

# Ecological ordination

## Homework Wk 11

### *The assignment*

#### Data loading and file preparation

Using [these data on wading bird counts in Southern Africa](#) and functions from the **vegan** package, perform a non-Euclidean ordination and necessary analyses to provide at least one customized biplot and answer the questions below.

You will again create your .Rmd file from scratch and upload the knitr-ed Word document to Blackboard. This time, **provide your R code at the end of the assignment as an Appendix**. To do so, insert the following R **markdown** code chunks at the end of your .Rmd file (obviously, don't use the double ## comment operators). *Practice using them now as they will be required in your final paper*. Example output follows on page 2 of this assignment.

This code chunk collects all your previous code chunks and compiles them at the end:

```
## # Appendix
## ## Full session script
## ```{r ref.label=knitr::all_labels(),echo=TRUE,eval=FALSE}
## ```
```

This code chunk reports information about the computer you used, the R version, and various package versions you have loaded:

```
## ## Session info
## ```{r sessionInfo, echo=FALSE}
## sessionInfo();
## ```
```

A handy code chunk option is `fig.cap`, which allows you to attach a caption to the figure produced by that code chunk. Practice using it to see how you can make your Word output even more professional.

```
## ```{r fig.cap='This is my ordination of African wader birds.'}
## plot(wader.ord)
## ```
```

#### Questions

1. Which function/distance measure did you choose, and why?
2. How can you be confident your ordination is a decent representation of variation in these data?
3. Which categorical variable(s) show the most difference in the bird communities? Which show the least? Provide evidence/examples.
4. Which bird species contribute the most to variation among habitat types?
5. Which bird species seems most abundant along Northern Namibian coastlines?

# Appendix

## Full session script

```
# Code Chunk 1
knitr::opts_chunk$set(message = FALSE, warning=FALSE,
                        echo=FALSE, eval=TRUE)

# Code Chunk 2
if (!require("pacman")) install.packages("pacman")
pacman::p_load(s20x,vegan)

# Code chunk 3
cat(" # Appendix
\ ## Full session script
\ ```{r ref.label=knitr::all_labels(),echo=TRUE,eval=FALSE}
\ ```")

# Code chunk 4
cat(" ## Session info
\ ```{r sessionInfo, echo=FALSE}
\ sessionInfo();
\ ```")

# Code chunk 5
cat("\ ```{r fig.cap='This is my ordination of African wader birds.'}
\ plot(wader.ord)
\ ```")
sessionInfo();
```

## Session information

```
## R version 3.3.1 (2016-06-21)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 7 x64 (build 7601) Service Pack 1
##
## locale:
## [1] LC_COLLATE=English_United States.1252
## [2] LC_CTYPE=English_United States.1252
## [3] LC_MONETARY=English_United States.1252
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.1252
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] vegan_2.4-1      lattice_0.20-33 permute_0.9-0   s20x_3.1-17
## [5] pacman_0.4.1
##
## loaded via a namespace (and not attached):
## [1] Rcpp_0.12.6      digest_0.6.10   MASS_7.3-45     grid_3.3.1
## [5] nlme_3.1-128     formatR_1.4     magrittr_1.5    evaluate_0.9
## [9] stringi_1.1.1    Matrix_1.2-6    rmarkdown_1.0   tools_3.3.1
## [13] stringr_1.1.0    parallel_3.3.1 yaml_2.1.13     cluster_2.0.4
## [17] mgcv_1.8-12      htmltools_0.3.5 knitr_1.14
```