Group C — Null models and assembly rules

Master FBE · 90 min · Realms: Oriental + Australian

You will test whether freshwater fish assemblages in the Oriental and Australian realms are assembled by environmental filtering (functional clustering) or competitive exclusion (functional overdispersion) using standardised effect sizes (SES-FRic).

Deliverable: 5-slide PPT presented to the class in 8 minutes.

```
library(FD); library(ggplot2); library(dplyr)

traits <- read.csv("fish_traits.csv", row.names=1)
env    <- read.csv("env_data.csv",    row.names=1)
comm   <- read.csv("fish_communities.csv", row.names=1)

my_realms <- c("Oriental","Australian")
sites     <- rownames(env[env$Realm %in% my_realms,])
```

Step 1 — Observed FD (20 min)

1a. Compute observed FRic for your basins.

```
sp_shared <- intersect(colnames(comm[sites,]),rownames(traits))
comm_sub  <- comm[sites,sp_shared]
tr_sub    <- traits[sp_shared,2:8]

set.seed(42)
fd_obs <- dbFD(tr_sub,as.matrix(comm_sub),m=3,
               calc.FRic=TRUE,calc.CWM=FALSE,print.pco=FALSE)$FRic

df <- data.frame(basin=rownames(comm_sub),
                 S=specnumber(comm_sub),
                 FRic=fd_obs,
                 Realm=env[rownames(comm_sub),"Realm"],
                 temp=env[rownames(comm_sub),"temp_mean"])
```

1b. Is FRic higher in species-rich or species-poor basins? Plot FRic vs S. This is the richness confound we need to correct for.

```
ggplot(df,aes(S,FRic,colour=Realm))+
  geom_point(size=2.5)+geom_smooth(method="lm",linetype=2)+theme_bw()
```

Step 2 — Null model and SES (40 min)

2a. Build a null model by randomly shuffling species identities in the trait matrix (nperm = 199 for speed). Compute SES-FRic.

```
set.seed(42)
null_FRic <- replicate(199, {
  tr_null <- tr_sub[sample(nrow(tr_sub)), , drop=FALSE]
  rownames(tr_null) <- rownames(tr_sub)
  tryCatch(
    dbFD(tr_null,as.matrix(comm_sub),m=3,
```

```
         print.pco=FALSE,calc.CWM=FALSE)$FRic,
    error=function(e) rep(NA,nrow(comm_sub))
  )
})

SES <- (fd_obs - rowMeans(null_FRic,na.rm=TRUE)) /
         apply(null_FRic,1,sd,na.rm=TRUE)
pval <- rowMeans(sweep(null_FRic,1,fd_obs,">="),na.rm=TRUE)

df$SES  <- SES
df$pval <- pval
df$pattern <- ifelse(SES>1.96,"overdispersed",
              ifelse(SES< -1.96,"clustered","random"))
print(df[,c("basin","Realm","SES","pval","pattern")])
```

2b. Plot SES-FRic by realm as a boxplot. Are assemblages more clustered or overdispersed? Add reference lines at ±1.96.

```
ggplot(df,aes(Realm,SES,fill=Realm))+
  geom_boxplot(alpha=0.7)+
  geom_hline(yintercept=c(-1.96,1.96),linetype=2,colour="red")+
  geom_hline(yintercept=0)+
  labs(y="SES-FRic",title="Functional assembly patterns")+
  theme_bw()+theme(legend.position="none")
```

2c. Does temperature predict SES-FRic? Hot = more filtering (clustering) or more competition (overdispersion)?

```
ggplot(df,aes(temp,SES,colour=Realm))+
  geom_point(size=2.5)+geom_smooth(method="lm")+
  geom_hline(yintercept=0,linetype=2)+
  labs(x="Mean temp (°C)",y="SES-FRic")+theme_bw()
cor.test(df$temp,df$SES,method="spearman")
```

Step 3 — Interpretation (15 min)

3a. Count the proportion of basins in each pattern category (clustered / random / overdispersed). Does the pattern differ between Oriental and Australian realms?

```
table(df$Realm,df$pattern)
```

3b. Propose a biological mechanism that could explain the dominant assembly pattern you found. Write 3–4 sentences.

Slide template (5 slides, 8 min)

Slide	Content	~Time

1 — Intro	What is a null model? What are SES thresholds (±1.96)?	45 sec
2 — SES figure	Boxplot of SES-FRic by realm with ±1.96 reference lines.	2 min
3 — Pattern	% clustered / random / overdispersed per realm.	2 min
4 — Mechanism	Proposed ecological mechanism for the dominant pattern.	2 min
5 — Limitation	One assumption of the null model you used.	30 sec