n <- apply(sapply(exanull.res, function(x) x[,i]), 1, IQR, na.rm=T)
  z <- (indices.red[,i] - median.n)/ifelse(IQR.n==0, 1, IQR.n) # sd is 0 when null model values are
constant (i.e. median.n==index);then the z-score should be 0
  z.rob.mat[,i] <- z
}
z.rob.mat
write.table(round(z.rob.mat[,c(1,4,5,6,2,3,7,8)], 2), file="exampleweb_z.robust.scores.txt",
sep="\t")

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# calculate p-values:
# note that this is not entirely correct, because NAs will also lead to a p-value of 0!
p.mat <- matrix(0, 11, 8)
colnames(p.mat) <- colnames(indices)[-c(2,8,10)]
rownames(p.mat) <- colnames(exa)
for (i in 1:8){

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null.vals <- sapply(exanull.res, function(x) x[,i])
p2 <- 1:3
for (j in 1:11){ # for each species, calculate the number of times the null model value was
higher than the observed:
  p.lower <- null.vals[j,] < indices.red[j,i]
  p.higher <- null.vals[j,] > indices.red[j,i]
  p.equal <- null.vals[j,] == indices.red[j,i]
  sample.size <- NCOL(null.vals) - max(sum(is.na(null.vals[j,])), sum(is.na(p.lower)),
sum(is.na(p.higher)), sum(is.na(p.equal)))
  #p2[j] <- sum(p.higher)/sample.size
  p2[j] <- (min(sum(p.lower, na.rm=T), sum(p.higher, na.rm=T))+sum(p.equal, na.rm=T)) /
sample.size #turn this into probabilities, acknowledging possible NAs (in NSI!)
}
# p2 <- colSums(p, na.rm=T)/colSums(!is.na(p))
p.mat[,i] <- p2 #ifelse(p2>0.5, 1-p2, p2)*2 #two-tailed test
}
p.mat
round(p.mat[,c(1,4,5,6,2,3,7,8)], 3)

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#----- calculate these indices for all webs -----

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webs <- data(package="bipartite")$results[,3]
data(list=webs)

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res <- lapply(webs, function(x) specieslevel(get(x), index="ALLBUTD")$"higher trophic
level"[-4])

```

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res

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save(res, file="allwebs_special_indices_obs.Rdata")

```

```

load(file="allwebs_special_indices_obs.Rdata")

