

Ecological ordination

Homework Week 11

The Solution

25 April 2019

Which function/distance measure did you choose, and why?

This ordination was fit with the `capscale` function using the Bray-Curtis distance measure and the `metaMDS` options because this fit these data best and had the maximal variance explained in the top two axes.

How can you be confident your ordination is a decent representation of variation in these data?

More than 70% of variation is explained by the first two axes (Table 1), after which further inertia is marginal (Fig. 1).

	MDS1	MDS2	MDS3	MDS4	MDS5
Eigenvalue	0.88	0.23	0.14	0.12	0.08
Proportion Explained	0.58	0.15	0.09	0.08	0.05
Cumulative Proportion	0.58	0.73	0.82	0.90	0.95

Table 1: Proportion variance explained by the first five axes of the MDS.

Which categorical variable(s) show the most difference in the bird communities? Which show the least? Provide evidence/examples.

As the only factor with $P > 0.10$, Location provides the least explanation of difference in the bird communities, while Habitat is the best (Table 2).

Term	R squared	P value
Country	0.20	0.04
Ocean	0.19	0.06
Location	0.58	0.46
Habitat	0.42	0.00

Table 2: Results of `factorfit` on wader data.

Which bird species contribute the most to variation among habitat types?

This is a case where a constrained ordination most directly answers the question. Fitting `Habitat` as a constraint, Whitefronted Plover and Avocet are at the opposite ends of the first (constrained) axis (-0.73 and 0.44, respectively; Table 3).

Which bird species seems most abundant along Northern Namibian coastlines?

Turnstones are the species most associated with Namibian coastlines (Fig. 2).

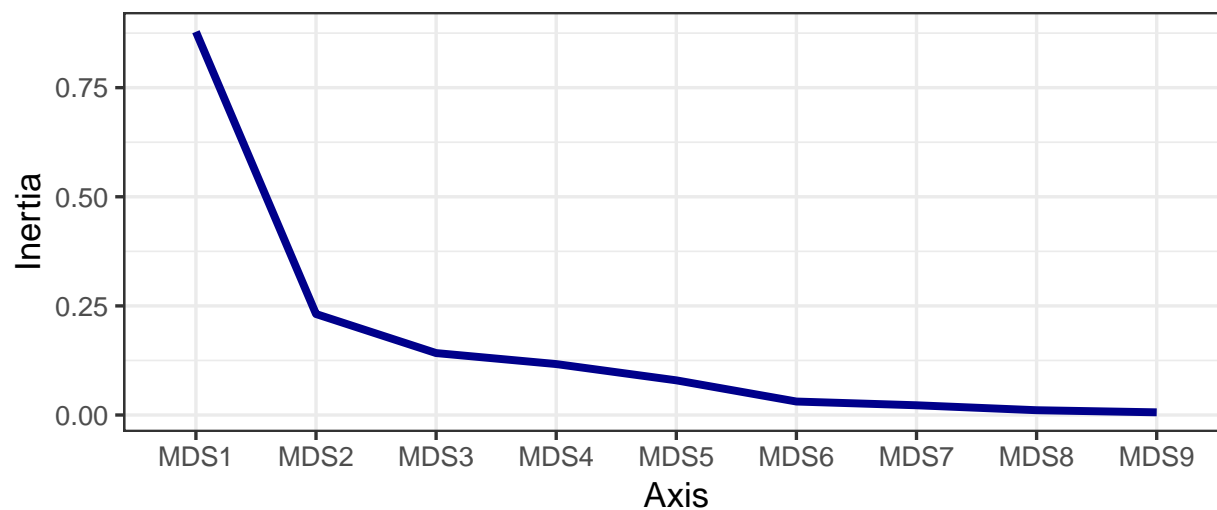


Figure 1: Screeplot for the Bray-Curtis MDS on the wader data.

