

2017-11-17

## Linear discriminant analysis

- ## Load the data

The variables are: Species, stage (1-5 for larvae, 6 for adults), sex (m male, f female, u undetermined), antseg1 - antseg4 (lengths of 1st to 4th antennal segments), midfem, midtib, hindfem, hindtib (lengths of middle and hind femora and tibiae). The values are raw measurements in millimeters.

```
## Observations: 541
## Variables: 11
## $ Species <chr> "canali", "canali", "canali", "canali", "canali", "can...
## $ stage <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 2, 2, 2, ...
## $ sex <chr> "u", "u", "u", "u", "u", "u", "u", "u", "u", "u", "u", ...
```

```
## $ antseg1 <dbl> 0.17, 0.20, 0.18, 0.16, 0.13, 0.18, 0.18, 0.18, 0.20, ...
## $ antseg2 <dbl> 0.15, 0.14, 0.14, 0.13, 0.13, 0.16, 0.12, 0.15, 0.15, ...
## $ antseg3 <dbl> 0.19, 0.18, 0.17, 0.14, 0.16, 0.18, 0.16, 0.16, 0.19, ...
## $ antseg4 <dbl> 0.72, 0.74, 0.62, 0.55, 0.56, 0.52, 0.72, 0.60, 0.67, ...
## $ midfem <dbl> 0.70, 0.76, 0.76, 0.70, 0.72, 0.76, 0.74, 0.76, 0.78, ...
## $ midtib <dbl> 0.80, 0.92, 0.94, 0.92, 0.92, 0.97, 0.91, 0.92, 0.95, ...
## $ hindfem <dbl> 0.43, 0.68, 0.79, 0.74, 0.68, 0.68, 0.70, 0.70, 0.78, ...
## $ hindtib <dbl> 0.72, 0.42, 0.40, 0.42, 0.38, 0.45, 0.42, 0.43, 0.44, ...
```

## Manipulate the data

For the purpose of this exercise let's limit the data to one species and only the measurements of the antennae.

```
morph_data %>%
  select(Species:antseg4, -sex) %>%
  filter(Species == "canali") %>%
  mutate_at(vars(antseg1:antseg4), scale)-> canal_data

head(canal_data)
```

```
## # A tibble: 6 x 6
##   Species stage antseg1 antseg2 antseg3 antseg4
##   <chr>   <int>   <dbl>   <dbl>   <dbl>   <dbl>
## 1 canali     1   -1.31   -1.33   -1.38   -1.27
## 2 canali     1   -1.26   -1.36   -1.42   -1.22
## 3 canali     1   -1.30   -1.36   -1.45   -1.51
## 4 canali     1   -1.33   -1.39   -1.55   -1.68
## 5 canali     1   -1.39   -1.39   -1.48   -1.65
## 6 canali     1   -1.30   -1.31   -1.42   -1.75
```

## Conduct the linear discriminant analysis using MASS::lda()

```
canal_lda<-MASS::lda(stage~antseg1 + antseg2 + antseg3 + antseg4, data = canal_data)

canal_lda
```

```
## Call:
## lda(stage ~ antseg1 + antseg2 + antseg3 + antseg4, data = canal_data)
##
## Prior probabilities of groups:
##      1      2      3      4      5      6
## 0.1111111 0.1111111 0.1111111 0.2222222 0.2222222 0.2222222
##
## Group means:
##      antseg1      antseg2      antseg3      antseg4
## 1 -1.3073501 -1.3594034 -1.4443907 -1.4868663
## 2 -1.1332171 -1.1490818 -1.1510214 -1.2348777
## 3 -0.8167818 -0.8640406 -0.8315750 -0.9156920
## 4 -0.3028084 -0.2399942 -0.1731241 -0.0805297
## 5  0.4283631  0.5487119  0.6043044  0.6886356
## 6  1.5031198  1.3775452  1.2823132  1.2106121
##
## Coefficients of linear discriminants:
```

```
##           LD1           LD2           LD3           LD4
## antseg1 14.5047455 -7.2205800  3.8168030  2.764369
## antseg2 -3.8449898  1.2049129 -8.6374675 -2.428811
## antseg3 -1.7878986  0.9023135  4.3236873 -3.984543
## antseg4 -0.2461576  5.5171016  0.5203163  3.569601
##
## Proportion of trace:
##      LD1      LD2      LD3      LD4
## 0.9719 0.0276 0.0003 0.0002

names(canal_lda)

## [1] "prior"   "counts"  "means"   "scaling" "lev"     "svd"     "N"
## [8] "call"    "terms"   "xlevels"
```