```

```

#----- calculate index correlations across webs -----

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index.cor.pearson <- index.cor.spear <- index.cor.ken <- array(NA, dim=c(11, 11, 21),
dimnames=list(colnames(res[[1]]), colnames(res[[1]]), webs))

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for (i in seq_along(res)){

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  r <- res[[i]]

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  index.cor.pearson[,i] <- cor(r, use="complete.obs", method="pearson")

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  index.cor.spear[,i] <- cor(r, use="complete.obs", method="spear")

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```

  index.cor.ken[,i] <- cor(r, use="complete.obs", method="ken")

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}

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index.cor.ken[,5]

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hist(index.cor.pearson[7,5,]) # not always normally distributed

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# summarise in means and median

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#apply(index.cor.pearson, c(1,2), mean, na.rm=T)
#apply(index.cor.pearson, c(1,2), sd, na.rm=T)
apply(index.cor.pearson, c(1,2), median, na.rm=T)
apply(index.cor.pearson, c(1,2), IQR, na.rm=T)

outmat <- round(apply(index.cor.pearson, c(1,2), median, na.rm=T),3)
outmat[lower.tri(outmat)] <- round(apply(index.cor.ken, c(1,2), median,
na.rm=T),3)[lower.tri(outmat)]
write.table(outmat, file="outmat.txt", sep="\t")
outmatqqr <- round(apply(index.cor.pearson, c(1,2), IQR, na.rm=T),3)
outmatqqr[lower.tri(outmat)] <- round(apply(index.cor.ken, c(1,2), IQR,
na.rm=T),3)[lower.tri(outmat)]
write.table(outmatqqr, file="outmatqqr.txt", sep="\t")

cc <- apply(index.cor.pearson, c(1,2), median, na.rm=T)
cc.red <- cc[-c(2,8, 10),-c(2,8,10)]
par(mar=c(5,5,1,1))
plot(cmd <- cmdscale(1-abs(cc.red), k=2), type="n", xlab="axis 1", ylab="axis 2", tcl=0.5,
cex.lab=1.5, las=1)
text(cmd, c("degree", "strength", "PSI", "NSI", "BC", "CC", "H", "d"), cex=1.25, font=2)
cmdscale(1-abs(cc.red), k=4, eig=T)

.8120/sum(cmdscale(1-abs(cc.red), k=4, eig=T)$eig)
.6073/sum(cmdscale(1-abs(cc.red), k=4, eig=T)$eig)

#----- null models -----
# Safariland
saf <- specieslevel(Safariland, index="ALLBUTD")$"higher trophic level"
write.table(round(saf[,c(1,7,8,6,3,5,10,12)],3), file="Safariland_indices.txt", sep="\t", quote=F)

#----- null models -----
nulls <- list()
for (i in seq_along(webs)){
  nulls[[i]] <- nullmodel(get(webs[i]))
}
save(nulls, file="nulls.Rdata")

## let's look at the specialisation values of an extreme specialist, Chalepogenus.caeruleus in
Safariland (web 1):
null.res.1 <- array(NA, dim=c(8, 27, 1000))
for (i in 1:1000){
  null.res.1[,i] <- t(specieslevel(nulls[[1]][[i]], index="ALLBUTD")$"higher trophic
level"[-c(2,4,9,11)])
}

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    print(i)
  }
save(null.res.1, file="null.res.1.Rdata")

null1.ind <- null.res.1[, 17, ]
(res[[1]][17, -c(2,8,10)] - apply(null1.ind, 1, mean))/apply(null1.ind, 1, sd)
#
#           degree strength      PSI node.specialisation.index
betweenness closeness partner.diversity    d
#Chalepogenus.caeruleus    -1.372702 9.918387 41.17186          19.00112
-0.750377 -5.935758      -1.481948 15.7503

praw <- rowSums(apply(null1.ind, 2, function(x) x > res[[1]][17, -c(2,8,10)])) / NCOL(null1.ind)
(p.value <- ifelse(praw > 0.5, 1-praw, praw))
#[1] 0.243 0.003 0.000 0.000 0.243 0.000 0.243 0.000

## let's look at the specialisation values of an extreme generalist, Corynura.prothysteres in
Safariland (web 1):
null1.ind <- null.res.1[, 24, ]
(res[[1]][24, -c(2,8,10)] - apply(null1.ind, 1, mean))/apply(null1.ind, 1, sd)
#
#           degree strength      PSI      NSI
betweenness closeness partner.diversity    d
#Corynura.prothysteres    0.004130498 -0.2206802 0.03651698 0.7250512 12.73813
8.95974      0.03052268 1.203328
praw <- rowSums(apply(null1.ind, 2, function(x) x > res[[1]][24, -c(2,8,10)])) / NCOL(null1.ind)
(p.value <- ifelse(praw > 0.5, 1-praw, praw))
#[1] 0.218 0.389 0.209 0.166 0.000 0.000 0.322 0.109

# the 8 indices for all pollinators in Safariland:
write.table(signif(res[[1]][,-c(2,8,10)], 3), file="obs.vals.Safariland.txt", sep="\t")

# now z-scores for all pollinators:
z.scores <- matrix(NA, 8, 27)
p.values <- matrix(NA, 8, 27)
for (i in 1:27){
  null1.ind <- null.res.1[, i, ]
  z.scores[,i] <- as.numeric(res[[1]][i, -c(2,8,10)] - apply(null1.ind, 1, mean,