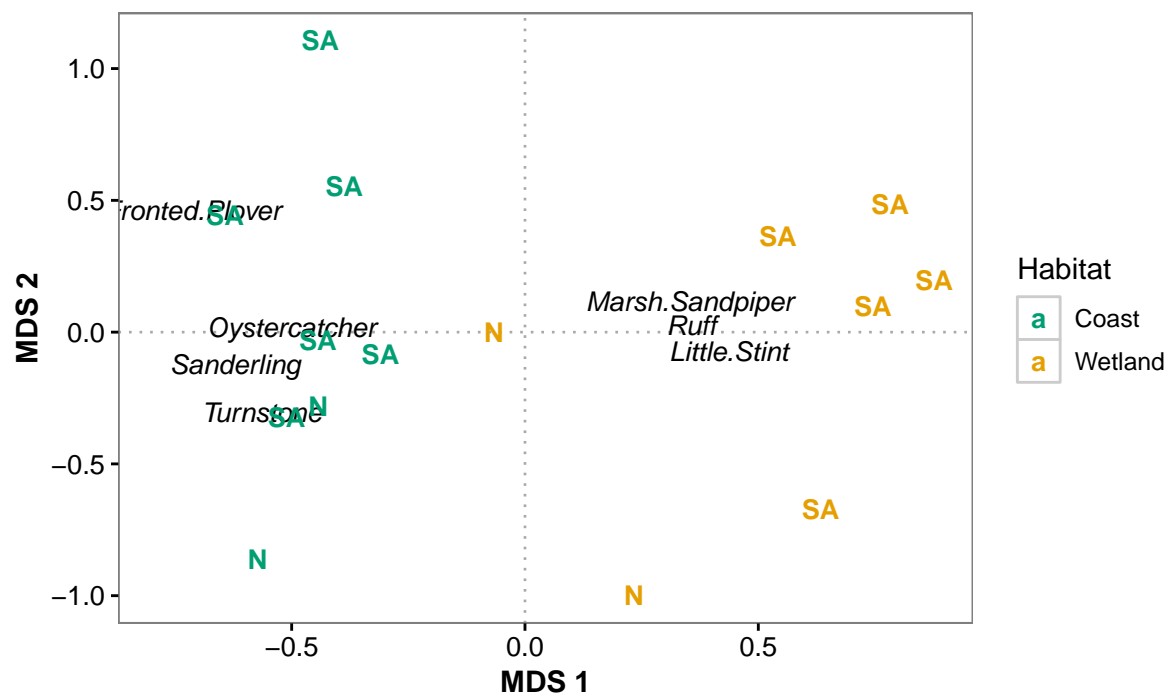


Figure 2: Species scores and site scores plotted by habitat and country (N=Namibia, SA=South Africa).

species	CAP1
WhiteFronted.Plover	-0.73
Sanderling	-0.60
Oystercatcher	-0.58
Turnstone	-0.51
Avocet	0.44
Little.Stint	0.38
BlackWinged.Stilt	0.31
Ruff	0.28
Marsh.Sandpiper	0.27
ThreeBanded.Plover	0.22
Kittlitz.Plover	0.22
Ringed.Plover	0.20
Whimbrel	-0.18
Greenshank	0.14
Common.Sandpiper	-0.14
Curlew.Sandpiper	0.14
BarTailed.Godwit	0.11
Grey.Plover	0.05
Knot	-0.03

Table 3: Species ranked by absolute value of species score along CAP1 in the constrained **capscale** model $[y_n] \sim \text{Habitat}$. CAP1 accounts for 75% of variance in the data. The constrained model is significantly better than the unconstrained ordination (Table 4).

Model 1: wader.comm \sim 1					
Model 2: wader.comm \sim Habitat					
ResDf	ResChiSquare	Df	ChiSquare	F	Pr(>F)
14	1.52				
13	0.77	1	0.75	12.60	0.0010

Table 4: Results of statistical comparison of constrained vs. unconstrained models.

