Supplemental material: Intraspecific variation and directional casque asymmetry in adult southern cassowaries (*Casuarius casuarius*)

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This document contains a supplemental table of specimen data, a figure depicting shape quantification (page 4), and the R code used in the analyses of the associated article (page 5). It is two R scripts concatenated, one for landmarking the data, and one for analysis of said data. This is meant to provide an easily readable document highlighting our approach to data quantification and analysis. These two R scripts can be found and downloaded on the following github repository: Intraspecific-variation-southern-cassowaries.

### Supplemental Table

Adult *Casuarius casuarius* specimen list, indicating sex, preparation history, and data collected.

| Specimen ID          | Sex | Type | LAT | ROS | DEV | DEG | GEO |
|----------------------|-----|------|-----|-----|-----|-----|-----|
| AMNH FLUID 12483     | M   | Fluid|x    | x   | R   | SM  | SPNG|
| AMNH FLUID 15259     | F   | Fluid|x    | x   | R   | SR  | SPNG|
| AMNH FLUID 15261     | M   | Fluid|x    | x   | R   | SM  | SPNG|
| AMNH FLUID 15262     | F   | Fluid|x    | x   | R   | SR  | SPNG|
| AMNH FLUID 6401      | U   | Fluid|x    | x   | R   | NM  | —   |
| AMNH SKIN 10804      | U   | Dried|x | x | R   | SM  | WIS |
| AMNH SKIN 11574      | M   | Dried|x | x | R   | SM  | WIS |
| AMNH SKIN 155232     | U   | Dried|x | x | R   | SM  | —   |
| AMNH SKIN 155401     | U   | Dried|x | x | R   | NM  | —   |
| AMNH SKIN 300522     | U   | Dried|x | x | L   | NM  | —   |
| AMNH SKIN 421657     | F   | Dried|x | x | R   | SR  | SPNG|
| AMNH SKIN 424915     | M   | Dried|x | x | R   | SM  | SPNG|
| BVZ Juliet 2020      | F   | Live|x | x | R   | SM  | —   |
| BVZ Romeo 2020       | M   | Live|x | x | L   | SM  | —   |
| CCP Dino 2019        | M   | Live|x | x | R   | SM  | —   |
| CCP Eyegore 2020     | M   | Live|x | x | L   | SM  | —   |
| CCP Fred 2020        | M   | Live|x | x | R   | SM  | —   |
| CCP Ginger 2019      | F   | Live|x | x | L   | SM  | —   |
| CCP Godiva 2020      | F   | Live|x | x | L   | SM  | —   |
| CCP Lucky 2019       | F   | Live|x | x | R   | SM  | —   |
| CCP Nemesis 2019     | F   | Live|x | x | R   | SM  | —   |
| CCP Pugsley 2019     | M   | Live|x | x | L   | SM  | —   |
| CCP Quattles 2020    | M   | Live|x | x | R   | SM  | —   |
| CCP Wednesday 2019   | F   | Live|x | x | R   | SM  | —   |
| DMNS ZB. 33689       | M   | Dried|x | — | L   | —   | —   |
| DMNS ZB. 33690       | F   | Dried|x | — | R   | —   | —   |
| DMNS ZB. 50012       | M   | Dried|— | — | R   | —   | —   |
| MOO 3914             | U   | Skel.|x | x | L   | NM  | —   |
| Specimen ID | Sex | Type | LAT | ROS | DEV | DEG | GEO |
|------------|-----|------|-----|-----|-----|-----|-----|
| MOO 6994   | M   | Skel.| x   | x   | R   | SM  | —   |
| MOO 8031   | F   | Skel.| x   | x   | L   | SR  | —   |
| MV 51886   | U   | Dried| x   | —   | R   | —   | —   |
| MV B17741  | U   | Dried| x   | x   | R   | NM  | —   |
| MV R11696  | F   | Dried| x   | x   | R   | SM  | AUS |
| MV R12279  | M   | Dried| x   | —   | N   | —   | AUS |
| MV R12282  | U   | Dried| x   | x   | R   | SM  | AUS |
| MV R3089   | U   | Dried| x   | x   | R   | SM  | AUS |
| MV R5243   | U   | Dried| x   | x   | R   | SM  | AUS |
| MV R8046   | U   | Dried| x   | x   | R   | SM  | AUS |
| NHMUK 1852.12.5.20 | U | Skel.| x   | x   | R   | SM  | —   |
| NHMUK 1878.3.29.1 | U | Dried| x   | —   | L   | —   | INDP |
| NHMUK 1916.5.30.1481 | U | Dried| x   | x   | R   | SM  | INDP |
| NHMUK 1916.5.30.1482 | U | Dried| x   | x   | R   | SR  | —   |
| NHMUK 1916.5.30.1483 | F | Dried| x   | x   | R   | SM  | INDP |
| NHMUK 1939.12.20.10 | U | Dried| x   | x   | R   | SM  | —   |
| NHMUK 1939.12.20.2 | U | Dried| x   | x   | N   | NM  | WIS |
| NHMUK 1939.12.20.3 | U | Dried| x   | x   | R   | SM  | AUS |
| NHMUK 1939.12.9 | U | Dried| x   | x   | R   | SR  | SPNG |
| NHMUK 1939.12.9.4 | F | Dried| x   | x   | R   | SM  | AUS |
| NHMUK 1939.12.9.877 | U | Dried| x   | x   | R   | SM  | —   |
| NHMUK 1939.12.9.880 | U | Dried| x   | x   | R   | SM  | INDP |
| NHMUK 1939.12.9.882 | U | Dried| x   | x   | R   | SM  | —   |
| NHMUK 1939.12.9.884 | U | Dried| x   | x   | R   | SM  | —   |
| NHMUK 1939.12.9.890 | U | Dried| x   | x   | L   | NM  | —   |
| NHMUK 1939.12.9.894 | M | Dried| x   | —   | R   | —   | —   |
| NHMUK 1939.12.9.895 | U | Dried| x   | x   | R   | SM  | WIS |
| NHMUK 1939.12.9.896 | U | Dried| x   | x   | R   | SM  | SPNG |
| NHMUK 1939.12.9.899 | U | Dried| —   | x   | R   | SM  | —   |
| NHMUK 1939.12.9.907 | M | Dried| x   | —   | R   | —   | WIS |
| NHMUK 1939.12.9.910 | U | Dried| x   | x   | R   | SM  | WIS |
| NHMUK 1939.12.9.919 | U | Dried| x   | x   | L   | SM  | INDP |
| NHMUK 1939.12.9.930 | U | Dried| x   | x   | R   | SM  | —   |
| NHMUK 1939.12.9.934 | F | Dried| x   | —   | R   | —   | —   |
| NHMUK 1939.12.9.944 | M | Dried| x   | x   | R   | SR  | AUS |
| NHMUK 1939.12.9.945 | M | Dried| —   | —   | R   | —   | —   |
| NHMUK 1939.12.9.946 | F | Dried| x   | x   | R   | SM  | AUS |
| NHMUK 1939.12.9.947 | M | Dried| x   | x   | R   | NM  | AUS |
| NHMUK 1939.12.9.948 | F | Dried| x   | x   | R   | SM  | AUS |
| NHMUK 1939.12.9.950 | M | Dried| x   | x   | R   | SM  | AUS |
| NHMUK 1939.12.9.953 | M | Dried| x   | x   | R   | SM  | AUS |
| NHMUK 1939.12.9.957 | M | Dried| —   | —   | R   | —   | —   |
| NHMUK 1939.12.9.964 | U | Dried| x   | x   | R   | SM  | INDP |
| NHMUK 1939.12.9.967 | M | Dried| x   | x   | R   | SM  | —   |
| NHMUK 1939.12.9.968 | U | Dried| x   | —   | R   | —   | —   |
| NHMUK 1939.12.9.969 | M | Dried| x   | x   | LS  | NM  | WIS |
| NHMUK 1939.12.9.975 | M | Dried| —   | —   | L   | —   | —   |
| NHMUK 1942.4.14.1 | F | Dried| x   | x   | R   | NM  | —   |
| NHMUK 1942.5.29.1 | F | Dried| x   | x   | R   | SM  | —   |
| NHMUK 1965.30.1484 | F | Dried| x   | x   | R   | SR  | INDP |
| NHMUK 1996.41.888 | M | Dried| x   | x   | R   | NM  | —   |
| NHMUK 1996.41.889 | M | Dried| x   | x   | R   | SM  | —   |
| Specimen ID       | Sex | Type | LAT | ROS | DEV | DEG | GEO      |
|-------------------|-----|------|-----|-----|-----|-----|----------|
| NHMUK 1996.41.890 | U   | Dried| x   | x   | R   | SM  | —        |
| NHMUK 1996.41.892 | M   | Dried| x   | x   | L   | NM  | —        |
| NHMUK 1996.41.895 | M   | Dried| x   | x   | L   | NM  | —        |
| NHMUK 1996.41.905 | F   | Dried| x   | x   | R   | SM  | WIS      |
| NHMUK 2002.10.1   | U   | Fluid| x   | x   | R   | NM  | —        |
| NHMUK S/1979.37.5 | U   | Skel.| x   | —   | R   | —   | —        |
| NHMUK S/2010.1.20 | U   | Skel.| x   | x   | R   | SM  | —        |
| QM Exhibition Mount A | U  | Dried| x   | x   | R   | SM  | —        |
| QM Exhibition Mount C | U  | Dried| x   | x   | R   | SM  | —        |
| QM 0.20563        | M   | Dried| x   | x   | R   | SM  | SPNG     |
| QM 0.26746        | U   | Dried| x   | x   | R   | SM  | —        |
| QM 0.26825        | U   | Dried| x   | x   | R   | SM  | —        |
| QM 0.26826        | U   | Dried| x   | x   | R   | SM  | —        |
| QM 0.26827        | U   | Dried| —   | x   | R   | NM  | —        |
| QM 0.30059        | F   | Dried| —   | —   | R   | —   | —        |
| QM 0.30105        | U   | Dried| —   | —   | LS  | —   | —        |
| QM 0.3435         | U   | Dried| x   | —   | R   | NM  | INDP     |
| QM 0.3510         | U   | Dried| x   | x   | L   | NM  | —        |
| QM 0.3775         | U   | Dried| x   | x   | L   | NM  | —        |
| QM 0.5400         | M   | Dried| x   | x   | RS  | SM  | AUS      |
| QM QEB1687        | U   | Dried| x   | —   | L   | —   | —        |
| QM QEB1688        | U   | Dried| —   | —   | R   | —   | —        |
| QM QEB26828       | U   | Dried| x   | x   | R   | NM  | —        |
| QM WSERZ214       | M   | Skel.| x   | x   | R   | SM  | —        |
| TLG 001           | U   | Skel.| x   | x   | R   | SM  | —        |
| TLG (SCZ) C022 (12126) | M  | Froz.| —   | —   | L   | —   | —        |
| UNE 01138         | U   | Froz.| x   | x   | LS  | NM  | AUS      |
| WTQLD Bob 2019    | M   | Live | x   | —   | R   | —   | AUS      |
| WTQLD Bumbella 2019 | F  | Live | x   | —   | R   | —   | AUS      |
| WTQLD Krakatoa 2019 | F  | Live | x   | —   | R   | —   | AUS      |
| WTQLD Relaxowary 2019 | M  | Live|x   | —   | L   | —   | AUS      |