## Explanation of the output

### Prior

From the raw data, the break down in proportions of the number of individuals in each group

```
canal_lda$prior

##           1           2           3           4           5           6
## 0.1111111 0.1111111 0.1111111 0.2222222 0.2222222 0.2222222
```

### Group means

The mean value for each of the variables for each group

```
canal_lda$means

##      antseg1      antseg2      antseg3      antseg4
## 1 -1.3073501 -1.3594034 -1.4443907 -1.4868663
## 2 -1.1332171 -1.1490818 -1.1510214 -1.2348777
## 3 -0.8167818 -0.8640406 -0.8315750 -0.9156920
## 4 -0.3028084 -0.2399942 -0.1731241 -0.0805297
## 5  0.4283631  0.5487119  0.6043044  0.6886356
## 6  1.5031198  1.3775452  1.2823132  1.2106121
```

### Coefficients

These are the coefficients to describe the linear discrimination. For example:  $LD1 = 14.5047455 \times \text{Group1} + -3.8449898 \times \text{Group2} + -1.7878986 \times \text{Group3} + \dots$

```
canal_lda$scaling

##           LD1           LD2           LD3           LD4
## antseg1 14.5047455 -7.2205800  3.8168030  2.764369
## antseg2 -3.8449898  1.2049129 -8.6374675 -2.428811
## antseg3 -1.7878986  0.9023135  4.3236873 -3.984543
## antseg4 -0.2461576  5.5171016  0.5203163  3.569601
```

You can also standardize the coefficients (loadings), which provides the relative strength of each factor on linear discriminant analysis

```
loadings <- canal_lda$scaling
col.ss <- colSums(loadings^2)
sweep(loadings, 2, sqrt(col.ss), "/")
```

```
##           LD1           LD2           LD3           LD4
## antseg1  0.95969829 -0.78391461  0.36703621  0.4257438
## antseg2 -0.25440157  0.13081342 -0.83060701 -0.3740641
## antseg3 -0.11829530  0.09796121  0.41577985 -0.6136643
## antseg4 -0.01628688  0.59897356  0.05003531  0.5497585
```

## Variation explained

The amount of variation explained by the each of the linear discriminant axis

```
prop = canal_lda$svd^2/sum(canal_lda$svd^2)
prop
```

```
## [1] 0.9719389713 0.0275790703 0.0003069345 0.0001750239
```

## Graphing the results

```
# extracting the data
lda_pred <- predict(canal_lda)
lda_scores<-data.frame(stage = lda_pred$class, lda_pred$x)

#developing hulls for each stage group

hull1<- lda_scores[lda_scores$stage ==1,][chull(lda_scores[lda_scores$stage ==1,c("LD1", "LD2")]),]
hull2<- lda_scores[lda_scores$stage ==2,][chull(lda_scores[lda_scores$stage ==2,c("LD1", "LD2")]),]
hull3<- lda_scores[lda_scores$stage ==3,][chull(lda_scores[lda_scores$stage ==3,c("LD1", "LD2")]),]
hull4<- lda_scores[lda_scores$stage ==4,][chull(lda_scores[lda_scores$stage ==4,c("LD1", "LD2")]),]
hull5<- lda_scores[lda_scores$stage ==5,][chull(lda_scores[lda_scores$stage ==5,c("LD1", "LD2")]),]
hull6<- lda_scores[lda_scores$stage ==6,][chull(lda_scores[lda_scores$stage ==6,c("LD1", "LD2")]),]

all_hulls <- rbind(hull1, hull2, hull3, hull4, hull5, hull6)

#plot using ggplot2

ggplot(data = lda_scores) +
  geom_point(aes(x = LD1, y = LD2, color = stage), size = 2) +
  geom_polygon(data = all_hulls, aes(x = LD1, y = LD2, color = stage, fill = stage), alpha = 0.25) +
  coord_equal() +
  theme_classic()
```

## Assessing the accuracy of the predictions

```
ct <- table(canal_data$stage, lda_pred$class)
ct
```

```
##
```

```
##      1  2  3  4  5  6
##    1  9  1  0  0  0  0
##    2  0 10  0  0  0  0
##    3  0  0 10  0  0  0
##    4  0  0  0 20  0  0
##    5  0  0  0  0 20  0
##    6  0  0  0  0  0 20

# percent correct for each stage
diag(prop.table(ct, 1))

##    1    2    3    4    5    6
## 0.9 1.0 1.0 1.0 1.0 1.0

# total percent correct
sum(diag(prop.table(ct)))

## [1] 0.9888889
```

## MANOVA and MANCOVA

Two common multivariate regression models are the multivariate analysis of variance (MANOVA; an extension of the univariate ANOVA) when all predictor variables are categorical, and the multivariate analysis of covariance (MANCOVA; extension of univariate ANCOVA) when predictor variables are categorical and continuous.