na.rm=T))/apply(null1.ind, 1, sd, na.rm=T)

  praw <- rowSums(apply(null1.ind, 2, function(x) x > res[[1]][i, -c(2,8,10)])) / NCOL(null1.ind)
  p.values[,i] <- ifelse(praw > 0.5, 1-praw, praw)

  print(i)
}

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#-----
# d' distribution:
data(memmott1999)
ind.names <- c("degree", "NSI", "BC", "CC", "strength", "PSI", "H", "d")
ds <- dfun(t(memmott1999))
hist(ds$dprime)
plot(density(ds$dprime, from=0, to=0.8), main="distribution of d' in Memmott 1999", las=1,
tcl=-0.5, log="", xlim=c(0,1))
rug(ds$dprime)

#require(MASS)
#fitdistr(unname(ds$dprime), dbeta, list(shape1=2, shape2=2))

mem <- res[[7]][,c(1,5,6,7,3,4,9,11)]
par(mfrow=c(2,4), mar=c(3,2.8,2,.2))
for (i in 1:8) hist(mem[,i], main=ind.names[i], col="grey80", las=1)
mtext("a", side=3, line=-2, outer=TRUE, adj=0.02, cex=2, font=2)

# same plot for one null model run:
set.seed(42)
mem.null <- nullmodel(memmott1999, 1)[[1]]
mem.null.res <- specieslevel(mem.null, index="ALLBUTD")$"higher trophic
level"[-c(2,4,9,11)][,c(1,4:6,2,3,7:8)]
par(mfrow=c(2,4), mar=c(3,2.8,2,.2))
for (i in 1:8) hist(mem.null.res[,i], main=ind.names[i], col="grey80", las=1)
mtext("b", side=3, line=-2, outer=TRUE, adj=0.02, cex=2, font=2)

#-----
# specialisation shift:
webs <- data(package="bipartite")$results[,3]
webs <- webs[c(1,15:21)]
data(list=webs)

specs <- NA
for (i in 1:length(webs)){
  specs <- c(specs, colnames(get(webs[i])))
}
sort(table(specs)) # two species in all 8 networks: Bombus dahlbomii and Syrphus octomaculatus

# for Bombus dahlbomii calculate the 8 specialisation indices in all 8 networks:
calc.ind <- function(web, focal.poll="Bombus dahlbomii") {
  # helper function to calculate the specialisation indices only for Bombus dahlbomii
  out <- specieslevel(web, index=c("degree", "NS", "BC", "CC", "strength", "PSI", "diversity",

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"d")$"higher trophic level"[focal.poll,]
  unlist(out)
}
ind.names <- c("degree", "NSI", "BC", "CC", "strength", "PSI", "H", "d")
vaz.obs <- t(sapply(webs, function(x) calc.ind(get(x))))
cattle <- c("grazed", "ungrazed")[c(2,1,1,2,2,1,2,1)] #taken from V 路 zquez & Simberloff
(2003), Fig. 1)
par(mfrow=c(2,4), mar=c(3,3,3,1))
for (i in c(1,4:6,2,3,7,8)) boxplot(unlist(vaz.obs[,i]) ~ cattle, main=ind.names[i], las=1, tcl=0.5,
notch=FALSE, col="grey80")

# now run the null models for these webs, adding another dimension of complexity:

>null.array <- array(NA, dim=c(8,8,1000), dimnames=list(rownames(vaz.obs), colnames(vaz.obs),
as.character(1:1000)))
#for (i in webs){
# web <- get(i)
# spec.index <- which(colnames(web) == "Bombus dahlbomii")
# null <- nullmodel(web, dim(null.array)[3])
# null.vals <- sapply(null, calc.ind, focal.poll=spec.index)
# null.array[i,,] <- unname(null.vals)
#}
#save(null.array, file="vazquez_null.array.Rdata")
load("vazquez_null.array.Rdata")

z.mat <- vaz.obs - apply(null.array, c(1,2), mean) / apply(null.array, c(1,2), sd)

matrix(rowSums(apply(null.array, 3, function(x) x > vaz.obs)), 8,8, byrow=F)

## make a panel plot depicting the 64 combinations of networks and indices, nullmodels vs.
observed
# make the plot window LARGE (at least A4)!
windows(width=15, height=10)
par(mfrow=c(8,8), mar=c(2,2.8,1,0.5), oma=c(0,2.5,2.8,0))

for (i in c(1,4,6,8,2,3,5,7)){#loop through the 8 sites, ungrazed first
  for (j in c(1,4:6,2:3,7:8)){# loop through the 8 indices
    xlims <- range(c(null.array[,j,], vaz.obs[,j]), na.rm=T)*c(0.9, 1.1)
#   xlims <- range(c(null.array[i,j,], vaz.obs[i,j]), na.rm=T)*c(0.9, 1.1)
    hist(null.array[i,j,], col={if(i %in%c(1,4,6,8)) "grey80" else "grey40"}, las=1, main="",
xlim=xlims)#paste(ind.names[j], rownames(z.mat)[i]))
    abline(v=vaz.obs[i,j], col="red", lwd=2)
  } #grazed sites are dark grey, ungrazed light grey
}
}

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```

mtext("degree", side=3, line=0, outer=T, cex=1.5, font=3, at=0.12, adj=1)
mtext("NSI", side=3, line=0, outer=T, cex=1.5, font=3, at=0.11*2, adj=1)
mtext("BC", side=3, line=0, outer=T, cex=1.5, font=3, at=0.115*3, adj=1)
mtext("CC", side=3, line=0, outer=T, cex=1.5, font=3, at=0.12*4, adj=1)
mtext("strength", side=3, line=0, outer=T, cex=1.5, font=3, at=0.123*5, adj=1)
mtext("PSI", side=3, line=0, outer=T, cex=1.5, font=3, at=0.12*6, adj=1)
mtext("H", side=3, line=0, outer=T, cex=1.5, font=3, at=0.119*7, adj=1)
mtext("d", side=3, line=0, outer=T, cex=1.5, font=3, at=0.12*8, adj=1)

mtext("Safariland", side=2, line=0, outer=T, cex=1, font=1, at=8*0.125, adj=1)