*F = female; M = male; U = unknown; Froz. = Frozen; Skel. = Skeleton; LAT = lateral; ROS = rostral; DEV = deviation type; DEG = degree of deviation; L = leftward; LS = leftward sinusoidal; N = none; R = rightward; RS = rightward sinusoidal; NM = none–minimal; SM = slight–moderate; SR = severe–radical; AUS = Australia; SPNG = southern Papua New Guinea; INDP = Indonesian Papua; WIS = islands west of New Guinea*
Figure 1: Exemplar harmonics (1–16; black outlines filled grey to blue) of casque outlines from an elliptical Fourier analysis. This type of analysis uses these harmonic coefficients to approximate shape of the casques across the sample. Considering that it is difficult to place homologous landmarks on cassowary casques, this non-landmark-based approach is a practical means to accurately capture shape data.
Data Landmarking

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written in R3.6.3 64-bit

PACKAGES

Load Momocs, a morphometrics package. we are using v1.3.0

```r
library(Momocs)
```

Load tibble, a package enabling tibble data structures instead of dataframes for momocs to use v3.0.3

```r
library(tibble)
```

Command to check which versions of packages are loaded and attached in the R session

```r
sessionInfo()
```

Command to ensure that no extraneous objects exist

```r
rm(list = ls())
```

LATERAL LANDMARKING

Data read-in and outline creation

Read in the factors list to categorize specimens, initialize as a tibble

```r
cass_info <- as_tibble(read.csv("FILE_PATH/all_cc_lat_fac_ldk.csv", header = T, row.names = 1))
```

Check the factors are correct

```r
cass_info
```

Create an object containing the filenames to reference them for import

```r
lf_lat <- list.files("FOLDER_PATH/caque_pics_oriented_ldk/Cc_LAT", full.names = TRUE)
```

Double-check the filenames in the object

```r
lf_lat
```

Import the binary mask jpegs using the file list

```r
cass_lat_all <- import_jpg(lf_lat)
```

Convert them to outline, simultaneously adding factors to the outlines

```r
cass_lat_all_out <- Out(cass_lat_all, fac = cass_info)
```

Interpolate to the average number of points stated in the object information

```r
cass_lat_all_out_int <- coo_interpolate(cass_lat_all_out, n = 5305)
```

Double check the point numbers are correct

```r
cass_lat_all_out_int
```
Landmark Assignment and Outline Processing
Make sure to save the object returned by the command. There does not seem to be a way to go back through the specimens or edit points. Landmarks must be assigned in the same order for each specimen (I did anterior first, posterior second)

```r
cass_lat_all_ldk <- def_ldk(cass_lat_all_out_int, 2)
```

Inspect to make sure all specimens have 2 landmarks assigned

```r
inspect(cass_lat_all_ldk)
cass_lat_all_ldk
```

Plot the outlines in their unaligned state, landmarks are red

```r
stack(cc_lat_all_ldk)
```

There are only two landmarks on the outlines at the ventral ends of the casques, so a Procrustes alignment cannot work. Bookstein coordinate alignment can, as it works on only two landmarks. These will be used to establish a new baseline calculated from the first and last landmarks (or just first and second if there are only two), which is exactly what is needed.

```r
cass_lat_all_ldk_bk <- coo_bookstein(cass_lat_all_ldk)
```

Plot the aligned outlines to make sure the outlines are aligned along the same baseline

```r
stack(cass_lat_all_ldk_bk)  
```

The start points for the outlines are inconsistent. Here I create a single origin for each outline. Write the coordinates out to a csv to create a vector for the coo_slide function, identifying which point is closest to the origin (0,0) of the aligned outlines using the csv in Microsoft Excel

```r
write.csv(bookstein_test$coo, file = "Bookstein_coords_lat.csv")
```

write a vector for sliding the coordinate start point to the same x-y coordinate for all outlines. Create the list of points to shift all outline starting points to the same location

```r
slide_vector <- c(200, 76, 259, 277, 289, 135, 147, 178, 242, 159, 223, 202, 359, 258, 275, 268, 281, 303, 384, 249, 389, 181, 167, 114, 273, 141, 282, 68, 65, 156, 134, 127, 5277, 71, 159, 212, 220, 261, 322, 101, 222, 197, 171, 190, 257, 155, 277, 113, 171, 180, 229, 215, 181, 101, 141, 49, 230, 88, 87, 166, 156, 132, 107, 117, 111, 80, 131, 182, 252, 221, 339, 381, 96, 5247, 163, 159, 267, 73, 246, 91, 234, 3, 29, 133, 141, 257, 219, 160, 90, 192, 121, 145, 31, 208, 92, 200, 103, 89, 71, 238, 199, 170, 75, 138, 170, 192, 237, 137, 174, 269, 209, 134, 224, 197, 233, 144, 1, 178, 289, 239, 328)
```

Slide the start points of all outlines to ~ (0,0) using coo_slide

```r
cass_lat_all_ldk_bk_slid <- coo_slide(cass_lat_all_ldk_bk, id = slide_vector)
```

Verify the start points are relatively the same for all specimens

```r
stack(cass_lat_all_ldk_bk_slid)
```

Save the data object for redundancy

```r
save(cass_lat_all_ldk_bk_slid, file = "cass_lat_all_ldk_bk_slid.RData")
```
Slicing the data to different analytical groups

Left/Right analysis

```r
cc_test_ldk_bk_slid <- slice(cass_lat_all_ldk_bk_slid, c(1, 2, 7, 8, 13, 14, 24, 25, 26, 27, 34, 36, 69, 70, 71, 78, 85, 86, 87, 89, 102:121))

Inspect that the correct specimens were sliced into this group
```

```r
cc_test_ldk_bk_slid
print(cc_test_ldk_bk_slid$fac[, 3], n = 40)

generate graph to visually double-check the start points

stack(cc_test_ldk_bk_slid)

save outline data object
```

```r
save(cc_test_ldk_bk_slid, file = "cc_test_ldk_bk_slid.RData")
```

All lateral outlines (excluding the test data)

```r
cc_lat_all_ldk_bk_slid <- slice(cass_lat_all_ldk_bk, c(1:101))
cc_lat_all_ldk_bk_slid_id_vector <- slide_vector[c(1:101)]
cc_lat_all_ldk_bk_slid <- coo_slide(cc_lat_all_ldk_bk_slid, id = cc_lat_all_ldk_bk_slid_id_vector)

Inspect that the correct specimens were sliced into this group
```

```r
cc_lat_all_ldk_bk_slid
print(cc_lat_all_ldk_bk_slid$fac[, 1], n = 100)

generate graph to visually double-check the start points

stack(cc_lat_all_ldk_bk_slid)

Save outline data object
```

```r
save(cc_lat_all_ldk_bk_slid, file = "cc_lat_all_ldk_bk_slid.RData")
```

lateral sex analysis

```r
cc_lat_sex_ldk_bk_slid <- slice(cass_lat_all_ldk_bk_slid, c(1:4, 7, 10:23, 25, 26, 27, 38, 42, 43, 54:59, 61, 63, 64, 65, 67, 68, 69, 77, 84, 87:90, 93:101))

Inspect that the correct specimens were sliced into this group
```

```r
cc_lat_sex_ldk_bk_slid
print(cc_lat_sex_ldk_bk_slid$fac[, 1], n = 53)

generate graph to visually double-check the start points

stack(cc_lat_sex_ldk_bk_slid)

Save outline data object
```
Save the file with the sliced data:
```
save(cc_lat_sex_ldk_bk_slid, file = "cc_lat_sex_ldk_bk_slid.RData")
```

**Lateral geography analysis**

```
cc_lat_geo_ldk_bk_slid <- slice(cass_lat_all_ldk_bk_slid, c(1:4, 6, 7, 10, 11,
25, 30:33, 35, 36, 38, 40, 41, 43, 45, 49:52, 54:60, 62, 63, 69, 76, 77, 81,
84, 87:90, 95, 97, 98))
```

Inspect that the correct specimens were sliced into this group
```
cc_lat_geo_ldk_bk_slid
```

Double check the geography data are accurate
```
print(cc_lat_geo_ldk_bk_slid$fac[, 2], n = 45)
```

Generate a graph to visually double-check the start points
```
stack(cc_lat_geo_ldk_bk_slid)
```

Save the outline data object
```
save(cc_lat_geo_ldk_bk_slid, file = "cc_lat_geo_ldk_bk_slid.RData")
```

**Lateral geography-sex analysis**

```
cc_lat_geo_sex_ldk_bk_slid <- slice(cass_lat_all_ldk_bk_slid, c(1:4, 10, 11, 25,
43, 54:59, 77, 84, 87:90, 95))
```

