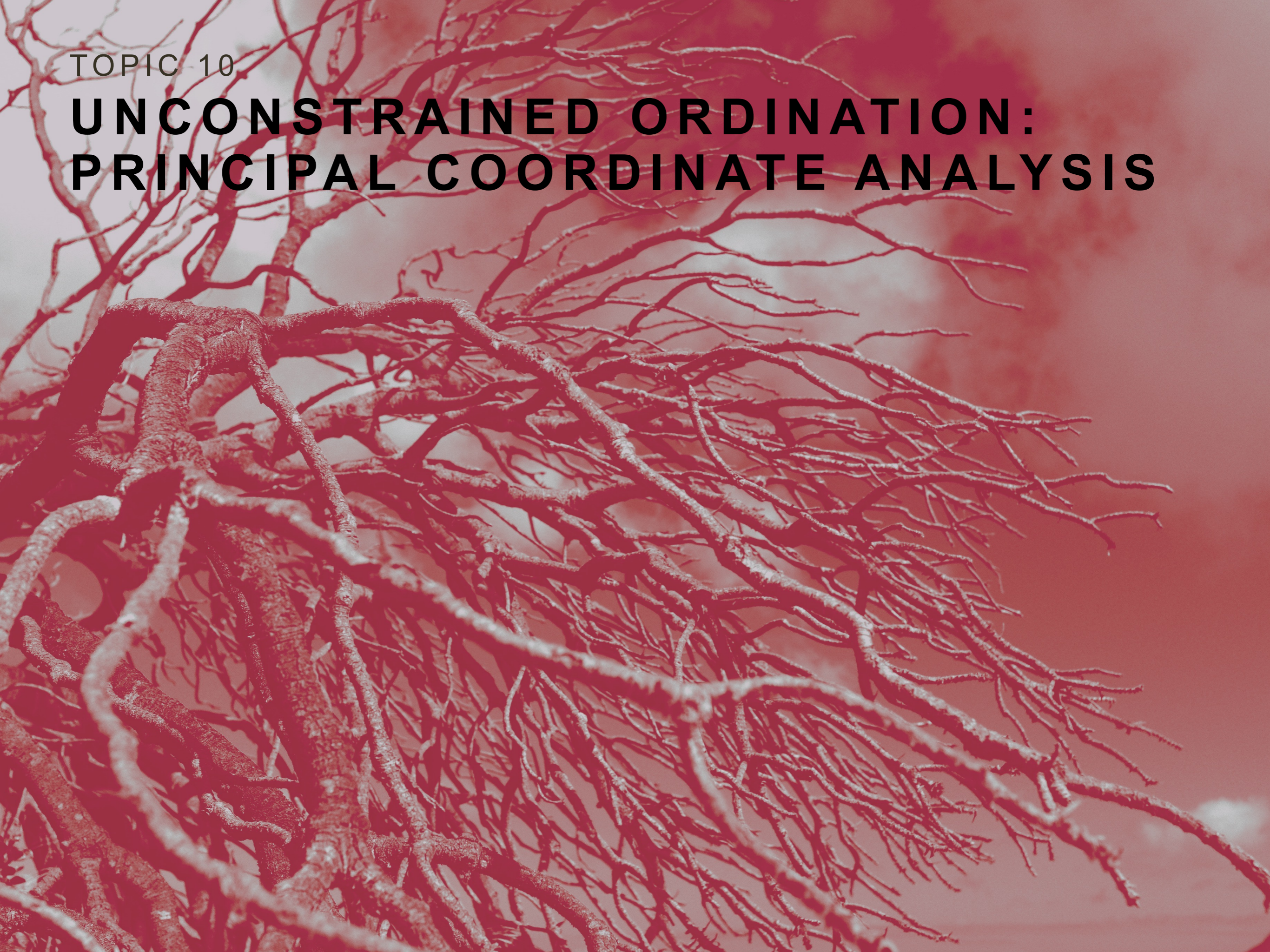


TOPIC 10

UNCONSTRAINED ORDINATION: PRINCIPAL COORDINATE ANALYSIS

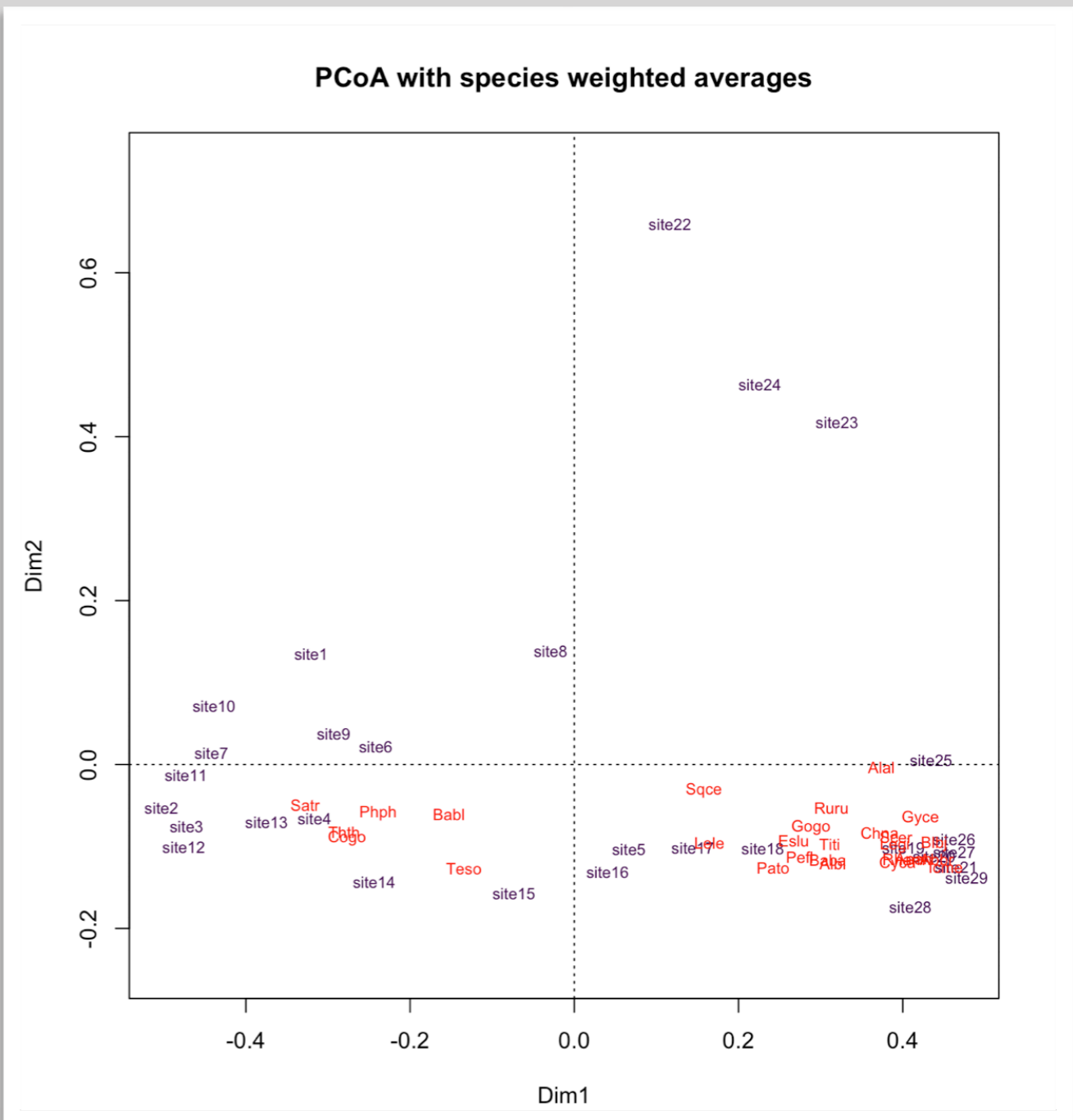


Principal Coordinates Analysis (PCoA)

- see <https://sites.google.com/site/mb3gustame/dissimilarity-based-methods/principal-coordinates-analysis> and https://www.davidzeleny.net/anadat-r/doku.php/en:pcoa_nmds
- a.k.a. 'Classical multidimensional scaling' (MDS), hence the base R function name `cmdscale()`
- PCoA is conceptually similar to PCA, which preserves Euclidean distances between objects, and CA which preserves χ^2 distances between objects
- **rather than using raw data as in a CA, PCoA takes a (dis)similarity matrix as input**
 - the strength of the method is that it can be used with other dissimilarities (as per **vegan's** `vegdist()` function) that are better suited for communities of species
 - if dissimilarities are Euclidean distances, then PCoA is equal to PCA
- also, (dis)similarity matrices calculated from **quantitative, semi-quantitative, qualitative, and mixed variables** can be handled by PCoA
- **info about original variables are not available** because the input is the square (site × site) dissimilarity matrix, not the raw species table