### Load the data

```
bryc_data <- read.table("http://ecology.msu.montana.edu/labds/R/labs/lab1/bryceveg.R")

bryc_data %>% rownames_to_column("site") -> bryc_data

bryc_site_data <- read.table("http://ecology.msu.montana.edu/labds/R/labs/lab2/brycesite.R")

bryc_site_data %>%
  rownames_to_column("site") %>%
  full_join(bryc_data, by = "site") -> bryc_site_data

glimpse(bryc_site_data)

## Observations: 160
## Variables: 182
## $ site      <chr> "bcnp__1", "bcnp__2", "bcnp__3", "bcnp__4", "bcnp__5"...
## $ plotcode  <int> 50001, 50002, 50003, 50004, 50005, 50006, 50007, 5000...
## $ annrad    <int> 241, 222, 231, 254, 232, 216, 288, 279, 187, 279, 271...
## $ asp       <int> 30, 50, 50, 360, 300, 330, 150, 220, 360, 125, 125, 2...
## $ av        <dbl> 1.00, 0.96, 0.96, 0.93, 0.48, 0.76, 0.25, 0.00, 0.93,...
## $ depth     <chr> "deep", "shallow", "shallow", "shallow", "shallow", "...
## $ east      <dbl> 388220.9, 388477.2, 388384.0, 388307.5, 389026.3, 389...
## $ elev      <int> 8720, 8360, 8560, 8660, 8480, 8560, 8560, 8680, 8240,...
## $ grorad    <int> 162, 156, 159, 166, 159, 155, 169, 169, 146, 167, 168...
## $ north     <int> 4144784, 4147573, 4147347, 4146971, 4146846, 4146853,...
## $ pos       <chr> "ridge", "mid_slope", "mid_slope", "ridge", "up_slope..."
```

```

## $ quad      <chr> "pc", "pc", "pc", "pc", "pc", "pc", "pc", "pc", "bp",...
## $ slope     <int> 9, 2, 2, 0, 2, 2, 3, 2, 3, 3, 2, 6, 3, 4, 3, 4, 2, 1,...
## $ junost     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ ameuta     <dbl> 0.0, 0.5, 0.0, 0.5, 0.0, 0.5, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0...
## $ arcpat     <dbl> 1.0, 0.5, 1.0, 1.0, 4.0, 1.0, 4.0, 2.0, 0.0, 5.0, 2.0...
## $ arttri     <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0...
## $ atrcan     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ berfre     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ ceamar     <dbl> 0.5, 0.0, 0.5, 0.5, 0.5, 1.0, 1.0, 0.0, 0.0, 0.5, 0.5...
## $ cerled     <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.5...
## $ cermon     <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0...
## $ chrdep     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ chrnau     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ chrpar     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ chrvis     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ eurlan     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ juncom     <dbl> 0.0, 2.0, 1.0, 0.0, 1.0, 0.5, 0.0, 0.5, 0.5, 0.0, 0.0...
## $ pacmyr     <dbl> 0.0, 0.5, 0.5, 0.0, 0.5, 0.5, 0.5, 0.5, 0.5, 0.0, 0.5...
## $ pruvir     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ purtri     <dbl> 0.0, 0.0, 0.0, 0.0, 0.5, 0.5, 0.5, 0.0, 0.0, 1.0, 1.0...
## $ quegam     <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0...
## $ rhutri     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ ribcer     <dbl> 0.0, 0.0, 0.5, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.5...
## $ roswoo     <dbl> 0.0, 0.5, 0.5, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0...
## $ samcoe     <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0...
## $ shearg     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ sherot     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ symore     <dbl> 1.0, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5...
## $ arcuva     <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ artarb     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ artfri     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ artpyg     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ atrcon     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ berrep     <dbl> 1.0, 0.0, 0.5, 1.0, 0.5, 1.0, 0.5, 0.0, 1.0, 0.5, 1.0...
## $ ericor     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ gutsar     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ tetcan     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ agrcri     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ agrdas     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ agrscr     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ agrsmi     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ bougra     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ broano     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ brocil     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ broine     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ carrss     <dbl> 0.5, 0.5, 0.5, 0.5, 1.0, 0.5, 0.5, 0.5, 0.5, 0.5, 0.5...
## $ elysal     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ fesovi     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ hiljam     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ junbal     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ koenit     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ muhmon     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ muhric     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...
## $ oryhym     <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,...