Inspect that the correct specimens were sliced into this group
```
cc_lat_geo_sex_ldk_bk_slid
```

Double check the sex and geography data are accurate
```
print(cc_lat_geo_sex_ldk_bk_slid$fac[, n = 21])
```

Generate a graph to visually double-check the start points
```
stack(cc_lat_geo_sex_ldk_bk_slid)
```

Save the outline data object
```
save(cc_lat_geo_sex_ldk_bk_slid, file = "cc_lat_geo_sex_ldk_bk_slid.RData")
```

**ANTERIOR LANDMARKING**

**Data read-in and outline creation**

Read in the factors list to categorize specimens
```
cass_info <- as_tibble(read.csv("FILE_PATH/all_cc_ant_fac_ldk.csv", header = T,
row.names = 1))
```

Check the factors are correct
```
cass_info
```

Create an object containing the filenames to reference them for import
lf_ant <- list.files("FOLDER_PATH/CC_ANT", full.names = TRUE)

Double-check the filenames in the object
lf_ant

Import the binary mask jpegs using the file list
cass_ant_all <- import_jpg(lf_ant)

Convert them to outline, simultaneously adding factors to the outlines
cass_ant_all_out <- Out(cass_ant_all, fac = cass_info)

Interpolate to the average number of points stated in the object information
cass_ant_all_out
cass_ant_all_out_int <- coo_interpolate(cass_ant_all_out, n = 3626)

Double check the point numbers are correct
cass_ant_all_out_int

Landmark Assignment and Outline Processing

Make sure to save the object returned by the command There does not seem to be a way to go back through the specimens or edit points. Landmarks must be assigned in the same order for each specimen (I did anatomical right first, left second)
cass_ant_all_ldk <- def_ldk(cass_ant_all_out_int, 2)

Inspect to make sure all specimens have 2 landmarks assigned
cass_ant_all_ldk
cass_ant_all_ldk$ldk

Plot the outlines in their unaligned state, landmarks are red
stack(cass_ant_all_ldk)

There are only two landmarks on the outlines at the ventral ends of the casques, so a Procrustes alignment cannot work. Bookstein coordinate alignment can, as it works on only two landmarks. These will be used to establish a new baseline calculated from the first and last landmarks (or just first and second if there are only two), which is exactly what is needed.
cass_ant_all_ldk_bk <- coo_bookstein(cass_ant_all_ldk)

Plot the aligned outlines to make sure the outlines are aligned along the same baseline
stack(cass_ant_all_ldk_bk) #(they are)

save this workspace
save.image("C:/Users/dik10/Documents/cass_ant_landmark_workspace.RData")

The start points for the outlines are inconsistent. Here I create a single origin for each outline Write the coordinates out to a csv to create a vector for the coo_slide function, identifying which point is closest to the origin (0,0) of the aligned outlines using the csv in Microsoft Excel
write.csv(cass_ant_all_ldk_bk$coo, file = "cc_ant_Bookstein_coo.csv")

write a vector for sliding the coordinate start point to the same x-y coordinate for all outlines Create the list of points to shift all outline starting points to the same location
slide_vector <- c(25, 3446, 3575, 3492, 3608, 58, 3616, 3608, 27, 3454, 3567, 3515, 46, 46, 47, 3589, 83, 51, 31, 3558, 40, 3584, 3534, 3530, 46, 3623, 8, 11, 3619, 3566, 3606, 3623, 3550, 3592, 3485, 3565, 3532, 3564, 2, 3552, 3541, 3612, 3600, 3567, 3597, 3617, 3526, 3623, 19, 31, 3525, 3539, 3564, 3617, 3584, 3510, 3525, 3499, 3579, 38, 3532, 3618, 3585, 3529, 18, 3611, 3613, 3614, 54, 3581, 31, 3573, 3571, 3610, 3527, 3603, 3589, 3586, 3509, 8, 15, 5, 19, 3610, 32, 3561)

Slide the start points of all outlines to ~ (0,0) using coo_slide

cass_ant_all_ldk_bk_slid <- coo_slide(cass_ant_all_ldk_bk_slid, 
id = slide_vector)

Verify the start points are relatively the same for all specimens

stack(cass_ant_all_ldk_bk_slid)

Save the data object for redundancy

save(cass_ant_all_ldk_bk_slid, file = "cass_ant_all_ldk_bk_slid.RData")

Slicing the data to different analytical populations

All anterior outlines

cc_ant_all_ldk_bk_slid <- cass_ant_all_ldk_bk_slid

Inspect that the correct specimens were sliced into this group

cc_ant_all_ldk_bk_slid

generate graph to visually double-check the start points

stack(cc_ant_all_ldk_bk_slid)

Save outline data object

save(cc_ant_all_ldk_bk_slid, file = "cc_ant_all_ldk_bk_slid.RData")

Anterior sex analysis

cc_ant_sex_ldk_bk_slid <- slice(cass_ant_all_ldk_bk_slid, c(1:4, 7, 11:26, 29, 41, 53:58, 60, 61, 63:67, 69, 70, 71, 76, 78, 85))

Inspect that the correct specimens were sliced into this group

cc_ant_sex_ldk_bk_slid

Double check the sex data are accurate

print(cc_ant_sex_ldk_bk_slid$fac[, 1], n = 42)

generate graph to visually double-check the start points

stack(cc_ant_sex_ldk_bk_slid)

Save outline data object

save(cc_ant_sex_ldk_bk_slid, file = "cc_ant_sex_ldk_bk_slid.RData")
Anterior geography analysis

\[ \text{cc\_ant\_geo\_ldk\_bk\_slid} \leftarrow \text{slice}(\text{cass\_ant\_all\_ldk\_bk\_slid}, \text{c}(1:4, 6, 7, 11, 12, 29:33, 35, 37, 39, 40, 41, 43, 47, 48, 50, 51, 53:59, 61, 62, 65, 71, 77, 78, 85)) \]

Inspect that the correct specimens were sliced into this group

\[ \text{cc\_ant\_geo\_ldk\_bk\_slid} \]

Double check the geography data are accurate

\[ \text{print}(\text{cc\_ant\_geo\_ldk\_bk\_slid$fac[, 2], n = 37}) \]

generate graph to visually double-check the start points

\[ \text{stack}(\text{cc\_ant\_geo\_ldk\_bk\_slid}) \]

Save outline data object

\[ \text{save}(\text{cc\_ant\_geo\_ldk\_bk\_slid, file = "cc\_ant\_geo\_ldk\_bk\_slid.RData"}) \]

Anterior geography-sex analysis

\[ \text{cc\_ant\_geo\_sex\_ldk\_bk\_slid} \leftarrow \text{slice}(\text{cass\_ant\_all\_ldk\_bk\_slid}, \text{c}(1:4, 11, 12, 29, 41, 53:58, 78, 85)) \]

Inspect that the correct specimens were sliced into this group

\[ \text{cc\_ant\_geo\_sex\_ldk\_bk\_slid} \]

Double check the sex and geography data are accurate

\[ \text{print}(\text{cc\_ant\_geo\_sex\_ldk\_bk\_slid$fac, n = 16}) \]

generate graph to visually double-check the start points

\[ \text{stack}(\text{cc\_ant\_geo\_sex\_ldk\_bk\_slid}) \]

Save outline data object

\[ \text{save}(\text{cc\_ant\_geo\_sex\_ldk\_bk\_slid, file = "cc\_ant\_geo\_sex\_ldk\_bk\_slid.RData"}) \]

Geometric Morphometric Analysis of Southern Cassowary Casque Outlines

LANDMARK-BOOKSTEIN ALIGNMENT with SINGLE ORIGIN

2021 David Ian Kay

written in R3.6.3 64-bit

cmd for clearing out all read in data, objects, attached data, etc.

\[ \text{rm(list = ls())} \]
PACKAGES
Read in Momocs, a morphometrics package. We are using v1.3.0
library(Momocs)

Read in tibble to coerce dataframes to tibble type for momocs to use v3.0.3
library(tibble)

Read in ggplot2 library, v3.3.2
library(ggplot2)

Packages necessary for the linear discriminant analysis (LDA) with the principal coordinate analysis (PCO) results
library(MASS)  #v7.3-51.5
library(vegan)  #v2.5-6

Command to display the loaded packages, versions, and other attached information
sessionInfo()

RIGHT/LEFT SPECIFICITY ANALYSIS

Initial Data read-in
Initial data read-in of the Out object with landmarks assigned created in the data_landmarking_.R script
load("FILE_PATH/cc_test_ldk_bk_slid.RData")

Check the objects from the loaded data file
ls()

Elliptical Fourier Transformation  Calibrate harmonics needed to capture 99.9% shape variance (or N-1 harmonics)
cc_test_ldk_bk_slid_harm <- calibrate_harmonicpower_efourier(cc_test_ldk_bk_slid, nb.h = 20, plot = T)
c_test_ldk_bk_slid_harm  #16 harmonics capture 99.9% shape variance

Altered graph to show more than the default 10 harmonics
cc_test_ldk_bk_slid_harm$gg + theme_minimal() + coord_cartesian(xlim = c(0.5, 17), ylim = c(0, 100)) + ggtitle("left/right landmark bk slid test Harmonic calibration")

Calibrate the chosen number of reconstructions
calibrate_reconstructions_efourier(cc_test_ldk_bk_slid, range = 1:16)

Elliptical Fourier transformation with the number of harmonics previously chosen from the calibration
cc_test_ldk_bk_slid_e_trans <- efourier(cc_test_ldk_bk_slid, nb.h = 16, norm = F)

Principal coordinate analysis  Using the MDS function in Momocs
cc_test_ldk_bk_slid_MDS_MOMOCS <- MDS(cc_test_ldk_bk_slid_e_trans, k = 39)
Examine the output for the MDS

```r
str(cc_test_ldk_bk_slid_MDS_MOMOCS)
summary(cc_test_ldk_bk_slid_MDS_MOMOCS)
cc_test_ldk_bk_slid_MDS_MOMOCS
```

