Multivariate Statistics in Ecology and Quantitative Genetics
Combining PCA and GLMs

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http://evol.bio.lmu.de/_statgen

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- Lets again try to predict the species richness on sandy beaches
- Data from the dutch National Institute for Coastal and Marine Management (RIKZ: Rijksinstituut voor Kust en Zee)
- see also

Zuur, Ieno, Smith (2007) *Analysing Ecological Data.* Springer

```
> rikz_data <- read.delim("RIKZGroups.txt")
> dim(rikz_data)
[1] 45 17
> colnames(rikz_data)
 [1] "Sample"         "Polychaeta"     "Crustacea"
 [4] "Mollusca"       "Insecta"        "week"
 [7] "angle1"         "angle2"         "exposure"
[10] "salinity"       "temperature"    "NAP"
[13] "penetrability"  "grainsize"      "humus"
[16] "chalk"          "sorting1"
```

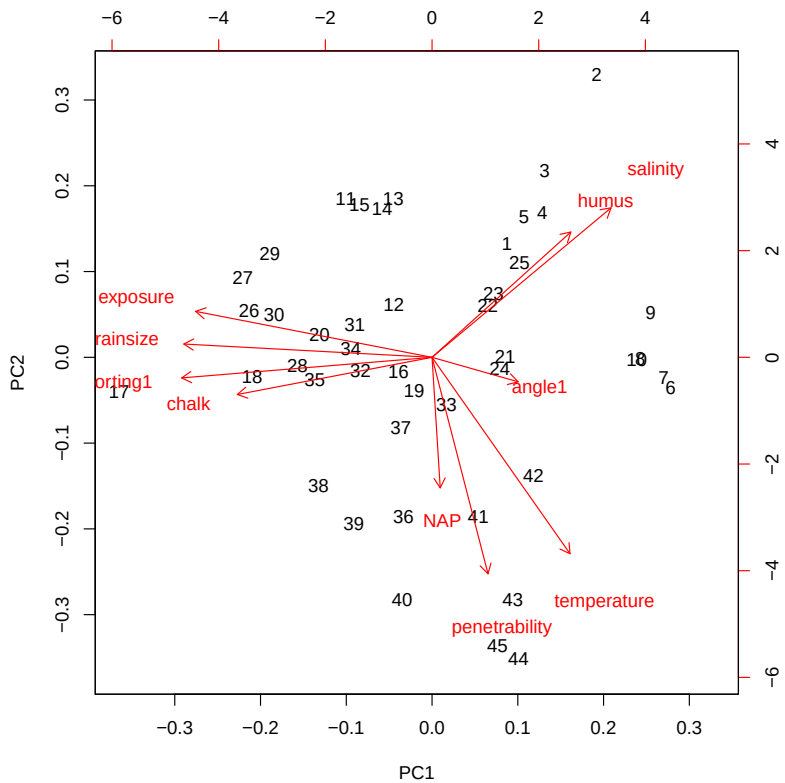
Meaning of the Variables

index i	index of sampling station
richness	Number of species that were found in a plot.
angle1	angle of the station
angle2	slope of the beach a the plot
exposure	index composed of wave action etc.
NAP	altitude of the plot compared to the mean sea level.
grainsize	average diameter of sand grains
humus	fraction of organic material
week	in which of 4 weeks was this plot probed.

(many more variables in original data set)

Explanatory Variables

```
> explanatory <- c(7, 9:17)
> pca <- prcomp(rikz_data[ , explanatory], scale = TRUE)
> biplot(pca, scale = 1)
```



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- Most likely, not more than one of each group will have a significant influence.
- We can use the biplot to manually choose only one of each group of highly correlated variables.
- Or we can use the PCA components as explanatory variables.

Model

We use the model

$$\text{Crustacea} = \beta_0 + \beta_1 Z_1 + \ldots + \beta_n Z_n + \varepsilon$$

where the Z_i are the values of the data's i-th PC.

Model

```
> rikz_data_pca <- data.frame(Crustacea = rikz_data$Crus
> fitted_model <- glm(Crustacea ~ ., data = rikz_data_pc
> summary(fitted_model)
Call:
glm(formula = Crustacea ~ ., data = rikz_data_pca)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-71.660   -8.869   -0.340    7.445  124.395

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  20.4444     5.2207   3.916 0.000412 ***
PC1           9.4165     2.7633   3.408 0.001701 **
PC2           3.3396     3.9664   0.842 0.405690
PC3           6.1369     4.8754   1.259 0.216693
```

Model

After dropping non-significant variables, only PC1 and PC9 remain:

```
> fitted_model_2 <- glm(Crustacea ~ PC1 + PC9, data = ri
> summary(fitted_model_2)
Call:
glm(formula = Crustacea ~ PC1 + PC9, data = rikz_data_pca

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-50.155  -19.186   -5.232   11.129  141.578

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   20.444      5.182   3.945 0.000297 ***
PC1            9.417      2.743   3.433 0.001354 **
PC9           32.881     15.120   2.175 0.035333 *
---
```

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To do so, we multiply the coefficients with the loadings of the corresponding principal component.

Interpretation

```
> pca$rotation[ , c(1,9)] %*%
+   fitted_model_2$coefficients[-1]
                              [,1]
angle1                   4.2215458
exposure               -22.0660880
salinity                 8.2313874
temperature            -16.0715593
NAP                      6.6778369
penetrability           11.3565887
grainsize                5.5566109
humus                    0.4565255
chalk                    7.0286887
sorting1                -9.2184292
```

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- As the variables were normalized, we can directly compare the factors. The larger absolute value, the larger is influence of the variable.
- We can use them to predict the species richness of new observations. We however need to apply the same normalization transformation, i.e. subtract mean and divide by the standard distribution of the training data.
- Maybe better suited: Linear Disriminant Analysis instead of PCA (not covered here).