Summarizing output from ordination

- Function `scores` will return scaled ordination scores from any ordination object in vegan.

```r
corr <- rda(env_data[,2:14], scale=TRUE)
scores(corr)
```

- Use choices option to specify which axes

```r
scores(corr, choices=c(3,4))
```

Remember to standardize your data for PCA

- Remember that PCA is simply trying to capture and summarize variability in the data you give it.

- Variance in the environmental dataset:

```r
rda(scale(env_data), scale=F)
```

PCA Centroids

- Use `tapply` function to calculate centroids

```r
drain_cent_axis1 <- tapply(pca_scores$sites[,1], env_data$drainage, mean)
drain_cent_axis2 <- tapply(pca_scores$sites[,2], env_data$drainage, mean)
```

- Interpretation of loadings

```r
PC1 PC2 PC3 PC4 PC5 PC6
drainage_area 1.2341 0.27768 -0.20500 0.008830 -0.019870 0.0983845
pH -0.1078 -0.89769 -0.66955 0.739094 -0.005982 -0.2322696
DO -0.6484 -1.03879 -0.25846 0.436499 -0.0006881 0.000000
Temp -0.9563 -0.17637 0.30958 0.784754 -0.225860 0.4920935
tds 0.3469 -0.19214 -0.77409 0.201544 -0.907196 -0.5841665
depth -1.1197 -0.05459 -0.17638 -0.418722 0.086392 -0.5040391
flow 0.6073 -0.92075 0.06458 -0.0005201 0.2150150
substrate 0.8694 -0.68232 0.34415 0.727371 -0.907196 -0.5841665
veg 0.6248 -0.53227 0.77886 -0.355169 -0.130040 -0.7226776
width 1.3432 -0.27171 -0.05106 -0.009342 0.085742 -0.1824708
canopy 1.0168 0.36131 -0.66089 0.094000 0.213493 0.0710733
turbidity 0.1470 0.51158 -0.13519 0.616221 1.028319 -0.6253680
```
metaNMDS output

global Multidimensional Scaling using monoMDS

Data: community[, 1:10]
Distance: bray shortest

Dimensions: 2
Stress: 0.01561306
Stress type 1, weak ties
Two convergent solutions found after 4 tries
Scaling: centring, PC rotation, halfchange scaling
Species: expanded scores based on 'community'

Scaling and Rotation

• NMDS axes are not in any particular order, values are arbitrary.
• By convention
  • all axes are centered (means=0)
  • Axes rotated to PCA axes. This will "order" them by importance
• Halfchange scaling – ordination scores are scaled to match the scale of the similarity matrix used (typically 0-1)
• Function MDSrotate() will rotate the axes to any vector (e.g. environmental variable).

Goodness of Fit

• Function goodness() returns goodness of fit statistics for each site. Relative measure of the total stress linked to each point.

• Higher values = more uncertainty and more stress

noshare option

• Using this option will invoke a function that will estimate dissimilarity for sites that do not share any species.
  • T/F – us or do not use
  • Value 0 to 1 – cutoff for when to use (proportion of sites with no shared species)
• Zerodist option – what to do with samples with no dissimilarity (ties)
noshare=0.0 noshare=0.1
NMDS stopping point

- isoMDS uses a stable stress value as a stopping point
- Set tolerance as an option
- "converged" when done

Procrustes Distance

- metaMDS uses a Procrustean analysis instead of stress values to assess differences in configurations for each iteration
  - Procrustes – son of Poseidon, had an iron bed that all visitors had to sleep in. He would stretch or cut limbs so they all fit.
  - Procrustes analysis – how much "cutting" and "stretching" is necessary to get one configuration (ordination) to match another.

Procrustes Statistic

- Any two configurations can be compared and their differences quantified with a Procrustes statistic – sum of squares of the residuals.
  - How different are these two configurations?
Procrustes Statistic

- You can also test the significance of Procrustes values (function `protest` compares observed vs. permuted values). This is testing for non-random concordance between two configurations.

```
Call:
procrustes(x = metanmds$points, y = metanmds_without_noshare$points)
Number of objects: 29    Number of dimensions: 2
Procrustes sum of squares:
9.477623
Procrustes root mean squared error:
0.571677
Quantiles of Procrustes errors:
       Min         1Q     Median         3Q        Max
0.03398588 0.14887655 0.25752112 0.53496706 2.15886845
Rotation matrix:
[,1]        [,2]
[1,] 0.99978430 0.02076904
[2,] 0.02076904 0.99978430
Translation of averages:
[,1]          [,2]
[1,] 3.450472e-17 -4.280952e-18
Scaling of target:
[1] 0.9371033
```

Protest – analysis of congruence

- Similar to Mantel tests, noise removed from data by working in fewer dimensions
- Generally more powerful than Mantel