mtext("vazllao", side=2, line=0, outer=T, cex=1, font=1, at=7*0.121, adj=1)
mtext("vazmasnc", side=2, line=0, outer=T, cex=1, font=1, at=6*0.124, adj=1)
mtext("vazquenc", side=2, line=0, outer=T, cex=1, font=1, at=5*0.123, adj=1)
mtext("vazarr", side=2, line=0, outer=T, cex=1, font=1, at=4*0.12, adj=1)
mtext("vazcer", side=2, line=0, outer=T, cex=1, font=1, at=3*0.122, adj=1)
mtext("vazmasc", side=2, line=0, outer=T, cex=1, font=1, at=2*0.124, adj=1)
mtext("vazquec", side=2, line=0, outer=T, cex=1, font=1, at=0.122, adj=1)

# now we examine the effect of grazing on the raw specialisation indices:
obs.data <- cbind.data.frame(cattle, vaz.obs)
colnames(obs.data)

# Next, we calculate the difference between the observed and the perfect generalist (i.e. mean of
null models):
windows(width=12.5, height=8)
par(tcl=0, mar=c(3,3,1,1), mfrow=c(2,4))

# degree:-----
index = "species.degree"
diffs <- obs.data[,index] - rowMeans(null.array[,index,])
zs <- (obs.data[,index] - rowMeans(null.array[,index,])) / apply(null.array[,index,], 1, sd)
zs <- ifelse(is.infinite(zs), NA, zs)/5
#plot all 3:
data2plot <- cbind(cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(1,4,6,8),],
cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(2,3,5,7),])
boxplot(data2plot, at=c(1,3,5,1.8,3.8,5.8), col=rep(c("grey80", "grey20"), each=3), las=1,
names=rep("", 6))
abline(h=0)
axis(side=2, at=seq(-6,6,by=2), tcl=0.5, labels=FALSE)
mtext("raw", side=1, line=0.75, outer=F, at=1.4, font=2, cex=1.5)
mtext("diff", side=1, line=0.75, outer=F, at=3.4, font=2, cex=1.5)
mtext("z/5", side=1, line=0.75, outer=F, at=5.4, font=2, cex=1.5)
legend("bottomleft", "degree", bty="n", cex=2, inset=c(-0.05,-0.025))
legend("topright", c("ungrazed", "grazed"), col=c("grey80", "grey20"), pch=15, bty="o", cex=2)

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# NSI:-----
index = "node.specialisation.index"
diffs <- obs.data[,index] - rowMeans(null.array[,index,])
zs <- (obs.data[,index] - rowMeans(null.array[,index,])) / apply(null.array[,index,], 1, sd)
zs <- ifelse(is.infinite(zs), NA, zs)/20
#plot all 3:
data2plot <- cbind(cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(1,4,6,8),],
cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(2,3,5,7),])
boxplot(data2plot, at=c(1,3,5,1.8,3.8,5.8), col=rep(c("grey80", "grey20"), each=3), las=1,
names=rep("", 6))
axis(side=2, at=c(0,0.5,1,1.5,2,2.5), tcl=0.5, labels=FALSE)
mtext("raw", side=1, line=0.75, outer=F, at=1.4, font=2, cex=1.5)
mtext("diff", side=1, line=0.75, outer=F, at=3.4, font=2, cex=1.5)
mtext("z/20", side=1, line=0.75, outer=F, at=5.4, font=2, cex=1.5)
legend("topleft", "NSI", bty="n", cex=2, inset=c(-0.05,-0.05))

# BC:-----
index = "betweenness"
diffs <- obs.data[,index] - rowMeans(null.array[,index,])
zs <- (obs.data[,index] - rowMeans(null.array[,index,])) / apply(null.array[,index,], 1, sd)
zs <- ifelse(is.infinite(zs), NA, zs)/100
#plot all 3:
data2plot <- cbind(cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(1,4,6,8),],
cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(2,3,5,7),])
boxplot(data2plot, at=c(1,3,5,1.8,3.8,5.8), col=rep(c("grey80", "grey20"), each=3), las=1,
names=rep("", 6))
abline(h=0)
boxplot(data2plot, at=c(1,3,5,1.8,3.8,5.8), col=rep(c("grey80", "grey20"), each=3), las=1,
names=rep("", 6), add=T)
axis(side=2, at=seq(0,0.3,by=0.1), tcl=0.5, labels=FALSE)
mtext("raw", side=1, line=0.75, outer=F, at=1.4, font=2, cex=1.5)
mtext("diff", side=1, line=0.75, outer=F, at=3.4, font=2, cex=1.5)
mtext("z/100", side=1, line=0.75, outer=F, at=5.4, font=2, cex=1.5)
legend("topleft", "BC", bty="n", cex=2, inset=c(-0.05,-0.05))

# CC:-----
index = "closeness"
diffs <- obs.data[,index] - rowMeans(null.array[,index,])
zs <- (obs.data[,index] - rowMeans(null.array[,index,])) / apply(null.array[,index,], 1, sd)
zs <- ifelse(is.infinite(zs), NA, zs)/100
#plot all 3:
data2plot <- cbind(cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(1,4,6,8),],
cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(2,3,5,7),])

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boxplot(data2plot, at=c(1,3,5,1.8,3.8,5.8), col=rep(c("grey80", "grey20"), each=3), las=1,
names=rep("", 6))
abline(h=0)
axis(side=2, at=seq(0,0.15,by=0.05), tcl=0.5, labels=FALSE)
mtext("raw", side=1, line=0.75, outer=F, at=1.4, font=2, cex=1.5)
mtext("diff", side=1, line=0.75, outer=F, at=3.4, font=2, cex=1.5)
mtext("z/100", side=1, line=0.75, outer=F, at=5.4, font=2, cex=1.5)
legend("topleft", "CC", bty="n", cex=2, inset=c(-0.05,-0.05))

