Group A — Functional space of freshwater fishes

Master FBE · 90 min · Realms: Neotropical + Nearctic

You will build and interpret a functional space for Neotropical and Nearctic freshwater fishes using FishMORPH morphological traits. Your goal: understand how these two realms differ in functional organisation.

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

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

# Load data
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)

# Filter your two realms
my_realms <- c("Neotropical","Nearctic")
sites     <- rownames(env[env$Realm %in% my_realms, ])
sp_realms <- unique(traits$Realm[traits$Realm %in% my_realms])
```

Step 1 — Explore traits (15 min)

1a. Compute trait completeness (% non-NA per trait). Drop species with more than 30% missing data.

```
colMeans(!is.na(traits[,2:8]))*100     # completeness per trait
complete <- rowMeans(!is.na(traits[,2:8]))
tr_clean <- traits[complete >= 0.70, ]
```

1b. Are any traits strongly correlated (|r| > 0.7)? If yes, does this affect the number of independent axes?

```
cor(tr_clean[,2:8], use="pairwise.complete.obs")
```

Step 2 — Build the functional space (25 min)

2a. Run a PCA on scaled traits. How many PC axes explain >70% of variance? What does PC1 represent biologically?

```
tr_sc <- scale(tr_clean[,2:8])
pca   <- prcomp(tr_sc, scale.=FALSE)
cumsum(summary(pca)$importance[2,])   # cumulative variance
sort(abs(pca$rotation[,1]), decreasing=TRUE)  # PC1 loadings
```

2b. Plot the functional space with funspace, colouring by realm. Which realm fills more of the trait space?

```
realm_vec <- tr_clean$Realm
funspace(x=pca, axes=c(1,2),
         group.vec = realm_vec,
         pnt       = TRUE,
         fill.col  = c("#8e44ad","#2980b9"))
```

2c. Compute pairwise functional overlap between the two realms. Is the overlap high or low? What does this mean for global fish functional diversity?

```
overlap <- fun_overlap(x=pca, axes=c(1,2), group.vec=realm_vec)
print(round(overlap, 3))
```

Step 3 — Functional uniqueness (20 min)

3a. Compute functional uniqueness per species. List the 5 most unique species and look up their names — are they known for unusual morphology?

```
uniq <- funspaceUniqueness(x=pca, axes=c(1,2))
tr_clean$uniqueness <- uniq
head(tr_clean[order(-uniq), c("Realm","uniqueness")], 5)
```

3b. Are Neotropical species on average more unique than Nearctic species? Test with a Wilcoxon test and plot a boxplot.

```
wilcox.test(uniqueness~Realm, data=tr_clean[tr_clean$Realm %in% my_realms,])
ggplot(tr_clean[tr_clean$Realm %in% my_realms,],
       aes(Realm,uniqueness,fill=Realm))+
  geom_boxplot(alpha=0.7)+theme_bw()
```

Slide template (5 slides, 8 min presentation)

Slide	Content	~Time
1 — Intro	Title + context: why compare Neotropical and Nearctic fish?	30 sec
2 — Figure	Your best funspace plot (PC1 vs PC2, both realms)	2 min
3 — Results	Overlap value + uniqueness comparison. Key numbers.	2 min
4 — Interpretation	What does low/high overlap mean ecologically? Which realm is more unique?	2 min
5 — Limitation	One methodological limitation of PCA for functional spaces.	1 min

Tip: use ggplot2 to save your best figure: ggsave('GroupA_fig.png', dpi=150, width=7, height=5)