```

[illegible]

```

## $ euprob <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ fraves <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ genaff <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ gerfre <dbl> 0.5, 0.5, 0.5, 0.0, 0.0, 0.5, 0.0, 0.0, 0.5, 0.0, 0.0...
## $ gerric <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0...
## $ gilcon <dbl> 0.0, 0.5, 0.0, 0.5, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0...
## $ haparm <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0...
## $ heddru <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ hymaca <dbl> 0.0, 0.0, 0.0, 0.0, 0.5, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0...
## $ hymfil <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0...
## $ hymric <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.5...
## $ ipoagg <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ irimis <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ ivesab <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ leppun <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ lesint <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ leueri <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ ligpor <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ linkin <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0...
## $ linlew <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ litinc <dbl> 0.0, 0.0, 0.0, 0.0, 0.5, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0...
## $ litmul <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.5, 0.5...
## $ lotuta <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0...
## $ lupkin <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ lupser <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ lyggra <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ lygspe <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ macgri <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.5, 0.0...
## $ molpar <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ oenbra <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ oencaae <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0...
## $ oencor <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ oenfla <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ oenlav <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ opueri <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ orofas <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ pedcan <dbl> 0.0, 0.0, 0.0, 0.0, 0.5, 0.0, 0.5, 0.0, 0.0, 0.5, 0.0...
## $ pedsim <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ pencae <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.5, 0.5...
## $ pencom <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ penlei <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ penuta <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ phllon <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ phycha <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ potcon <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ potcri <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ potgra <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ pteand <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.5, 0.0...
## $ pyrvir <dbl> 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.5, 0.0, 0.0...
## $ salibe <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ sclwhi <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ senmul <dbl> 0.0, 0.5, 0.5, 0.5, 0.5, 0.0, 0.5, 0.5, 0.0, 0.5, 0.5...
## $ sphcoc <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ stapin <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...

```



```
## $ steten <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ strcor <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ swerad <dbl> 0.0, 0.5, 0.0, 0.0, 0.5, 0.5, 0.0, 0.0, 0.0, 0.0, 0.0, ...
## $ taroff <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ thafen <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ towmin <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ tradub <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ valacu <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, ...
## $ vicame <dbl> 0.0, 0.5, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, 0.0, ...
```

## Using MANOVA and MANCOVA

### MANOVA

-Independent variable is a categorical variable - Interpret like ANOVA - default test statistic is “Pillai” but “Wilks”, “Hotelling-Lawley”, “Roy” are also available. See `?summary.manova`. Wilks’ statistic is most popular in the literature, but the default Pillai–Bartlett statistic is recommended by Hand and Taylor (1987)

As a **reminder**:

-R provides Type I sequential SS, not the default Type III marginal SS reported by SAS and SPSS. In a nonorthogonal design with more than one term on the right hand side of the equation order will matter (i.e., A+B and B+A will produce different results)! - Type I sequential SS: tests the main effect of factor A, followed by the main effect of factor B after the main effect of A, followed by the interaction effect AB after the main effects. - Type II: tests for each main effect after the other main effect. No significant interaction is assumed (in other words, you should test for interaction first ( $SS(AB | A, B)$ ) and only if AB is not significant, continue with the analysis for main effects). - Type III: tests for the presence of a main effect after the other main effect and interaction. This approach is therefore valid in the presence of significant interactions. If the interactions are not significant, type II gives a more powerful test.