```

```

# strength:-----
#par(tcl=0, mar=c(3,3,1,1))#, mfrow=c(2,4)
index = "strength"
diffs <- obs.data[,index] - rowMeans(null.array[,index,])
zs <- (obs.data[,index] - rowMeans(null.array[,index,])) / apply(null.array[,index,], 1, sd)
zs <- ifelse(is.infinite(zs), NA, zs)
#plot all 3:
data2plot <- cbind(cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(1,4,6,8),],
cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(2,3,5,7),])
boxplot(data2plot, at=c(1,3,5,1.8,3.8,5.8), col=rep(c("grey80", "grey20"), each=3), las=1,
names=rep("", 6))
abline(h=0)
boxplot(data2plot, at=c(1,3,5,1.8,3.8,5.8), col=rep(c("grey80", "grey20"), each=3), las=1,
names=rep("", 6), add=TRUE)
axis(side=2, at=c(-4,-2, 0,2), tcl=0.5, labels=FALSE)
mtext("raw", side=1, line=0.75, outer=F, at=1.4, font=2, cex=1.5)
mtext("diff", side=1, line=0.75, outer=F, at=3.4, font=2, cex=1.5)
mtext("z", side=1, line=0.75, outer=F, at=5.4, font=2, cex=1.5)
legend("bottomleft", "strength", bty="n", cex=2, inset=c(-0.05,0))