Plot out results (first two principal coordinates only)

```r
plot_MDS(cc_test_ldk_bk_slid_MDS_MOMOCS)
plot_MDS(cc_test_ldk_bk_slid_MDS_MOMOCS, ~side)
plot_MDS(cc_test_ldk_bk_slid_MDS_MOMOCS, ~side, chullfilled = T)
```

Using the capland function in vegan package. To set up a PCO, the “formula” portion of the function call is

```r
cc_test_ldk_bk_slid_PCO_MOMOCS <- capscale(cc_test_ldk_bk_slid_e_trans ~ 1,
distance = "euclidean")
```

look at output to determine number of axes to explain 99% of variance

```r
summary(cc_test_ldk_bk_slid_PCO_MOMOCS)
```

Extract site score data

```r
cc_test_ldk_bk_slid_slid_MDS_MOMOCS_scores <- scores(cc_test_ldk_bk_slid_slid_MDS_MOMOCS,
choices = c(1, 2, 3, 4, 5, 6, 7, 8), display = c("sites"))
```

Write results to csv to be used in the MANOVA and LDA and to have a separate copy

```r
write.csv(cc_test_ldk_bk_slid_PCO_MOMOCS_scores,
file = "FILE_PATH/cc_test_ldk_bk_slid_PCO_MOMOCS.csv")
```

Read in the data for the MANOVA and LDA

```r
cc_test_ldk_bk_slid_PCO_MOMOCS_dat <- read.csv("FILE_PATH/cc_test_ldk_bk_slid_PCO_MOMOCS.csv",
header = T, row.names = 1)
cc_test_ldk_bk_slid_PCO_MOMOCS_dat
```

Read in the factor data for sides

```r
cass_info <- read.csv("FILE_PATH/test_info.csv", header = T, row.names = 1)
```

Create a dataframe of the principal coordinates and the side factor data

```r
cc_test_ldk_bk_slid_PCO_MOMOCS_dat_fac <- cbind(cc_test_ldk_bk_slid_PCO_MOMOCS_dat,
cass_info$fac.side)
cc_test_ldk_bk_slid_PCO_MOMOCS_dat_fac
```

**MANOVA** Run a multiple analysis of variance on the principal coordinates

```r
cc_test_ldk_bk_slid_PCO_MANOVA <- aov(MDS1 + MDS2 +
MDS3 + MDS4 + MDS5 + MDS6 + MDS7 + MDS8 ~ fac.side,
data = cc_test_ldk_bk_slid_PCO_MOMOCS_dat_fac)
```

Look at the output

```r
summary(cc_test_ldk_bk_slid_PCO_MANOVA)
cc_test_ldk_bk_slid_PCO_MANOVA
```

**LDA** Use the data from the 8 principal coordinates produced

```r
```
cc_test_ldk_bk_slid_PCO_MOMOCS_lda <- lda(fac.side ~ MDS1 + MDS2 + MDS3 + MDS4 + MDS5 + MDS6 + MDS7 + MDS8, data = cc_test_ldk_bk_slid_PCO_MOMOCS_dat_fac)

Use the predict function to test the LDA, but establish the principal coordinate data as a dataframe
cc_test_ldk_bk_slid_PCO_MOMOCS_lda_predict <- predict(cc_test_ldk_bk_slid_PCO_MOMOCS_lda, newdata = as.data.frame(cc_test_ldk_bk_slid_PCO_MOMOCS_dat))

Check the predicted portion for a % correct
cc_test_ldk_bk_slid_PCO_MOMOCS_lda_predict$class

Build a CV table
CV.fac_all <- cc_test_ldk_bk_slid_PCO_MOMOCS_lda_predict$class
CV.tab_all <- table(cc_test_ldk_bk_slid_PCO_MOMOCS_dat[, 9], CV.fac_all)
names(dimnames(CV.tab_all)) <- c("actual", "classified")
CV.correct_all <- sum(diag(CV.tab_all))/sum(CV.tab_all)
tab_all <- CV.tab_all
ce_all <- sapply(seq_along(1:nrow(tab_all)), function(i) 1 - (sum(tab_all[i, -i])/sum(tab_all[i, ])))
names(ce_all) <- rownames(tab_all)

Correct classification rate
ce_all

Classification table
tab_all

PCA  Running a principal components analysis as well, mostly to check to see if the results would show a "horseshoe" shape due to the outlines being auto-correlated
cc_test_ldk_bk_slid_PCA <- PCA(cc_test_ldk_bk_slid_e_trans)

Output of PCA
cc_test_ldk_bk_slid_PCA
summary(cc_test_ldk_bk_slid_PCA)

Plot the PCA results
plot_PCA(cc_test_ldk_bk_slid_PCA)
plot_PCA(cc_test_ldk_bk_slid_PCA, "side")
plot_PCA(cc_test_ldk_bk_slid_PCA, "side", chullfilled = T)

MANOVA  MANOVA of the principal component data
cc_test_ldk_bk_slid_MANOVA <- MANOVA(cc_test_ldk_bk_slid_PCA, "side")
cc_test_ldk_bk_slid_MANOVA

Pairwise MANOVA
cc_test_ldk_bk_slid_MANOVA_PW <- MANOVA_PW(cc_test_ldk_bk_slid_PCA, "side")
cc_test_ldk_bk_slid_MANOVA_PW

LDA  LDA of the principal components
cc_test_ldk_bk_slid_LDA <- LDA(cc_test_ldk_bk_slid_PCA, "side")
cc_test_ldk_bk_slid_LDA
plot_CV(cc_test_ldk_bk_slid_LDA)

**Workspace save/load**   Save workspace, commented to prevent erroneous execution

```r
# save.image('FILE_PATH/cass_test_ldk_bk_slid.RData')
```

load workspace, commented to prevent erroneous execution

```r
# load('FILE_PATH/cass_test_ldk_bk_slid.RData')
```

Check the objects in the R session

```r
ls()
```

**ALL CASQUE ANALYSIS**

**CC LATERAL ASPECT**

**Initial Data read-in**   Initial data read-in of the Out object with landmarks assigned created in the data_landmarking_2.R script

```r
load("FILE_PATH/cc_lat_all_ldk_bk_slid.RData")
ls()
```

**Elliptical Fourier Transformation**   Calibrate harmonics needed to capture 99.9% shape variance (or a maximum of N-1 harmonics)

```r
cal_cc_lat_all_ldk_bk_slid <- calibrate_harmonicpower_efourier(cc_lat_all_ldk_bk_slid,
                   nb.h = 20, plot = T)
cal_cc_lat_all_ldk_bk_slid
```

Altered graph to show more than the default 10 harmonics

```r
cal_cc_lat_all_ldk_bk_slid$gg + theme_minimal() + coord_cartesian(xlim = c(0.5, 17),
                                                        ylim = c(0, 100)) + ggtitle("Southern Cassowary lateral landmark Bookstein slid
Harmonic calibration")
```

Visualize the reconstruction at various harmonics

```r
cal_cc_lat_all_ldk_bk_slid_recon <- calibrate_reconstructions_efourier(cc_lat_all_ldk_bk_slid,
                                          range = 1:16)
cal_cc_lat_all_ldk_bk_slid_recon
```

Elliptical Fourier transformation with the number of harmonics previously chosen from the calibration.

```r
cc_lat_all_ldk_bk_slid_ef <- efourier(cc_lat_all_ldk_bk_slid, nb.h = 16,
                             norm = F)
```

**PCA**   Orinate the data with a Principal Components Analysis

```r
cc_lat_all_ldk_bk_slid_PCA <- PCA(cc_lat_all_ldk_bk_slid_ef)
cc_lat_all_ldk_bk_slid_PCA
summary(cc_lat_all_ldk_bk_slid_PCA)
```

Plot out the results, export to an svg
PCA plot with point labels, export to an svg

```R
plot_PCA(cc_lat_all_ldk_bk_slid_PCA, labelpoints = T)
svg(filename = "FILE_PATH/cc_lat_all_ldk_bk_slid_PCA_002.svg")
dev.off()
```

Plotting sex results Plot with point labels, export to an svg

```R
plot(cc_lat_all_ldk_bk_slid_PCA, "sex", ellipses = T)
plot_PCA(cc_lat_all_ldk_bk_slid_PCA, "sex", labelpoints = T)
svg(filename = "FILE_PATH/cc_lat_all_ldk_bk_slid_PCA_003.svg")
dev.off()
```

Plot with convex hulls, export to an svg

```R
plot_PCA(cc_lat_all_ldk_bk_slid_PCA, "sex")
svg(filename = "FILE_PATH/cc_lat_all_ldk_bk_slid_PCA_004.svg")
dev.off()
```

Plot with convex hulls filled in, export to an svg

```R
plot_PCA(cc_lat_all_ldk_bk_slid_PCA, "sex", chullfilled = T)
svg(filename = "FILE_PATH/cc_lat_all_ldk_bk_slid_PCA_005.svg")
dev.off()
```

Plotting geography results Plot with point labels, export to an svg

```R
plot_PCA(cc_lat_all_ldk_bk_slid_PCA, "geo", labelpoints = T)
svg(filename = "FILE_PATH/cc_lat_all_ldk_bk_slid_PCA_006.svg")
dev.off()
```

Plot with convex hulls, export to an svg

```R
plot_PCA(cc_lat_all_ldk_bk_slid_PCA, "geo")
svg(filename = "FILE_PATH/cc_lat_all_ldk_bk_slid_PCA_007.svg")
dev.off()
```

Plot with convex hulls filled in, export to an svg

```R
plot_PCA(cc_lat_all_ldk_bk_slid_PCA, "geo", chullfilled = T)
svg(filename = "FILE_PATH/cc_lat_all_ldk_bk_slid_PCA_008.svg")
dev.off()
```