- NOTE: when data is balanced, the factors are orthogonal, and types I, II and III all give the same results.
- If you wish to find ways to produce Type II or III SS then you will need to find a package to help. For example, `regr0` has a `drop1()` function for `mlm` models. Install via `install.packages("regr0", repos="http://R-Forge.R-project.org")`

```
man_out <- manova(cbind(junost,ameuta,arcpat,arttri,atrcan) ~ pos,data = bryc_site_data)
summary(man_out)
```

```
##           Df Pillai approx F num Df den Df Pr(>F)
## pos         4 0.18304    1.477     20   616 0.08253 .
## Residuals 155
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

### MANCOVA

- When you have a categorical and continuous independent variables

```
man_out <- manova(cbind(arcpat, artarb, carrss, purtri,sticom) ~ pos + elev, data = bryc_site_data)
summary(man_out)
```

```
##           Df Pillai approx F num Df den Df Pr(>F)
## pos         4 0.2700    2.2150     20   612 0.0018133 **
## elev         1 0.1438    5.0387      5   150 0.0002688 ***
```

```
## Residuals 154
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## ANOSIM

Analysis of similarities (ANOSIM) provides a way to test statistically whether there is a significant difference between two or more groups of sampling units.

The R-statistic in ANOSIM is a ratio between within-group and between-group dissimilarities

```
# create the y variable
y<-cbind(bryc_site_data$arcpat,bryc_site_data$artarb,bryc_site_data$carrss,bryc_site_data$purtri,bryc_s

# convert to an x variable
x <- as.factor(bryc_site_data$pos)

# analysis
anosim_out <- anosim(y, x, distance = "euclidean", permutations = 999)
summary(anosim_out)
```

```
##
## Call:
## anosim(dat = y, grouping = x, permutations = 999, distance = "euclidean")
## Dissimilarity: euclidean
##
## ANOSIM statistic R: 0.0162
##      Significance: 0.23
##
## Permutation: free
## Number of permutations: 999
##
## Upper quantiles of permutations (null model):
##      90%      95%    97.5%      99%
## 0.0306 0.0391 0.0484 0.0597
##
## Dissimilarity ranks between and within classes:
##           0%      25%      50%      75%      100%      N
## Between   198 2978.50 6359.50 9536.000 12720.0 9823
## bottom    198 4155.00 6932.50 9591.125 12485.0 190
## low_slope 198 4070.00 6876.75 10634.500 12716.5 528
## mid_slope 198 3220.75 7323.50 10180.000 12704.0 1431
## ridge     198 2978.50 6196.50 8470.000 11827.5 153
## up_slope  198 1628.50 3863.50 6932.500 11978.0 595
perms<-permustats(anosim_out)
summary(perms)
```

```
##
##      statistic      SES      mean lower      median      upper Pr(perm)
## R      0.0162   0.6818   0.0014      -0.0009   0.0391      0.23
##
## (Interval (Upper - Lower) = 0.95)
```

```
densityplot(perms)
```

```
anosim_out$perm
```

```
##          TRUE          TRUE          TRUE          TRUE
## 0.012078652347 -0.032816017834 0.017721471214 0.011803572877
##          TRUE          TRUE          TRUE          TRUE
## 0.004734578709 -0.004219384521 -0.006707258341 0.016295295913
##          TRUE          TRUE          TRUE          TRUE
## 0.002899227968 -0.001738925337 0.001169614851 0.067735367506
##          TRUE          TRUE          TRUE          TRUE
## 0.036388642310 -0.013310536081 -0.023454355064 -0.015490790372
##          TRUE          TRUE          TRUE          TRUE
## -0.025731632147 0.009431240868 0.004536000006 -0.007285529643
##          TRUE          TRUE          TRUE          TRUE
## -0.014542560378 0.003889942771 -0.025675091157 -0.005015596915
##          TRUE          TRUE          TRUE          TRUE
## -0.020152312078 0.031368477137 0.030313525585 0.001268183823
##          TRUE          TRUE          TRUE          TRUE
## 0.035143299782 0.047068704611 -0.017929608120 -0.005932938451
##          TRUE          TRUE          TRUE          TRUE
## 0.011635285246 0.014903382553 0.018450565341 -0.035794909210
##          TRUE          TRUE          TRUE          TRUE
## -0.032275276537 0.007655453196 -0.020202422365 0.024910645734
##          TRUE          TRUE          TRUE          TRUE
## 0.049297839273 -0.012026047088 -0.029110773286 0.013193518371
##          TRUE          TRUE          TRUE          TRUE
## 0.041795176769 -0.023410078092 -0.025611451796 -0.019900144185
##          TRUE          TRUE          TRUE          TRUE
## -0.012362095244 -0.008055948943 -0.016157018229 -0.002089662202
##          TRUE          TRUE          TRUE          TRUE
## 0.030722033356 0.003735746461 0.003236787163 0.028683641075
##          TRUE          TRUE          TRUE          TRUE
## -0.020587807717 0.030652771522 -0.018545585127 0.009550296724
##          TRUE          TRUE          TRUE          TRUE
## -0.018332633980 0.028345730475 0.016714240398 -0.018479661637
##          TRUE          TRUE          TRUE          TRUE
## 0.002430559741 0.025239314394 -0.001905842490 0.024376440561
##          TRUE          TRUE          TRUE          TRUE
## -0.023718822116 -0.003969114212 -0.006093635744 -0.008669466119
##          TRUE          TRUE          TRUE          TRUE
## 0.012239525342 0.002360911362 0.070208025510 0.007586402205
##          TRUE          TRUE          TRUE          TRUE
## -0.000979786122 0.022236668072 0.002502175985 0.005311444392
##          TRUE          TRUE          TRUE          TRUE
## -0.002999729664 -0.000617382626 -0.003416776566 -0.012635523112
##          TRUE          TRUE          TRUE          TRUE
## -0.002709223536 0.006289754615 0.083762049793 -0.022178967448
##          TRUE          TRUE          TRUE          TRUE
## -0.002933243927 -0.002617085267 0.013480967280 -0.003705525671
##          TRUE          TRUE          TRUE          TRUE
## -0.031143789078 0.022922152897 -0.004941942524 0.049637120351
```