```

```

# PSI:-----
#par(tcl=0, mar=c(3,3,1,1))#, mfrow=c(2,4)
index = "Pollination.Service.Index.PSI"
diffs <- obs.data[,index] - rowMeans(null.array[,index,])
zs <- (obs.data[,index] - rowMeans(null.array[,index,])) / apply(null.array[,index,], 1, sd)
zs <- ifelse(is.infinite(zs), NA, zs)/100
#plot all 3:
data2plot <- cbind(cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(1,4,6,8),],
cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(2,3,5,7),])
boxplot(data2plot, at=c(1,3,5,1.8,3.8,5.8), col=rep(c("grey80", "grey20"), each=3), las=1,
names=rep("", 6))
axis(side=2, at=c(0,0.5,1,1.5,2,2.5), tcl=0.5, labels=FALSE)
mtext("raw", side=1, line=0.75, outer=F, at=1.4, font=2, cex=1.5)
mtext("diff", side=1, line=0.75, outer=F, at=3.4, font=2, cex=1.5)
mtext("z/100", side=1, line=0.75, outer=F, at=5.4, font=2, cex=1.5)

```

```
legend("topleft", "PSI", bty="n", cex=2, inset=c(-0.05,-0.05))
```

```
# partner.diversity:-----  
#par(tcl=0, mar=c(3,3,1,1))#, mfrow=c(2,4)  
index = "partner.diversity"  
diffs <- obs.data[,index] - rowMeans(null.array[,index,])  
zs <- (obs.data[,index] - rowMeans(null.array[,index,])) / apply(null.array[,index,], 1, sd)  
zs <- ifelse(is.infinite(zs), NA, zs)/20  
#plot all 3:  
data2plot <- cbind(cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(1,4,6,8),],  
cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(2,3,5,7),])  
boxplot(data2plot, at=c(1,3,5,1.8,3.8,5.8), col=rep(c("grey80", "grey20"), each=3), las=1,  
names=rep("", 6))  
abline(h=0)  
axis(side=2, at=seq(-1,1,by=0.5), tcl=0.5, labels=FALSE)  
mtext("raw", side=1, line=0.75, outer=F, at=1.4, font=2, cex=1.5)  
mtext("diff", side=1, line=0.75, outer=F, at=3.4, font=2, cex=1.5)  
mtext("z/20", side=1, line=0.75, outer=F, at=5.4, font=2, cex=1.5)  
legend("topright", "H", bty="n", cex=2, inset=c(0.05,-0.05))
```

```
# d':-----  
#par(tcl=0, mar=c(3,3,1,1))#, mfrow=c(2,4)  
index = "d"  
diffs <- obs.data[,index] - rowMeans(null.array[,index,])  
zs <- (obs.data[,index] - rowMeans(null.array[,index,])) / apply(null.array[,index,], 1, sd)  
zs <- ifelse(is.infinite(zs), NA, zs)/100  
#plot all 3:  
data2plot <- cbind(cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(1,4,6,8),],  
cbind(raw=obs.data[,index], diff=diffs, z=zs)[c(2,3,5,7),])  
boxplot(data2plot, at=c(1,3,5,1.8,3.8,5.8), col=rep(c("grey80", "grey20"), each=3), las=1,  
names=rep("", 6))  
axis(side=2, at=c(0,0.5,1,1.5,2,2.5), tcl=0.5, labels=FALSE)  
mtext("raw", side=1, line=0.75, outer=F, at=1.4, font=2, cex=1.5)  
mtext("diff", side=1, line=0.75, outer=F, at=3.4, font=2, cex=1.5)  
mtext("z/100", side=1, line=0.75, outer=F, at=5.4, font=2, cex=1.5)  
legend("topleft", "d'", bty="n", cex=2, inset=c(-0.05,-0.05))
```