Appendix

Full session script

```
knitr::opts_chunk$set(message = FALSE, warning=FALSE,
                        echo=FALSE, eval=TRUE, fig.align = 'center')
if (!require("pacman")) install.packages("pacman")
source('https://raw.githubusercontent.com/devanmcg/rangeR/master/R/CustomGGplotThemes.R')
source("https://raw.githubusercontent.com/devanmcg/rangeR/master/R/CustomCommunityFunctions.R")
pacman::p_load(vegan, tidyverse, broom, ggordiplots, RVAideMemoire, xtable)
waders <- read_csv("C:/Users/Devan.McGranahan/GoogleDrive/Teaching/Classes/Analysis of Ecosystems/comp
wader.comm <- waders %>%
  select(., .data$Oystercatcher :.data$BlackWinged.Stilt)
wader.mds <- capscale(wader.comm ~ 1, distance="bray", metaMDSdist=TRUE,
                     engine=monoMDS, autotransform=TRUE)

var.view(wader.mds, 5) %>%
  xtable("Proportion variance explained by the first five axes of the MDS.", label="VarView") %>%
  print(comment=FALSE, include.rownames=TRUE)

enframe(wader.mds$CA$eig) %>%
  plyr::rename(c("value"="Inertia")) %>%
  slice(1:9) %>%
ggplot() + theme_bw(14) +
  geom_line(aes(x=name, y=Inertia, group=1),
            color="darkblue", size=1.5) +
  labs(x="Axis")
w.fit <- envfit(wader.mds ~ Country + Ocean + Location + Habitat, data=waders)$factors
hab.cap <- capscale(wader.comm ~ waders$Habitat, distance="bray", metaMDSdist=TRUE,
                  engine=monoMDS, autotransform=TRUE)
scores(hab.cap, display="species") %>%
  as.data.frame() %>%
  rownames_to_column("species") %>%
  select(-MDS1) %>%
  arrange(desc(abs(CAP1))) %>%
  xtable("Species ranked by absolute value of species score along \\texttt{CAP1} in the constrain
  print(comment=FALSE, include.rownames=FALSE)
spp.sc <- scores(wader.mds, display="species") %>%
  as.data.frame() %>%
  rownames_to_column("species")

site.sc <- scores(wader.mds, display="sites") %>%
  as.data.frame() %>%
  mutate(Country = ifelse(waders$Country == "Namibia", "N", "SA"),
         Habitat = waders$Habitat)

ggplot() + theme_ord(12) +
  geom_vline(xintercept = 0, lty=3, color="darkgrey") +
  geom_hline(yintercept = 0, lty=3, color="darkgrey") +
  labs(x="MDS 1", y="MDS 2") +
  geom_text(data=filter(spp.sc, abs(MDS1) > 0.3),
            aes(x=MDS1*1.0, y=MDS2*1.5,
                label=species),
```

```

    fontface="italic",
    check_overlap = TRUE) +
geom_text(data=site.sc, aes(x=MDS1, y=MDS2,
                           label=Country,
                           color=Habitat),
          fontface="bold",
          check_overlap = TRUE) +
scale_color_manual(name="Habitat", values = cbPal5)

```

Session info

```

## R version 3.5.3 (2019-03-11)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 17763)
##
## Matrix products: default
##
## 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] xtable_1.8-3      RVAideMemoire_0.9-73 ggordiplots_0.3.0
## [4] broom_0.5.2       forcats_0.4.0       stringr_1.4.0
## [7] dplyr_0.8.0.1     purrr_0.3.2         readr_1.3.1
## [10] tidyr_0.8.3       tibble_2.1.1        ggplot2_3.1.1
## [13] tidyverse_1.2.1   vegan_2.5-4         lattice_0.20-38
## [16] permute_0.9-5     pacman_0.5.1
##
## loaded via a namespace (and not attached):
## [1] tidyselect_0.2.5 xfun_0.6             splines_3.5.3       haven_2.1.0
## [5] colorspace_1.4-1 generics_0.0.2       htmltools_0.3.6     yaml_2.2.0
## [9] mgcv_1.8-28      rlang_0.3.4         pillar_1.3.1        withr_2.1.2
## [13] glue_1.3.1       modelr_0.1.4        readxl_1.3.1        plyr_1.8.4
## [17] munsell_0.5.0    gtable_0.3.0        cellranger_1.1.0    rvest_0.3.2
## [21] evaluate_0.13    labeling_0.3         knitr_1.22          parallel_3.5.3
## [25] Rcpp_1.0.1       backports_1.1.3     scales_1.0.0        jsonlite_1.6
## [29] hms_0.4.2        digest_0.6.18       stringi_1.4.3       grid_3.5.3
## [33] cli_1.1.0        tools_3.5.3         magrittr_1.5         lazyeval_0.2.2
## [37] cluster_2.0.7-1  crayon_1.3.4        pkgconfig_2.0.2     MASS_7.3-51.3
## [41] Matrix_1.2-17    xml2_1.2.0          lubridate_1.7.4     assertthat_0.2.1
## [45] rmarkdown_1.12   httr_1.4.0          rstudioapi_0.10     R6_2.4.0
## [49] nlme_3.1-137     compiler_3.5.3

```