##	TRUE	TRUE	TRUE	TRUE
##	0.047784691350	-0.002477191122	0.036622572309	-0.017504303212
##	TRUE	TRUE	TRUE	TRUE
##	0.027081376962	-0.016201787166	0.002422758560	-0.007491312138
##	TRUE	TRUE	TRUE	TRUE
##	0.003756971295	0.030327652047	-0.025838845670	0.038526341512
##	TRUE	TRUE	TRUE	TRUE
##	0.000108478580	-0.015819986140	-0.010123156396	-0.018910589017
##	TRUE	TRUE	TRUE	TRUE
##	0.016024679281	-0.024761966475	-0.008181611205	0.025938363434
##	TRUE	TRUE	TRUE	TRUE
##	-0.008660153899	-0.017313947376	0.015878740978	-0.006940907216
##	TRUE	TRUE	TRUE	TRUE
##	0.028394294582	-0.029461475011	0.013336504876	-0.000246475140
##	TRUE	TRUE	TRUE	TRUE
##	-0.037311746881	0.015677878146	-0.012692872332	-0.023783304848
##	TRUE	TRUE	TRUE	TRUE
##	-0.010715062193	0.036900884700	-0.021717503014	0.009536205402
##	TRUE	TRUE	TRUE	TRUE
##	-0.012915522245	-0.021244793634	-0.011697132444	0.004635306928
##	TRUE	TRUE	TRUE	TRUE
##	-0.009363630636	0.010524671216	0.033652712030	-0.011949019214
##	TRUE	TRUE	TRUE	TRUE
##	-0.005924680444	-0.017771440939	0.015909102330	0.033855823850
##	TRUE	TRUE	TRUE	TRUE
##	0.031891015679	-0.029328292693	0.020172939525	-0.025474895994
##	TRUE	TRUE	TRUE	TRUE
##	-0.005541192676	0.005377684146	-0.018967867956	-0.000395330101
##	TRUE	TRUE	TRUE	TRUE
##	-0.009409453787	0.021226274615	-0.027636244721	-0.019704411859
##	TRUE	TRUE	TRUE	TRUE
##	0.019164092248	-0.011834039651	-0.022434403403	-0.024216305515
##	TRUE	TRUE	TRUE	TRUE
##	0.011027039138	-0.007523149389	-0.020542898218	0.019169960703
##	TRUE	TRUE	TRUE	TRUE
##	0.003758306632	-0.018047855745	-0.018721955063	-0.011167003564
##	TRUE	TRUE	TRUE	TRUE
##	-0.005782150765	-0.029653377027	0.029399346690	-0.012074330071
##	TRUE	TRUE	TRUE	TRUE
##	0.013768978436	-0.029600666347	-0.006440893705	-0.015581347321
##	TRUE	TRUE	TRUE	TRUE
##	0.059676501906	-0.016182178793	-0.016812633668	-0.001615512064
##	TRUE	TRUE	TRUE	TRUE
##	0.020565634091	-0.010793495685	0.059868755326	0.015634795950
##	TRUE	TRUE	TRUE	TRUE
##	0.021532910212	0.027928051046	0.014141326681	0.012403736681
##	TRUE	TRUE	TRUE	TRUE
##	-0.028038884036	0.007138572267	0.031340540476	-0.022386682668
##	TRUE	TRUE	TRUE	TRUE
##	-0.007771065287	-0.003847879648	0.009890245470	0.017634358030
##	TRUE	TRUE	TRUE	TRUE
##	-0.023568210133	-0.003508703992	-0.027319769798	0.004390764513
##	TRUE	TRUE	TRUE	TRUE
##	0.014816937038	-0.028451678942	-0.009985159835	-0.014860476060