**Outlier Identification** Identify potential outliers using the “Which_out” function

```R
which_out(cc_lat_all_ldk_bk_slid_PCA)
```
save workspace, commented to prevent erroneous execution

```r
# save.image('FILE_PATH/cass_lat_all_ldk_bk_slid.RData')
```

load workspace, commented to prevent erroneous execution

```r
# load('FILE_PATH/cass_lat_sex_ldk_bk_slid.RData')
```

Check the objects in the R session

```r
ls()
```

**CC ANTERIOR ASPECT**

**Initial Data read-in**  Initial data read-in of the Out object with landmarks assigned created in the data_landmarking_2.R script

```r
load("FILE_PATH/cc_ant_all_ldk_bk_slid.RData")
```

Check the objects from the loaded data file

```r
ls()
```

**Elliptical Fourier Transformation**  Calibrate harmonics needed to capture 99.9% shape variance (or a maximum of N-1 harmonics)

```r
cal_cc_ant_all_ldk_bk_slid <- calibrate_harmonicpower_efourier(cc_ant_all_ldk_bk_slid, nb.h = 20, plot = T)
cal_cc_ant_all_ldk_bk_slid
```

## 14 harmonics capture 99.9% of shape

Altered graph to show more than the default 10 harmonics

```r
cal_cc_ant_all_ldk_bk_slid$gg + theme_minimal() + coord_cartesian(xlim = c(0.5, 15), ylim = c(0, 100)) + ggtitle("Southern Cassowary anterior all landmark Bookstein-slid Harmonic calibration")
```

Calibrate the chosen number of reconstructions

```r
cal_cc_ant_all_ldk_bk_slid_recon <- calibrate_reconstructions_efourier(cc_ant_all_ldk_bk_slid, range = 1:14)
cal_cc_ant_all_ldk_bk_slid_recon
```

Elliptical Fourier transformation with the number of harmonics previously chosen from the calibration

```r
cc_ant_all_ldk_bk_slid_ef <- efourier(cc_ant_all_ldk_bk_slid, nb.h = 14, norm = F)
```

**PCA**  Ordinate the data with a Principal Components Analysis

```r
cc_ant_all_ldk_bk_slid_PCA <- PCA(cc_ant_all_ldk_bk_slid_ef)
```

PCA output

```r
cc_ant_all_ldk_bk_slid_PCA
summary(cc_ant_all_ldk_bk_slid_PCA)
```

Plot out the results, export to an svg

```r
plot_PCA(cc_ant_all_ldk_bk_slid_PCA)
svg(filename = "FILE_PATH/cc_ant_all_ldk_bk_slid_PCA_001.svg")
plot_PCA(cc_ant_all_ldk_bk_slid_PCA)
dev.off()
```
PCA plot with point labels, export to an svg

```r
plot_PCA(cc_ant_all_ldk_bk_slid_PCA, labelpoints = T)
svg(filename = "FILE_PATH/cc_ant_all_ldk_bk_slid_PCA_002.svg")
plot_PCA(cc_ant_all_ldk_bk_slid_PCA, labelpoints = T)
dev.off()
```

Plotting sex results Plot with point labels, export to an svg

```r
plot_PCA(cc_ant_all_ldk_bk_slid_PCA, "sex", labelpoints = T)
svg(filename = "FILE_PATH/cc_ant_all_ldk_bk_slid_PCA_003.svg")
plot_PCA(cc_ant_all_ldk_bk_slid_PCA, "sex", labelpoints = T)
dev.off()
```

Plot with convex hulls, export to an svg

```r
plot_PCA(cc_ant_all_ldk_bk_slid_PCA, "sex")
svg(filename = "FILE_PATH/cc_ant_all_ldk_bk_slid_PCA_004.svg")
plot_PCA(cc_ant_all_ldk_bk_slid_PCA, "sex")
dev.off()
```

Plot with convex hulls filled in, export to an svg

```r
plot_PCA(cc_ant_all_ldk_bk_slid_PCA, 'sex', chullfilled=T)
svg(filename = "FILE_PATH/cc_ant_all_ldk_bk_slid_PCA_005.svg")
plot_PCA(cc_ant_all_ldk_bk_slid_PCA, "sex", chullfilled = T)
dev.off()
```

Plotting geography results Plot with point labels, export to an svg

```r
plot_PCA(cc_ant_all_ldk_bk_slid_PCA, "geo", labelpoints = T)
svg(filename = "FILE_PATH/cc_ant_all_ldk_bk_slid_PCA_006.svg")
plot_PCA(cc_ant_all_ldk_bk_slid_PCA, "geo", labelpoints = T)
dev.off()
```

Plot with convex hulls, export to an svg

```r
plot_PCA(cc_ant_all_ldk_bk_slid_PCA, "geo")
svg(filename = "FILE_PATH/cc_ant_all_ldk_bk_slid_PCA_007.svg")
plot_PCA(cc_ant_all_ldk_bk_slid_PCA, "geo")
dev.off()
```

Plot with convex hulls filled in, export to an svg

```r
plot_PCA(cc_ant_all_ldk_bk_slid_PCA, "geo", chullfilled = T)
svg(filename = "FILE_PATH/cc_ant_all_ldk_bk_slid_PCA_008.svg")
plot_PCA(cc_ant_all_ldk_bk_slid_PCA, "geo", chullfilled = T)
dev.off()
```

**Outlier Identification** Identify potential outliers using the “Which_out” function

```r
which_out(cc_ant_all_ldk_bk_slid_PCA)
```

**Workspace save/load** save the workspace for future access

```r
# save.image('FILE_PATH/cass_ant_all_ldk_bk_slid.RData')
```

command to load the workspace

```r
# load('FILE_PATH/cass_ant_all_ldk_bk_slid.RData')
```

Check the objects in the R session
SEX CASQUE ANALYSIS

CC SEX LATERAL ASPECT

**Initial Data read-in**  Initial data read-in of the Out object with landmarks assigned created in the data_landmarking_2.R script

```r
# load('FILE_PATH/cc_lat_sex_ldk_bk_slid.RData')
ls()
stack(cc_lat_sex_ldk_bk_slid)
```

**Elliptical Fourier Transformation**  Calibrate harmonics needed to capture 99.9% shape variance (or N-1 harmonics)

```r
cal_cc_lat_sex_ldk_bk_slid <- calibrate_harmonicpower_efourier(cc_lat_sex_ldk_bk_slid, nb.h = 20, plot = T)
cal_cc_lat_sex_ldk_bk_slid
```

Altered graph to show more than the default 10 harmonics

```r
cal_cc_lat_sex_ldk_bk_slid$gg + theme_minimal() + coord_cartesian(xlim = c(0.5, 17), ylim = c(0, 100)) + ggtitle("Southern Cassowary known-sex lateral landmark Bookstein slid Harmonic calibration")
```

Calibrate the chosen number of reconstructions

```r
cal_cc_lat_sex_ldk_bk_slid_recon <- calibrate_reconstructions_efourier(cc_lat_sex_ldk_bk_slid, range = 1:16)
cal_cc_lat_sex_ldk_bk_slid_recon
```

Elliptical Fourier transformation with the number of harmonics previously chosen from the calibration

```r
cc_lat_sex_ldk_bk_slid_ef <- efourier(cc_lat_sex_ldk_bk_slid, nb.h = 16, norm = F)
```

**PCA**  Ordinate the data with a Principal Components Analysis

```r
cc_lat_sex_ldk_bk_slid_PCA <- PCA(cc_lat_sex_ldk_bk_slid_ef, fac = "sex")
cc_lat_sex_ldk_bk_slid_PCA
summary(cc_lat_sex_ldk_bk_slid_PCA)
```

Plot out the results

```r
plot_PCA(cc_lat_sex_ldk_bk_slid_PCA)
svg(filename = "FILE_PATH/cc_lat_sex_ldk_bk_slid_PCA_001.svg")
plot_PCA(cc_lat_sex_ldk_bk_slid_PCA)
dev.off()
```

Plot with convex hulls, export to an svg

```r
plot_PCA(cc_lat_sex_ldk_bk_slid_PCA, "sex")
svg(filename = "FILE_PATH/cc_lat_sex_ldk_bk_slid_PCA_002.svg")
plot_PCA(cc_lat_sex_ldk_bk_slid_PCA, "sex")
dev.off()
```

Plot with convex hulls filled in, export to an svg
LDA  Run an LDA on the PCA results, retaining the number of axes capturing 99% variance or supported by sample size

```r
cc_lat_sex_ldk_bk_slid_LDA <- LDA(cc_lat_sex_ldk_bk_slid_PCA, "sex", retain = 9)
```

**LDA output**

```
cc_lat_sex_ldk_bk_slid_LDA
```

Create an LDA plot, and an LDA cross-validation plot

```r
plot_LDA(cc_lat_sex_ldk_bk_slid_LDA, "sex")
plot_CV(cc_lat_sex_ldk_bk_slid_LDA)
```

**MANOVA**  MANOVA of the PCA ordinated results, retaining the number of axes capturing 99% variance or supported by sample size

```r
cc_lat_sex_ldk_bk_slid_MANOVA <- MANOVA(cc_lat_sex_ldk_bk_slid_PCA, fac = "sex", retain = 9)
```

**MANOVA output**

```
cc_lat_sex_ldk_bk_slid_MANOVA
```

Pairwise MANOVA

```r
cc_lat_sex_ldk_bk_slid_PW_MANOVA <- MANOVA_PW(cc_lat_sex_ldk_bk_slid_PCA, fac = "sex")
```

**Pairwise MANOVA output**

```
cc_lat_sex_ldk_bk_slid_PW_MANOVA
```

**Workspace save/load**  save the workspace for future access, commented to prevent erroneous execution

```r
# save.image('FILE_PATH/cass_lat_sex_ldk_bk_slid.RData')
```

command to load the workspace, commented to prevent erroneous execution

```r
# load('FILE_PATH/cass_lat_sex_ldk_bk_slid.RData')
```

**CC SEX ANTERIOR ASPECT**

**Initial Data read-in**  Initial data read-in of the Out object with landmarks assigned created in the data_landmarking_2.R script

```r
# load('FILE_PATH/cc_ant_sex_ldk_bk_slid.RData')
ls()
```

