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```
# PCA on Trebic grasslands - biplots with two different scalings
grasslands.spe <- read.delim
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/data/grasslands-spe.txt', row.names = 1)
grasslands.env <- read.delim
('https://raw.githubusercontent.com/zdealveindy/anadat-r/master/data/grasslands-env.txt')

library (vegan)
library (RColorBrewer)

cols <- brewer.pal (6, 'Dark2')

PCA <- rda (log1p (grasslands.spe))
groups <- as.numeric (grasslands.env$classification)

png ('pca_grasslands.png', width = 8, height = 4, units = 'in', res = 300,
pointsize = 10)
par (mfrow = c(1,2))
biplot (PCA, display = 'sites', scaling = 'species', type = 'n', main =
'Grasslands dataset: sample scores\n(scaling = 1, focus on sites)')
points (PCA, display = 'sites', pch = as.character (groups), scaling =
'species', col = cols[groups])
biplot (PCA, display = 'species', scaling = 'species', main = 'Grasslands
dataset: species scores\n(scaling = 2, focus on species)')
dev.off ()
```

From:

<https://www.davidzeleny.net/anadat-r/> - **Analysis of community ecology data in R**

Permanent link:

[https://www.davidzeleny.net/anadat-r/doku.php/en:pca\\_rscript](https://www.davidzeleny.net/anadat-r/doku.php/en:pca_rscript)

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