Basics in Community Ecology

Master FBE · CRBE · Université de Toulouse

Based on LTOM.01.002 (University of Tartu, 2023). Covers diversity indices, beta diversity, dark diversity, ordination, environment–community links, constrained ordination, and spatial analysis.

Community ecology asks: how many species, which ones, and why? The primary data structure is the **species × site matrix**.

1. The community matrix

```
library(vegan)
data(dune); data(dune.env)

dim(dune)              # 20 sites × 30 species
rowSums(dune)          # total abundance per site
specnumber(dune)       # species richness per site

# Standardise
dune_pa  <- decostand(dune,"pa")      # presence/absence
dune_rel <- decostand(dune,"total")   # relative abundance
dune_hel <- decostand(dune,"hellinger") # square-root of rel. ab.
```

2. Alpha diversity

Index	Formula	Range	Code
Richness S	Count species	>0	specnumber(comm)
Shannon H'	-Σp■ln(p■)	0–ln(S)	diversity(comm,'shannon')
Simpson 1-D	1-Σp■²	0–1	diversity(comm,'simpson')
Pielou J	H'/ln(S)	0–1	H/log(specnumber(comm))
Chao1	Richness estimator	≥S	estimateR(comm)[2,]
ACE	Abundance-based est.	≥S	estimateR(comm)[4,]

```
S <- specnumber(dune)
H <- diversity(dune,"shannon")
D <- diversity(dune,"simpson")
J <- H/log(S)          # evenness

# Rarefaction (standardise richness to min sample size)
min_n  <- min(rowSums(dune))
S_rare <- rarefy(dune,min_n)

# Rarefaction curves — saturation?
rarecurve(dune,step=2,col="#27ae60",label=FALSE)

# Hill numbers (unify richness, Shannon, Simpson)
library(vegan)
```

```
renyi(dune,scales=c(0,1,2))  # q=0: richness; q=1: exp(H); q=2: 1/D
```

3. Beta diversity

Beta diversity = variation in composition between sites. Decompose into **replacement** (species swap) and **nestedness** (subset effect).

```
library(betapart)

d_bray <- vegdist(dune,"bray")          # abundance
d_jacc <- vegdist(dune,"jaccard",binary=TRUE) # presence

# Decompose beta into nestedness + replacement
beta_pair <- beta.pair(decostand(dune,"pa"))
beta_pair$beta.sor    # total Sørensen beta
beta_pair$beta.sim    # replacement (Simpson turnover)
beta_pair$beta.sne    # nestedness

# Whittaker beta: gamma/mean(alpha) - 1
beta_w <- ncol(dune)/mean(specnumber(dune)) - 1
cat("Whittaker beta:",round(beta_w,2))
```

4. Dark diversity

*Pärtel et al. (2011) TREE. **Dark diversity** = ecologically suitable but absent species.*

Observed diversity (S) + Dark diversity (DD) = **Species pool**. **Completeness** = S/(S+DD). Communities with low completeness are below their potential.

```
# Beals smoothing: habitat suitability via co-occurrence
beals_scores <- beals(dune)

# Dark diversity: suitable but absent
threshold <- 0.3
dark <- (dune==0) & (beals_scores>threshold)
DD   <- rowSums(dark)
S    <- rowSums(dune>0)

results <- data.frame(
  S=S, DD=DD,
  completeness=round(S/(S+DD),2),
  community_openness=round(DD/(S+DD),2)
)
print(results)

# Visualise completeness vs observed richness
library(ggplot2)
df <- cbind(results, Management=dune.env$Management)
ggplot(df,aes(S,DD,colour=Management)) +
  geom_point(size=3,alpha=0.8) +
  geom_smooth(method="lm",se=TRUE,linetype=2,colour="grey50") +
  labs(x="Observed richness",y="Dark diversity",
       title="Dark diversity vs observed richness") +
  theme_bw()
```

5. Unconstrained ordination

Method	Type	Dissimilarity	Best for
PCA	Linear	Euclidean	Environmental variables, standardised data
CA/DCA	Unimodal	Chi-square	Long turnover gradients
NMDS	Non-metric	Any	Ecology: robust, no assumptions
PCoA	Distance-based	Any	Any dissimilarity matrix
db-RDA	Constrained	Any	Env effects + any dissimilarity