**Elliptical Fourier Transformation**  Calibrate harmonics needed to capture 99.9% shape variance (or N-1 harmonics)

```r
cal_cc_ant_ldk_bk_slid <- calibrate_harmonicpower_efourier(cc_ant_sex_ldk_bk_slid, nb.h = 20, plot = T)
cal_cc_ant_ldk_bk_slid
```

```r
##14 harmonics capture 99.9% of the shape
```
Altered graph to show more than the default 10 harmonics

```r
cal_cc_ant_ldk_bk_slid$gg + theme_minimal() + coord_cartesian(xlim = c(0.5, 15),
ylim = c(0, 100)) + ggtitle("Southern Cassowary known sex anterior landmark Bookstein-
slid Harmonic calibration")
```

Calibrate the chosen number of reconstructions

```r
cal_cc_ant_sex_ldk_bk_slid_recon <- calibrate_reconstructions_efourier(cc_ant_sex_ldk_bk_slid,
range = 1:14)
cal_cc_ant_sex_ldk_bk_slid_recon
```

Elliptical Fourier transformation with the number of harmonics previously chosen from the calibration

```r
cc_ant_sex_ldk_bk_slid_ef <- efourier(cc_ant_sex_ldk_bk_slid, nb.h = 14,
norm = F)
```

**PCA**  
Ordinate the data with a Principal Components Analysis

```r
cc_ant_sex_ldk_bk_slid_PCA <- PCA(cc_ant_sex_ldk_bk_slid_ef, fac = "sex")
```

PCA output

```r
cc_ant_sex_ldk_bk_slid_PCA
summary(cc_ant_sex_ldk_bk_slid_PCA)
```

Plot out the results, export to an svg

```r
plot_PCA(cc_ant_sex_ldk_bk_slid_PCA)
svg(filename = "FILE_PATH/cc_ant_sex_ldk_bk_slid_PCA_001.svg")
```

Plot with convex hulls, export to an svg

```r
plot_PCA(cc_ant_sex_ldk_bk_slid_PCA, "sex")
svg(filename = "FILE_PATH/cc_ant_sex_ldk_bk_slid_PCA_002.svg")
```

Plot with convex hulls filled in, export to an svg

```r
plot_PCA(cc_ant_sex_ldk_bk_slid_PCA, "sex", chullfilled = T)
svg(filename = "FILE_PATH/cc_ant_sex_ldk_bk_slid_PCA_003.svg")
```

**LDA**  
Run an LDA on the PCA results, retaining the number of axes capturing 99% variance or supported by sample size

```r
cc_ant_sex_ldk_bk_slid_LDA <- LDA(cc_ant_sex_ldk_bk_slid_PCA, "sex", retain = 9)
cc_ant_sex_ldk_bk_slid_LDA
```

Create an LDA plot, and an LDA cross-validation plot

```r
plot_LDA(cc_ant_sex_ldk_bk_slid_LDA, "sex")
plot_CV(cc_ant_sex_ldk_bk_slid_LDA)
```

**MANOVA**  
MANOVA of the PCA ordinated results, retaining the number of axes capturing 99% variance or supported by sample size
cc_ant_sex_ldk_bk_slid_MANOVA <- MANOVA(cc_ant_sex_ldk_bk_slid_PCA, fac = "sex", retain = 9)

MANOVA output
cc_ant_sex_ldk_bk_slid_MANOVA

Pairwise MANOVA
cc_ant_sex_ldk_bk_slid_PW_MANOVA <- MANOVA_PW(cc_ant_sex_ldk_bk_slid_PCA, fac = "sex")

Pairwise MANOVA output
cc_ant_sex_ldk_bk_slid_PW_MANOVA

Workspace save/load  save the workspace for future access, commented to prevent erroneous execution
# save.image("FILE_PATH/cass_ant_sex_ldk_bk_slid.RData")

command to load the workspace, commented to prevent erroneous execution
# load("FILE_PATH/cass_ant_sex_ldk_bk_slid.RData")

GEOGRAPHY CASQUE ANALYSIS

CC GEOGRAPHY LATERAL ASPECT

Initial Data read-in  Initial data read-in of the Out object with landmarks assigned created in the data_landmarking_2.R script
# load("FILE_PATH/cc_lat_geo_ldk_bk_slid.RData")
ls()

Elliptical Fourier Transformation  Calibrate harmonics needed to capture 99.9% shape variance (or N-1 harmonics)

cal_cc_lat_geo_ldk_bk_slid <- calibrate_harmonicpower_efourier(cc_lat_geo_ldk_bk_slid, nb.h = 20, plot = T)
cal_cc_lat_geo_ldk_bk_slid
##15 harmonics capture 99.9% of the shape

Altered graph to show more than the default 10 harmonics

cal_cc_lat_geo_ldk_bk_slid$gg + theme_minimal() + coord_cartesian(xlim = c(0.5, 16), ylim = c(0, 100)) + ggtitle("Southern Cassowary lateral aspect landmark Bookstein slid geography Harmonic calibration")

Calibrate the chosen number of reconstructions

cal_cc_lat_geo_ldk_bk_slid_recon <- calibrate_reconstructions_efourier(cc_lat_geo_ldk_bk_slid, range = 1:15)
cal_cc_lat_geo_ldk_bk_slid_recon

Elliptical Fourier transformation with the number of harmonics previously chosen from the calibration

cal_cc_lat_geo_ldk_bk_slid_ef <- efourier(cc_lat_geo_ldk_bk_slid, nb.h = 15, norm = F)

PCA  Ordinate the data with a Principal Components Analysis
cc_lat_geo_ldk_bk_slid_PCA <- PCA(cc_lat_geo_ldk_bk_slid_ef, fac = "geo")

PCA output
cc_lat_geo_ldk_bk_slid_PCA
summary(cc_lat_geo_ldk_bk_slid_PCA)

Plot out the results
plot_PCA(cc_lat_geo_ldk_bk_slid_PCA)
svg(filename = "FILE_PATH/cc_lat_geo_ldk_bk_slid_PCA_001.svg")
plot_PCA(cc_lat_geo_ldk_bk_slid_PCA)
dev.off()

Plot with convex hulls, export to an svg
plot_PCA(cc_lat_geo_ldk_bk_slid_PCA, "geo")
svg(filename = "FILE_PATH/cc_lat_geo_ldk_bk_slid_PCA_002.svg")
plot_PCA(cc_lat_geo_ldk_bk_slid_PCA, "geo")
dev.off()

Plot with convex hulls filled in, export to an svg
plot_PCA(cc_lat_geo_ldk_bk_slid_PCA, "geo", chullfilled = T)
svg(filename = "FILE_PATH/cc_lat_geo_ldk_bk_slid_PCA_003.svg")
plot_PCA(cc_lat_geo_ldk_bk_slid_PCA, "geo", chullfilled = T)
dev.off()

LDA Run an LDA on the PCA results, retaining the number of axes capturing 99% variance or supported by sample size
cc_lat_geo_ldk_bk_slid_LDA <- LDA(cc_lat_geo_ldk_bk_slid_PCA, "geo", retain = 8)

LDA output
cc_lat_geo_ldk_bk_slid_LDA

Create an LDA plot, and an LDA cross-validation plot
plot_LDA(cc_lat_geo_ldk_bk_slid_LDA, "geo")
plot_CV(cc_lat_geo_ldk_bk_slid_LDA)

MANOVA MANOVA of the PCA ordinated results, retaining the number of axes capturing 99% variance or supported by sample size
cc_lat_geo_ldk_bk_slid_MANOVA <- MANOVA(cc_lat_geo_ldk_bk_slid_PCA, fac = "geo", retain = 8)

MANOVA output
cc_lat_geo_ldk_bk_slid_MANOVA

Pairwise MANOVA
cc_lat_geo_ldk_bk_slid_PW_MANOVA <- MANOVA_PW(cc_lat_geo_ldk_bk_slid_PCA, fac = "geo")

Pairwise MANOVA output
cc_lat_geo_ldk_bk_slid_PW_MANOVA
Workspace save/load  save the workspace for future access, commented to prevent erroneous execution

```r
# save.image('FILE_PATH/Bookstein_slid/cass_lat_geo_ldk_bk_slid.RData')
```

command to load the workspace, commented to prevent erroneous execution

```r
# load('FILE_PATH/cass_lat_geo_ldk_bk_slid.RData')
```

### CC GEOGRAPHY ANTERIOR ASPECT

#### Initial Data read-in  Initial data read-in of the Out object with landmarks assigned created in the data_landmarking_2.R script

```r
# load('FILE_PATH/cc_ant_geo_ldk_bk_slid.RData')
ls()
stack(cc_ant_geo_ldk_bk_slid)
```

#### Elliptical Fourier Transformation  Calibrate harmonics needed to capture 99.9% shape variance (or N-1 harmonics)

```r
cal_cc_ant_ldk_bk_slid <- calibrate_harmonicpower_efourier(cc_ant_geo_ldk_bk_slid,
               nb.h = 20, plot = T)
cal_cc_ant_ldk_bk_slid
```

Altered graph to show more than the default 10 harmonics

```r
cal_cc_ant_ldk_bk_slid$gg + theme_minimal() + coord_cartesian(xlim = c(0.5, 15),
         ylim = c(0, 100)) + ggtitle("Southern Cassowary known geo anterior landmark Bookstein
Harmonic calibration")
```

calibrate the reconstructions

```r
cal_cc_ant_geo_ldk_bk_slid_recon <- calibrate_reconstructions_efourier(cc_ant_geo_ldk_bk_slid,
               range = 1:14)
cal_cc_ant_geo_ldk_bk_slid_recon
```

elliptical Fourier transformation with the number of harmonics previously chosen from the calibration.

```r
cc_ant_geo_ldk_bk_slid_ef <- efourier(cc_ant_geo_ldk_bk_slid, nb.h = 14,
               norm = F)
```