##	TRUE	TRUE	TRUE	TRUE
##	-0.013897451934	0.041070299496	-0.007655523477	0.031221238637
##	TRUE	TRUE	TRUE	TRUE
##	-0.008659064545	-0.002027287897	-0.021083990920	0.002900739007
##	TRUE	TRUE	TRUE	TRUE
##	-0.032883206381	-0.002351247737	0.006276541804	-0.028551266987
##	TRUE	TRUE	TRUE	TRUE
##	-0.018811317236	-0.011185979409	0.064857926620	-0.007894267717
##	TRUE	TRUE	TRUE	TRUE
##	0.027960380263	-0.004500578429	-0.019591224459	0.013376670415
##	TRUE	TRUE	TRUE	TRUE
##	0.042293081853	0.003264512981	0.027037170271	-0.029178278097
##	TRUE	TRUE	TRUE	TRUE
##	-0.013554445968	0.009487360172	-0.033981978078	0.035240463136
##	TRUE	TRUE	TRUE	TRUE
##	0.005196148564	0.038549850476	-0.010010250119	0.014347706564
##	TRUE	TRUE	TRUE	TRUE
##	0.051560216804	0.011381290049	0.019906504607	0.003842854563
##	TRUE	TRUE	TRUE	TRUE
##	-0.014067637150	-0.001988457696	-0.006333996445	0.007020148939
##	TRUE	TRUE	TRUE	TRUE
##	-0.012485051690	0.024363614295	0.012334053162	0.018201981774
##	TRUE	TRUE	TRUE	TRUE
##	-0.001207777384	0.005498110480	-0.023043071197	0.015431789551
##	TRUE	TRUE	TRUE	TRUE
##	-0.019108640612	-0.013769716386	0.030102999129	0.010515710401
##	TRUE	TRUE	TRUE	TRUE
##	-0.007612476421	-0.015140580614	-0.014218459976	0.048247280278
##	TRUE	TRUE	TRUE	TRUE
##	0.005978023652	0.031671493267	0.037773246455	-0.018760363579
##	TRUE	TRUE	TRUE	TRUE
##	-0.025357737722	0.033152276833	-0.004140283361	-0.026007344144
##	TRUE	TRUE	TRUE	TRUE
##	0.004526582365	-0.003189101568	0.009610738304	-0.017156869549
##	TRUE	TRUE	TRUE	TRUE
##	-0.009792695572	0.002001670507	-0.036522035471	0.012979513010
##	TRUE	TRUE	TRUE	TRUE
##	-0.024229061499	0.009807735686	0.032760109373	-0.009429237862
##	TRUE	TRUE	TRUE	TRUE
##	0.022742128354	0.018917933372	-0.014518805431	0.008692693959
##	TRUE	TRUE	TRUE	TRUE
##	0.001589578410	-0.000496112921	-0.021450892394	-0.017467159753
##	TRUE	TRUE	TRUE	TRUE
##	-0.025558635694	0.013680740758	-0.005879770945	0.010421990811
##	TRUE	TRUE	TRUE	TRUE
##	-0.014020443521	-0.000560173968	0.006863141393	-0.007140259008
##	TRUE	TRUE	TRUE	TRUE
##	0.009741882476	-0.007334234311	-0.025826651933	0.009689347498
##	TRUE	TRUE	TRUE	TRUE
##	0.001848985237	0.014592635524	-0.004504127615	-0.042621434250
##	TRUE	TRUE	TRUE	TRUE
##	0.003179683926	-0.011291822455	0.000892918921	-0.008114949764
##	TRUE	TRUE	TRUE	TRUE
##	0.005382568669	0.025261523161	-0.017505392566	-0.006871083135