NMDS:

```
ord <- metaMDS(dune,distance="bray",k=2,trymax=50)
cat("Stress:",round(ord$stress,3))  # <0.1 excellent, <0.2 ok

site_sc <- as.data.frame(scores(ord,"sites"))
site_sc$Management <- dune.env$Management

library(ggplot2)
ggplot(site_sc,aes(NMDS1,NMDS2,colour=Management)) +
  geom_point(size=3,alpha=0.8) +
  stat_ellipse(linewidth=0.7,linetype=2) +
  theme_bw()
```

PCoA (works with any dissimilarity):

```
pcoa <- cmdscale(d_bray,k=4,eig=TRUE)
eig_pct <- 100*pcoa$eig/sum(abs(pcoa$eig))
cat(sprintf("PC1=%.1f%%  PC2=%.1f%%\n",eig_pct[1],eig_pct[2]))

df_pc <- data.frame(pcoa$points[,1:2],Management=dune.env$Management)
names(df_pc)[1:2] <- c("PC1","PC2")
ggplot(df_pc,aes(PC1,PC2,colour=Management))+geom_point(size=3)+theme_bw()
```

6. Environment–community relationships

envfit — overlay environmental vectors on ordination:

```
ef <- envfit(ord,dune.env,permutations=999)
plot(ord);plot(ef,p.max=0.05,col="#c0392b")
```

PERMANOVA — do groups differ in composition?

```
adonis2(dune~Management+Moisture,data=dune.env,
        permutations=999,by="margin")
```

ANOSIM — simpler test for group differences:

```
ano <- anosim(d_bray,dune.env$Management,permutations=999)
print(ano)    # R: 0=no diff, 1=perfect; p-value
```

Indicator species analysis (IndVal):

```
library(indicspecies)
indval <- multipatt(dune,dune.env$Management,
                    func="IndVal.g",permutations=999)
summary(indval,alpha=0.05)
```

Mantel test:

```
geo_dist <- dist(matrix(rnorm(40),20,2))  # simulated coords
mantel(d_bray,geo_dist,method="pearson",permutations=999)
mantel.partial(d_bray,geo_dist,d_jacc,permutations=999)
```

7. Constrained ordination (RDA/CCA)

```
# RDA: linear; use Hellinger-transformed data
rda_mod <- rda(dune_hel~A1+Moisture+Management,data=dune.env)

RsquareAdj(rda_mod)      # adjusted R²
anova(rda_mod,by="axis",permutations=999)    # test axes
anova(rda_mod,by="margin",permutations=999)  # test terms

# Triplot
plot(rda_mod,scaling=2,display=c("sp","wa","bp"))

# db-RDA (distance-based: any dissimilarity)
dbRDA <- capscale(dune~Management,data=dune.env,
                  distance="bray")
anova(dbRDA)
```

8. Diversity partitioning

Total diversity (gamma) = mean alpha + beta (additive) or alpha × beta (multiplicative).

```
# Additive partitioning
part <- adipart(dune,dune.env$Management,index="shannon",
               permutations=999)
print(part)   # alpha, beta, gamma with significance test

# Multiplicative Whittaker
alpha <- mean(specnumber(dune))
gamma <- specnumber(colSums(dune>0))  # regional richness
beta  <- gamma/alpha
cat(sprintf("alpha=%.1f  gamma=%d  beta_mult=%.2f\n",alpha,gamma,beta))
```

9. Spatial analysis in R

From LTOM session 9: Mantel tests and basic GIS.

```
# Moran's I: spatial autocorrelation in species richness
library(ape)
coords <- cbind(runif(20),runif(20))  # simulated coordinates
w <- 1/as.matrix(dist(coords))       # inverse distance weights
diag(w) <- 0
Moran.I(specnumber(dune),weight=w)

# Simple species richness map
library(sf); library(ggplot2)
pts <- st_as_sf(as.data.frame(coords),
                coords=c("V1","V2"),crs=4326)
pts$S <- specnumber(dune)
ggplot(pts)+geom_sf(aes(colour=S,size=S))+
  scale_colour_viridis_c()+theme_minimal()
```

References: Oksanen et al. vegan · Pärtel et al. (2011) TREE · Anderson (2001) PERMANOVA · LTOM.01.002 (Tartu 2023) · Dufrêne & Legendre (1997) IndVal