#### PCA  Ordinate the data with a Principal Components Analysis

```r
cc_ant_geo_ldk_bk_slid_PCA <- PCA(cc_ant_geo_ldk_bk_slid_ef)
cc_ant_geo_ldk_bk_slid_PCA
summary(cc_ant_geo_ldk_bk_slid_PCA)
```

Plot out the results, export to an svg

```r
plot_PCA(cc_ant_geo_ldk_bk_slid_PCA)
svg(filename = "FILE_PATH/cc_ant_geo_ldk_bk_slid_PCA_001.svg")
plot_PCA(cc_ant_geo_ldk_bk_slid_PCA)
dev.off()
```

Plot with convex hulls, export to an svg

```r
plot_PCA(cc_ant_geo_ldk_bk_slid_PCA, "geo")
svg(filename = "FILE_PATH/cc_ant_geo_ldk_bk_slid_PCA_002.svg")
plot_PCA(cc_ant_geo_ldk_bk_slid_PCA, "geo")
dev.off()
```
Plot with convex hulls filled in, export to an svg

```r
plot_PCA(cc_ant_geo_ldk_bk_slid_PCA, "geo", chullfilled = T)
svg(filename = "FILE_PATH/cc_ant_geo_ldk_bk_slid_PCA_003.svg")
plot_PCA(cc_ant_geo_ldk_bk_slid_PCA, "geo", chullfilled = T)
dev.off()
```

```r
cc_ant_geo_ldk_bk_slid_LDA <- LDA(cc_ant_geo_ldk_bk_slid_PCA, "geo", retain = 6)
cc_ant_geo_ldk_bk_slid_LDA
```

**LDA**  
Create an LDA plot, and an LDA cross-validation plot

```r
plot_LDA(cc_ant_geo_ldk_bk_slid_LDA, "geo")
plot_CV(cc_ant_geo_ldk_bk_slid_LDA)
```

```r
cc_ant_geo_ldk_bk_slid_MANOVA <- MANOVA(cc_ant_geo_ldk_bk_slid_PCA, fac = "geo", retain = 6)
cc_ant_geo_ldk_bk_slid_MANOVA
cc_ant_geo_ldk_bk_slid_PW_MANOVA <- MANOVA_PW(cc_ant_geo_ldk_bk_slid_PCA, fac = "geo")
cc_ant_geo_ldk_bk_slid_PW_MANOVA
```

**MANOVA**

**Workspace save/load**  
save the workspace for future access, commented to prevent erroneous execution

```r
# save.image('FILE_PATH/cass_ant_geo_ldk_bk_slid.RData')
```

command to load the workspace, commented to prevent erroneous execution

```r
# load('FILE_PATH/cass_ant_geo_ldk_bk_slid.RData')
```

**GEOGRAPHY-SEX CASQUE ANALYSIS**

This section of code investigates potential shape differences between sexes by geographic location. As no reliably significant differences were found, this was not discussed at length in the article.

**CC LATERAL GEO-SEX**

**Initial Data read-in**  
Initial data read-in of the Out object with landmarks assigned created in the data_landmarking_2.R script

```r
# load('FILE_PATH/cc_lat_geo_sex_ldk_bk_slid.RData')
ls()
```

**Elliptical Fourier Transformation**  
Calibrate harmonics needed to capture 99.9% shape variance (or N-1 harmonics)

```r
cal_cc_lat_geo_sex_ldk_bk_slid <- calibrate_harmonicpower_efourier(cc_lat_geo_sex_ldk_bk_slid,
  nb.h = 20, plot = T)
cal_cc_lat_geo_sex_ldk_bk_slid #16 harmonics capture 99.9% of the shape
```

Altered graph to show more than the default 10 harmonics
Calibrate the chosen number of reconstructions

```r
cal_cc_lat_geo_sex_ldk_bk_slid_recon <- calibrate_reconstructions_efourier(cc_lat_geo_sex_ldk_bk_slid, range = 1:16)
```

Calibrate the chosen number of reconstructions

```r
cal_cc_lat_geo_sex_ldk_bk_slid_recon
```

Elliptical Fourier transformation with the number of harmonics previously chosen from the calibration

```r
cc_lat_geo_sex_ldk_bk_slid_ef <- efourier(cc_lat_geo_sex_ldk_bk_slid, nb.h = 16, norm = F)
```

**PCA** Ordinate the data with a Principal Components Analysis

```r
cc_lat_geo_sex_ldk_bk_slid_PCA <- PCA(cc_lat_geo_sex_ldk_bk_slid_ef, fac = c("sex", "geo"))
```

PCA output

```r
cc_lat_geo_sex_ldk_bk_slid_PCA
summary(cc_lat_geo_sex_ldk_bk_slid_PCA)
```

Plot out the results

```r
plot_PCA(cc_lat_geo_sex_ldk_bk_slid_PCA)
plot_PCA(cc_lat_geo_sex_ldk_bk_slid_PCA, ~sex + geo)
```

Plot with convex hulls

```r
plot_PCA(cc_lat_geo_sex_ldk_bk_slid_PCA, ~sex + geo, chullfilled = T)
```

Plot with 95% CI ellipses

```r
plot(cc_lat_geo_sex_ldk_bk_slid_PCA, ~sex + geo, ellipses = T)
```

**MANOVA** MANOVA of the PCA ordinated results, retaining the number of axes capturing 99% variance or supported by sample size

```r
cc_lat_geo_sex_ldk_bk_slid_MANOVA <- MANOVA(cc_lat_geo_sex_ldk_bk_slid_PCA, fac = "sex", retain = 3)
```

MANOVA output

```r
cc_lat_geo_sex_ldk_bk_slid_MANOVA
```

Pairwise MANOVA

```r
cc_lat_geo_sex_ldk_bk_slid_PW_MANOVA <- MANOVA_PW(cc_lat_geo_sex_ldk_bk_slid_PCA, ~sex + geo)
```

Pairwise MANOVA output

```r
cc_lat_geo_sex_ldk_bk_slid_PW_MANOVA
```
slice the data to just the SPNG  
Check factors for accuracy

PCA  
Ordinate the data with a Principal Components Analysis

Plot out the results, export to an svg

Plot with convex hulls, export to an svg

Plot with convex hulls filled in, export to an svg

LDA  
Run an LDA on the PCA results, retaining the number of axes capturing 99% variance or supported by sample size

LDA output

Create an LDA plot, and an LDA cross-validation plot

MANOVA  
MANOVA of the PCA ordinated results, retaining the number of axes capturing 99% variance or supported by sample size

MANOVA output
cc_lat_geo_sex_ldk_bk_slid_SPNG_MANOVA

Pairwise MANOVA

cc_lat_geo_sex_ldk_bk_slid_SPNG_PW_MANOVA <- MANOVA_PW(cc_lat_geo_sex_ldk_bk_slid_SPNG_PCA, fac = "sex")

Pairwise MANOVA output

cc_lat_geo_sex_ldk_bk_slid_SPNG_PW_MANOVA

cc_lat_geo_sex_ldk_bk_slid_AUS_ef <- slice(cc_lat_geo_sex_ldk_bk_slid_ef, c(7:14, 16:21))

Slice the data to just the AUS Check factors for accuracy

cc_lat_geo_sex_ldk_bk_slid_AUS_ef$fac

PCA Ordinate the data with a Principal Components Analysis

cc_lat_geo_sex_ldk_bk_slid_AUS_PCA <- PCA(cc_lat_geo_sex_ldk_bk_slid_AUS_ef, fac = "sex")
cc_lat_geo_sex_ldk_bk_slid_AUS_PCA
summary(cc_lat_geo_sex_ldk_bk_slid_AUS_PCA)

Plot out the results, export to an svg

plot_PCA(cc_lat_geo_sex_ldk_bk_slid_AUS_PCA)
svg(filename = "FILE_PATH/cc_lat_geo_sex_ldk_bk_slid_AUS_PCA_001.svg")
plot_PCA(cc_lat_geo_sex_ldk_bk_slid_AUS_PCA)
dev.off()

Plot with convex hulls, export to an svg

plot_PCA(cc_lat_geo_sex_ldk_bk_slid_AUS_PCA, "sex")
svg(filename = "FILE_PATH/cc_lat_geo_sex_ldk_bk_slid_AUS_PCA_002.svg")
plot_PCA(cc_lat_geo_sex_ldk_bk_slid_AUS_PCA, "sex")
dev.off()

Plot with convex hulls filled in, export to an svg

plot_PCA(cc_lat_geo_sex_ldk_bk_slid_AUS_PCA, "sex", chullfilled = T)
svg(filename = "FILE_PATH/cc_lat_geo_sex_ldk_bk_slid_AUS_PCA_003.svg")
plot_PCA(cc_lat_geo_sex_ldk_bk_slid_AUS_PCA, "sex", chullfilled = T)
dev.off()

LDA Run an LDA on the PCA results, retaining the number of axes capturing 99% variance or supported by sample size

cc_lat_geo_sex_ldk_bk_slid_AUS_LDA <- LDA(cc_lat_geo_sex_ldk_bk_slid_AUS_PCA, "sex", retain = 6)

LDA output

cc_lat_geo_sex_ldk_bk_slid_AUS_LDA

Create an LDA plot, and an LDA cross-validation plot
MANOVA of the PCA ordinated results, retaining the number of axes capturing 99% variance or supported by sample size

```
cc_lat_geo_sex_ldk_bk_slid_AUS_MANOVA <- MANOVA(cc_lat_geo_sex_ldk_bk_slid_AUS_PCA, fac = "sex", retain = 6)
```

Pairwise MANOVA

```
cc_lat_geo_sex_ldk_bk_slid_AUS_PW_MANOVA <- MANOVA_PW(cc_lat_geo_sex_ldk_bk_slid_AUS_PCA, fac = "sex")
```

Workspace save/load  save the workspace for future access, commented to prevent erroneous execution

```
# save.image('FILE_PATH/cass_lat_geo_sex_ldk_bk_slid.RData')
```

command to load the workspace, commented to prevent erroneous execution

```
# load('FILE_PATH/cass_lat_geo_sex_ldk_bk_slid.RData')
```

