

Ordinations: Principal components analysis

Class work:

Two functions are commonly used to run principal components analysis:

- *rda* available in the *vegan* r-package.
- *princomp*

We are going to apply these two functions to climate data associated with the arctic pollen data used by Frechette et al. (2008). This data is available in the *palaeoSig* package and called *arctic.env* you can load this data as follows: `data(arctic.env)`

From this data create a subset containing temperatures of the warmest and coldest month, annual mean temperature, July and January precipitation and the sum of annual precipitation.

Run pca on this data set using *rda* and *princomp*. Explore differences between pca using the covariance matrix/centered variables and correlation matrix/standardized variables.

- look at variances explained (function *summary* is pretty handy)
- Make screeplots (`screeplot(...,bstick=TRUE)`)
- Why are the variances explained so different? (look at the covariance and correlation matrix)

Make ordination biplots using *biplot* for *princomp* (make sure to set `pc.biplot=TRUE`) and *plot* for *rda* using `plot` for *rda*, I suggest using

```
plot(my.rda.object,scaling=1,display='sites',xlim=c(-1,1),ylim=c(-1,1)) points(my.rda.object,display='sites',scaling=1,...)
points(my.rda.object,display='species',scaling=0,pch = 15,col=4) text(my.rda.object,display='species',scaling=0,pos=1)
```

Interpret the biplot for standardized variables/correlation matrix.

The sites in the arctic pollen dataset are from three biomes. Color code the sites in your biplot. Which axis does discriminate between the biomes? Which variables have high loadings on this axis? (*my.rda.object\$C.Aeig* is helpful)

PCA on a pollen dataset

Take the pollen dataset you plotted in lab 5.

- Constrain the dataset to 9000 cal BP and present
- Only use species/taxa that have an average > 2%
- Square root transform the data (*sqr*t)
- Run a principal components analysis on this data
- Make a scree plot
- How many significant axes are there? (`screeplot(...,bstick=TRUE)`)
- Plot PC1 (`scores(my.rda.object)`)
- Make a PCA biplot
- Can you relate the PCA biplot to the pollen diagram?