##	TRUE	TRUE	TRUE	TRUE
##	0.003021446465	-0.004635096085	-0.012465302756	-0.004739674074
##	TRUE	TRUE	TRUE	TRUE
##	0.005018618994	-0.010571091755	-0.018288392149	-0.023958761132
##	TRUE	TRUE	TRUE	TRUE
##	-0.003297474726	0.008710650731	0.010062785097	0.004368626027
##	TRUE	TRUE	TRUE	TRUE
##	-0.010048658634	-0.020159761855	0.025426577870	-0.013231856606
##	TRUE	TRUE	TRUE	TRUE
##	-0.017868077186	-0.007484389469	-0.015123045528	0.011652890613
##	TRUE	TRUE	TRUE	TRUE
##	0.016809752151	-0.022569588728	-0.013471444217	0.008934354857
##	TRUE	TRUE	TRUE	TRUE
##	-0.010445570056	0.015801853666	0.004341111052	0.030355167022
##	TRUE	TRUE	TRUE	TRUE
##	-0.016226385484	0.039032399182	-0.002552883659	0.024432454444
##	TRUE	TRUE	TRUE	TRUE
##	-0.008061782258	-0.028884714750	0.014605461789	-0.025987278945
##	TRUE	TRUE	TRUE	TRUE
##	-0.010023252087	0.055255305760	0.019590802773	-0.007973931125
##	TRUE	TRUE	TRUE	TRUE
##	-0.003278569162	-0.008144854290	0.004817685881	0.012909442946
##	TRUE	TRUE	TRUE	TRUE
##	-0.006461696853	0.004972479578	-0.015714318797	-0.011486465426
##	TRUE	TRUE	TRUE	TRUE
##	-0.000272373654	-0.014675039887	0.013698451546	0.015172593567
##	TRUE	TRUE	TRUE	TRUE
##	0.000127946391	0.010382809206	0.009100709763	0.010114160440
##	TRUE	TRUE	TRUE	TRUE
##	0.026539124625	0.013419858032	-0.009418766007	-0.004363776644
##	TRUE	TRUE	TRUE	TRUE
##	-0.008304743353	0.018814269034	-0.016577157489	0.047403839116
##	TRUE	TRUE	TRUE	TRUE
##	0.007123988978	-0.005488657698	0.028541076256	-0.012164570755
##	TRUE	TRUE	TRUE	TRUE
##	0.036866095651	-0.013549245181	0.024796298698	0.008732789216
##	TRUE	TRUE	TRUE	TRUE
##	-0.024148168176	0.009221382080	0.021833782774	-0.015261182650
##	TRUE	TRUE	TRUE	TRUE
##	-0.005295420345	0.000205431091	-0.001279534189	-0.007710658848
##	TRUE	TRUE	TRUE	TRUE
##	-0.025022673499	0.034885614837	-0.018933676295	0.016418322640
##	TRUE	TRUE	TRUE	TRUE
##	-0.019500878353	0.018849796033	-0.009329298413	0.010791176415
##	TRUE	TRUE	TRUE	TRUE
##	0.001049153377	-0.026835218086	-0.015958017841	0.022661867558
##	TRUE	TRUE	TRUE	TRUE
##	0.000606207962	-0.010694259044	-0.031323145952	-0.013937195787
##	TRUE	TRUE	TRUE	TRUE
##	-0.005008006577	0.012179821712	-0.027725431192	0.000923315413
##	TRUE	TRUE	TRUE	TRUE
##	0.022946645793	0.007044606694	0.001388820999	0.013420982526
##	TRUE	TRUE	TRUE	TRUE
##	-0.013408577946	0.055418357464	-0.012794252540	0.007997018403

##	TRUE	TRUE	TRUE	TRUE
##	0.001014258907	0.007536151356	-0.019089875610	0.010397849320
##	TRUE	TRUE	TRUE	TRUE
##	-0.004150438952	0.016292800940	0.001230196993	-0.010706171658
##	TRUE	TRUE	TRUE	TRUE
##	-0.009117331198	-0.021540816814	0.041437025268	-0.035358886464
##	TRUE	TRUE	TRUE	TRUE
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```

R value is supposed to vary between 0 and 1 (not between -1 and +1) but you can obtained negative values but they are always close to 0. R value close to 1 indicates high separation between levels of your factor (e.g. control vs treatment samples), while R value close to 0 indicate no separation between levels of your factor.