CC ANTERIOR GEO-SEX

Initial Data read-in  Initial data read-in of the Out object with landmarks assigned created in the data_landmarking_2.R script

```
# load('FILE_PATH/cc_ant_geo sexe_ldk_bk_slid.RData')
ls()
stack(cc_ant_geo sexe_ldk_bk_slid)
```

Elliptical Fourier Transformation  Calibrate harmonics needed to capture 99.9% shape variance (or N-1 harmonics)

```
cal_cc_ant_geo sexe_ldk_bk_slid <- calibrate_harmonicpower_efourier(cc_ant_geo sexe_ldk_bk_slid, nb.h = 20, plot = T)
```

```
cal_cc_ant_geo sexe_ldk_bk_slid  ##14 harmonics capture 99.9% of the shape
```

Altered graph to show more than the default 10 harmonics

```
cal_cc_ant_geo sexe_ldk_bk slid$gg + theme_minimal() + coord cartesian(xlim = c(0.5, 15), ylim = c(0, 100)) + ggtitle("Southern Cassowary anterior aspect landmark Bookstein geography-sex Harmonic calibration")
```

Calibrate the chosen number of reconstructions

```
cal_cc_ant_geo sexe_ldk_bk slid recon <- calibrate_reconstructions_efourier(cc_ant_geo sexe_ldk_bk slid, range = 1:14)
```

Elliptical Fourier transformation with the number of harmonics previously chosen from the calibration
PCA Run a Principal Component Analysis to ordinate the data

```r
cc_ant_geo_sex_ldk bk_slid ef <- efourier(cc_ant_geo_sex_ldk bk_slid, nb.h = 14,
norm = F)
```

PCA output

```r
cc_ant_geo_sex_ldk bk_slid PCA <- PCA(cc_ant_geo_sex_ldk bk_slid ef)
summary(cc_ant_geo_sex_ldk bk_slid PCA)
```

Plot out the results, export to an svg

```r
plot_PCA(cc_ant_geo_sex_ldk bk_slid PCA)
svg(filename = "FILE PATH/cc_ant_geo_sex_ldk bk_slid PCA_001.svg")
plot_PCA(cc_ant_geo_sex_ldk bk_slid PCA)
dev.off()
```

Plot with convex hulls, export to an svg

```r
plot_PCA(cc_ant_geo_sex_ldk bk_slid PCA, "sex")
svg(filename = "FILE PATH/Bookstein_slid/cc_ant_geo seks ldk bk slid PCA_002.svg")
plot_PCA(cc_ant_geo_sex ldk bk slid PCA, "sex")
dev.off()
```

Plot with convex hulls filled in, export to an svg

```r
plot_PCA(cc_ant_geo_sex ldk bk slid PCA, "sex", chullfilled = T)
svg(filename = "FILE PATH/cc_ant_geo_sex ldk bk slid PCA_003.svg")
plot_PCA(cc_ant_geo_sex ldk bk slid PCA, "sex", chullfilled = T)
dev.off()
```

MANOVA MANOVA of the PCA ordinated results, retaining the number of axes capturing 99% variance or supported by sample size

```r
cc_ant_geo_sex ldk bk slid MANOVA <- MANOVA(cc_ant_geo_sex ldk bk slid PCA, fac = "sex", retain = 3)
```

MANOVA output

```r
cc_ant_geo_sex ldk bk slid MANOVA
```

Pairwise MANOVA

```r
cc_ant_geo_sex ldk bk slid PW MANOVA <- MANOVA_PW(cc_ant_geo_sex ldk bk slid PCA, ~sex + geo)
```

Pairwise MANOVA output

```r
cc_ant_geo_sex ldk bk slid PW MANOVA
```

Slice the data to just the SPNG Check factors for accuracy

```r
cc_ant_geo_sex ldk bk slid SPNG ef <- slice(cc_ant_geo_sex ldk bk slid ef,
c(1:6, 15))
cc_ant_geo_sex ldk bk slid SPNG ef$fac
```
**PCA**  Ordinate the data with a Principal Components Analysis

```r
cc_ant_geo_sex_ldk_bk_slid_SPNG_PCA <- PCA(cc_ant_geo_sex_ldk_bk_slid_SPNG_ef)
cc_ant_geo_sex_ldk_bk_slid_SPNG_PCA
summary(cc_ant_geo_sex_ldk_bk_slid_SPNG_PCA)
```

Plot out the results, export to an svg

```r
plot_PCA(cc_ant_geo_sex_ldk_bk_slid_SPNG_PCA)
svg(filename = "FILE_PATH/cc_ant_geo_sex_ldk_bk_slid_SPNG_PCA_001.svg")
plot_PCA(cc_ant_geo_sex_ldk_bk_slid_SPNG_PCA)
dev.off()
```

Plot with convex hulls, export to an svg

```r
plot_PCA(cc_ant_geo_sex_ldk_bk_slid_SPNG_PCA, "sex")
svg(filename = "FILE_PATH/cc_ant_geo_sex_ldk_bk_slid_SPNG_PCA_002.svg")
plot_PCA(cc_ant_geo_sex_ldk_bk_slid_SPNG_PCA, "sex")
dev.off()
```

Plot with convex hulls filled in, export to an svg

```r
plot_PCA(cc_ant_geo_sex_ldk_bk_slid_SPNG_PCA, "sex", chullfilled = T)
svg(filename = "FILE_PATH/cc_ant_geo_sex_ldk_bk_slid_SPNG_PCA_003.svg")
plot_PCA(cc_ant_geo_sex_ldk_bk_slid_SPNG_PCA, "sex", chullfilled = T)
dev.off()
```

**LDA**  Run an LDA on the PCA results, retaining the number of axes capturing 99% variance or supported by sample size

```r
cc_ant_geo_sex_ldk_bk_slid_SPNG_LDA <- LDA(cc_ant_geo_sex_ldk_bk_slid_SPNG_PCA, "sex", retain = 3)
```

LDA output

```r
cc_ant_geo_sex_ldk_bk_slid_SPNG_LDA
```

Create an LDA plot, and an LDA cross-validation plot

```r
plot_LDA(cc_ant_geo_sex_ldk_bk_slid_SPNG_LDA, "sex")
plot_CV(cc_ant_geo_sex_ldk_bk_slid_SPNG_LDA)
```

```r
cc_ant_geo_sex_ldk_bk_slid_SPNG_MANOVA <- MANOVA(cc_ant_geo_sex_ldk_bk_slid_SPNG_PCA, fac = "sex", retain = 3)
cc_ant_geo_sex_ldk_bk_slid_SPNG_MANOVA
cc_ant_geo_sex_ldk_bk_slid_SPNG_PW_MANOVA <- MANOVA_PW(cc_ant_geo_sex_ldk_bk_slid_SPNG_PCA, fac = "sex")
cc_ant_geo_sex_ldk_bk_slid_SPNG_PW_MANOVA
```

**MANOVA**

```r
cc_ant_geo_sex_ldk_bk_slid_AUS Ef <- slice(cc_ant_geo_sex_ldk_bk_slid_ef, c(7:14, 16))
slice the data to just the AUS  Check factors for accuracy
```
### PCA
Ordinate the data with a Principal Components Analysis

```r
cc_ant_geo_sex_ldk_bk_slid_AUS_PCA <- PCA(cc_ant_geo_sex_ldk_bk_slid_AUS_ef)
summary(cc_ant_geo_sex_ldk_bk_slid_AUS_PCA)
```

Plot out the results, export to an svg

```r
plot_PCA(cc_ant_geo_sex_ldk_bk_slid_AUS_PCA)
svg(filename = "FILE_PATH/cc_ant_geo_sex_ldk_bk_slid_AUS_PCA_001.svg")
```

Plot with convex hulls, export to an svg

```r
plot_PCA(cc_ant_geo_sex_ldk_bk_slid_AUS_PCA, "sex")
svg(filename = "FILE_PATH/cc_ant_geo_sex_ldk_bk_slid_AUS_PCA_002.svg")
```

Plot with convex hulls filled in, export to an svg

```r
plot_PCA(cc_ant_geo_sex_ldk_bk_slid_AUS_PCA, "sex", chullfilled = T)
svg(filename = "FILE_PATH/cc_ant_geo_sex_ldk_bk_slid_AUS_PCA_003.svg")
```

### LDA
Run an LDA on the PCA results, retaining the number of axes capturing 99% variance or supported by sample size

```r
cc_ant_geo_sex_ldk_bk_slid_AUS_LDA <- LDA(cc_ant_geo sexe ldk_bk_slid_AUS_PCA, "sex", retain = 4)
LDA output
cc_ant_geo_sex_ldk_bk_slid_AUS_LDA
```

Create an LDA plot, and an LDA cross-validation plot

```r
plot_LDA(cc_ant_geo sexe ldk_bk_slid_AUS_LDA, "sex")
plot_CV(cc_ant_geo sexe ldk_bk_slid_AUS_LDA)
```

### MANOVA
MANOVA of the PCA ordinated results, retaining the number of axes capturing 99% variance or supported by sample size

```r
cc_ant_geo sexe ldk_bk_slid_AUS_MANOVA <- MANOVA(cc_ant_geo sexe ldk_bk_slid_AUS_PCA, fac = "sex", retain = 4)
MANOVA output
cc_ant_geo sexe ldk_bk_slid_AUS_MANOVA
```

Pairwise MANOVA

```r
cc_ant_geo sexe ldk_bk_slid_AUS_PW_MANOVA <- MANOVA_PW(cc_ant_geo sexe ldk_bk_slid_AUS_PCA, fac = "sex")
Pairwise MANOVA output
```
Workspace save/load  save the workspace for future access, commented to prevent erroneous execution

```r
# save.image('FILE_PATH/cass_ant_geo_sex_ldk bk slid.RData')
```

command to load the workspace, commented to prevent erroneous execution

```r
# load('FILE_PATH/cass_ant_geo_sex_ldk bk slid.RData')
```