The problem is that the specialisation index values are affected by the network properties (such as number of species, sampling intensity, etc.). Thus, we need to calculate a corrected value (e.g. the z-score). Or, we explore the t-statistic between the two grazing types but compute the significance level from the null model. This latter approach is also usable for nonnormally distributed data, using Fisher's signed rank test, rather than the t-test.

```

obs.t.PSI <- t.test(obs.data$Pollination.Service.Index.PSI[obs.data$cattle=="grazed"],
obs.data$Pollination.Service.Index.PSI[obs.data$cattle=="ungrazed"], var.equal=F)$statistic
null.t.PSI <- apply(null.array[, 3, ], 2, function(x) t.test(x[obs.data$cattle=="grazed"],
x[obs.data$cattle=="ungrazed"]))$statistic)
plot(density(null.t.PSI)); abline(v=obs.t.PSI, col="red")
sum(null.t.PSI > obs.t.PSI) # 25
# this means that the observed difference statistics is significantly higher than would be expected
for a generalist

```

```

obs.degree.dev <- anova(glm(species.degree ~ cattle, family=poisson, data=obs.data),
test="Chisq")$Deviance[2]
obs.NSI.F <- anova(lm(node.specialisation.index ~ cattle, data=obs.data))$"F value"[1]
obs.BC.F <- anova(lm(betweenness ~ cattle, data=obs.data))$"F value"[1]
obs.CC.F <- anova(lm(closeness ~ cattle, data=obs.data))$"F value"[1]
obs.strength.F <- anova(lm(strength ~ cattle, data=obs.data))$"F value"[1]
obs.PSI.F <- anova(lm(Pollination.Service.Index.PSI ~ cattle, data=obs.data))$"F value"[1]
obs.H.F <- anova(lm(partner.diversity ~ cattle, data=obs.data))$"F value"[1]
obs.d.F <- anova(lm(d ~ cattle, data=obs.data))$"F value"[1]
# none of the indices hints at a change in specialisation of Bombus dahlbomii under change in
grazing

```

```

# use nullmodels to get a F-value distribution:
dimnames(null.array)[1:2]

```

```

null.degree.dev <- apply(null.array[, 1, ], 2, function(x) anova(glm(x ~ cattle, family=poisson,
data=obs.data))$Deviance[2])
sum(null.degree.dev > obs.degree.dev) #150
null.NSI.F <- apply(null.array[, 4, ], 2, function(x) anova(lm(x ~ cattle, data=obs.data))$"F
value"[1])
sum(null.NSI.F > obs.NSI.F) #964
null.BC.F <- apply(null.array[, "betweenness", ], 2, function(x) anova(lm(x ~ cattle,
data=obs.data))$"F value"[1])
sum(null.BC.F > obs.BC.F) #987
null.CC.F <- apply(null.array[, "closeness", ], 2, function(x) anova(lm(x ~ cattle,
data=obs.data))$"F value"[1])
sum(null.CC.F > obs.CC.F) #943
null.strength.F <- apply(null.array[, "strength", ], 2, function(x) anova(lm(x ~ cattle,
data=obs.data))$"F value"[1])
sum(null.strength.F > obs.strength.F) #131
null.PSI.F <- apply(null.array[, 3, ], 2, function(x) anova(lm(x ~ cattle, data=obs.data))$"F
value"[1])
sum(null.PSI.F > obs.PSI.F) #975
null.H.F <- apply(null.array[, 7, ], 2, function(x) anova(lm(x ~ cattle, data=obs.data))$"F
value"[1])

```

```

sum(null.H.F > obs.H.F) #893
null.d.F <- apply(null.array[, 8, ], 2, function(x) anova(lm(x ~ cattle, data=obs.data))$F
value"[1])
sum(null.d.F > obs.d.F) #686

#####
#####
#####
# this is nothing new: it repeats the analysis of Bombus for a different species:
#####
#####
webs <- data(package="bipartite")$results[,3]
webs <- webs[c(1,15:21)]
data(list=webs)

specs <- NA
for (i in 1:length(webs)){
  specs <- c(specs, colnames(get(webs[i])))
}
sort(table(specs)) # two species in all 8 networks: Bombus dahlbomii and Syrphus octomaculatus
# We pick a third one here, Vespula germanica, which is present in 7 of the 8 networks.

# for Vespula germanica calculate the 8 specialisation indices in all 8 networks:
calc.ind <- function(web, focal.poll="Vespula germanica") {
  # helper function to calculate the specialisation indices only for Vespula germanica
  out <- specieslevel(web, index=c("degree", "NS", "BC", "CC", "strength", "PSI", "diversity",
"d"))$"higher trophic level"[focal.poll,]
  unlist(out)
}
ind.names <- c("degree", "NSI", "BC", "CC", "strength", "PSI", "H", "d")
vaz.obs <- t(sapply(webs, function(x) calc.ind(get(x))))
cattle <- c("grazed", "ungrazed")[c(2,1,1,2,2,1,2,1)] #taken from V 路 zquez & Simberloff
(2003), Fig. 1)
par(mfrow=c(2,4), mar=c(3,3,3,1))
for (i in c(1,4:6,2,3,7,8)) boxplot(unlist(vaz.obs[,i]) ~ cattle, main=ind.names[i], las=1, tcl=0.5,
notch=FALSE, col="grey80")

# now run the null models for these webs, adding another dimension of complexity:

#null.array <- array(NA, dim=c(8,8,1000), dimnames=list(rownames(vaz.obs), colnames(vaz.obs),
as.character(1:1000)))
#for (i in webs){
#  web <- get(i)