- **the proportion of a given eigenvalue to the sum of all eigenvalues** reveals the relative 'importance' of each axis

Principal Coordinate Analysis (PCoA)

```
spe.bray <- vegdist(spe)
spe.b.pcoa <- cmdscale(spe.bray, k = (nrow(spe) - 1), eig = TRUE)
# Plot of the sites
# dev.new(title = "PCoA on fish species - Percentage difference")
ordiplot(scores(spe.b.pcoa, choices = c(1, 2)), type = "t",
         main = "PCoA with species weighted averages")
abline(v = 0, h = 0, lty = 3)
# Add weighted average projection of species
spe.wa <- wascores(spe.b.pcoa$points[,1:2], spe)
text(spe.wa, rownames(spe.wa), cex = 0.7, col = "red")
```



Questions (for yourself):

1. produce the code to run this analysis on the seaweed species data
2. what is the importance of the first three Dims?
3. how does the interpretation compare to that in the CA?
4. produce a multivariate analysis of the seaweed environmental data, and use this to explain the patterns observed in the species data (re-use your earlier results if you have done this before)

Principal Coordinates Analysis (PCoA)

Update:

I now use the **vegan** function `capscale()` for PCoA – see the Supplementary Material at https://github.com/ajsmit/Quantitative_Ecology/blob/main/jupyter_lab/14-PCoA.ipynb