```

```

# spec.index <- which(colnames(web) == "Vespula germanica")
# if (length(spec.index) == 0){
#   null.array[i,,] <- matrix(NA, 8, 1000)
# } else {
#   null <- nullmodel(web, dim(null.array)[3])
#   null.vals <- sapply(null, calc.ind, focal.poll=spec.index)
#   null.array[i,,] <- unname(null.vals)
# }
# print(i)
#}
#save(null.array, file="vazquez_Vespula.germanica_null.array.Rdata")
load("vazquez_Vespula.germanica_null.array.Rdata")

z.mat <- vaz.obs - apply(null.array, c(1,2), mean) / apply(null.array, c(1,2), sd)

matrix(rowSums(apply(null.array, 3, function(x) x > vaz.obs)), 8,8, byrow=F)

## make a panel plot depicting the 64 combinations of networks and indices, nullmodels vs.
observed
# make the plot window LARGE (at least A4!)
windows(width=15, height=10)
par(mfrow=c(7,8), mar=c(2,2.8,1,0.5), oma=c(0,2.5,2.8,0))
for (i in c(1,4,6,8,2,3,7)) {#loop through the 8 sites, ungrazed first
  for (j in c(1,4:6,2:3,7:8)) {# loop through the 8 indices
    xlims <- range(c(null.array[,j,], vaz.obs[,j]), na.rm=T)*c(0.9, 1.1)
    hist(null.array[i,j,], col={if(i %in% c(1,4,6,8)) "grey80" else "grey40"}, las=1, main="",
    xlim=xlims)#paste(ind.names[j], rownames(z.mat)[i]))
    abline(v=vaz.obs[i,j], col="red", lwd=2)
  } #grazed sites are dark grey, ungrazed light grey
}
mtext("degree", side=3, line=0, outer=T, cex=1.5, font=3, at=0.12, adj=1)
mtext("NSI", side=3, line=0, outer=T, cex=1.5, font=3, at=0.11*2, adj=1)
mtext("BC", side=3, line=0, outer=T, cex=1.5, font=3, at=0.115*3, adj=1)
mtext("CC", side=3, line=0, outer=T, cex=1.5, font=3, at=0.12*4, adj=1)
mtext("strength", side=3, line=0, outer=T, cex=1.5, font=3, at=0.123*5, adj=1)
mtext("PSI", side=3, line=0, outer=T, cex=1.5, font=3, at=0.12*6, adj=1)
mtext("H", side=3, line=0, outer=T, cex=1.5, font=3, at=0.119*7, adj=1)
mtext("d", side=3, line=0, outer=T, cex=1.5, font=3, at=0.12*8, adj=1)

mtext("Safariland", side=2, line=0, outer=T, cex=1, font=1, at=7*0.14, adj=1)
mtext("vazllao", side=2, line=0, outer=T, cex=1, font=1, at=6*0.14, adj=1)
mtext("vazmasnc", side=2, line=0, outer=T, cex=1, font=1, at=5*0.14, adj=1)
mtext("vazquenc", side=2, line=0, outer=T, cex=1, font=1, at=4*0.14, adj=1)
mtext("vazarr", side=2, line=0, outer=T, cex=1, font=1, at=3*0.14, adj=1)

```

```
mtext("vazcer", side=2, line=0, outer=T, cex=1, font=1, at=2*0.14, adj=1)
#mtext("vazmasc", side=2, line=0, outer=T, cex=1, font=1, at=2*0.124, adj=1)
mtext("vazquec", side=2, line=0, outer=T, cex=1, font=1, at=0.14, adj=1)
```