Morphometry-Geometry on mandibles of cervids

Berlioz et al., 2024

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CONTEXT : In this study, we investigate the relationships between mandibular morphology, size (2D landmarks and semi-landmarks) and environmental contexts at different scales of ecosystem structure: (i) at the inter-specific scale, between two cervid species, (ii) between populations of the same species from contrasting ecosystems, (iii) at the intra-population scale between contrasted local habitats

For this study, we needed the following packages :

Here are the datasets we analyzed: (1) ALL_Cervids (2) ALL_Cervus (3) All_Rusa

1 DATASET 1 : ALL_Cervids

1. Can we identify shape and size differences at the inter-specific scale, between the two cervid species ? ## Part 1 : data preparation :

```
# Descriptive factors :
Descriptive_ALL_Cervids <- read_excel("Descriptive_ALL_Cervids.xlsx") # importing environmental information
View(Descriptive_ALL_Cervids)
summary(Descriptive_ALL_Cervids)
```

```
##   TPS POSITION       Ref                Length        Species         
##  Min.   :  1.0   Length:315         Min.   :18.41   Length:315        
##  1st Qu.: 79.5   Class :character   1st Qu.:21.11   Class :character  
##  Median :158.0   Mode  :character   Median :25.09   Mode  :character  
##  Mean   :158.0                      Mean   :24.83                     
##  3rd Qu.:236.5                      3rd Qu.:27.48                     
##  Max.   :315.0                      Max.   :35.88                     
##                                                                       
##      Sex                Pop                 Lat              Long        
##  Length:315         Length:315         Min.   :-34.55   Min.   :-65.298  
##  Class :character   Class :character   1st Qu.: 38.35   1st Qu.:-21.574  
##  Mode  :character   Mode  :character   Median : 63.25   Median : -4.162  
##                                        Mean   : 89.58   Mean   :-12.762  
##                                        3rd Qu.:165.20   3rd Qu.: -2.130  
##                                        Max.   :165.76   Max.   : 42.545  
##                                                                          
##  Vegetation_type       Climat             Genet           Herb_Monocots  
##  Length:315         Length:315         Length:315         Min.   :32.86  
##  Class :character   Class :character   Class :character   1st Qu.:49.14  
##  Mode  :character   Mode  :character   Mode  :character   Median :55.50  
##                                                           Mean   :51.55  
##                                                           3rd Qu.:57.10  
##                                                           Max.   :57.10  
##                                                           NA's   :158
```

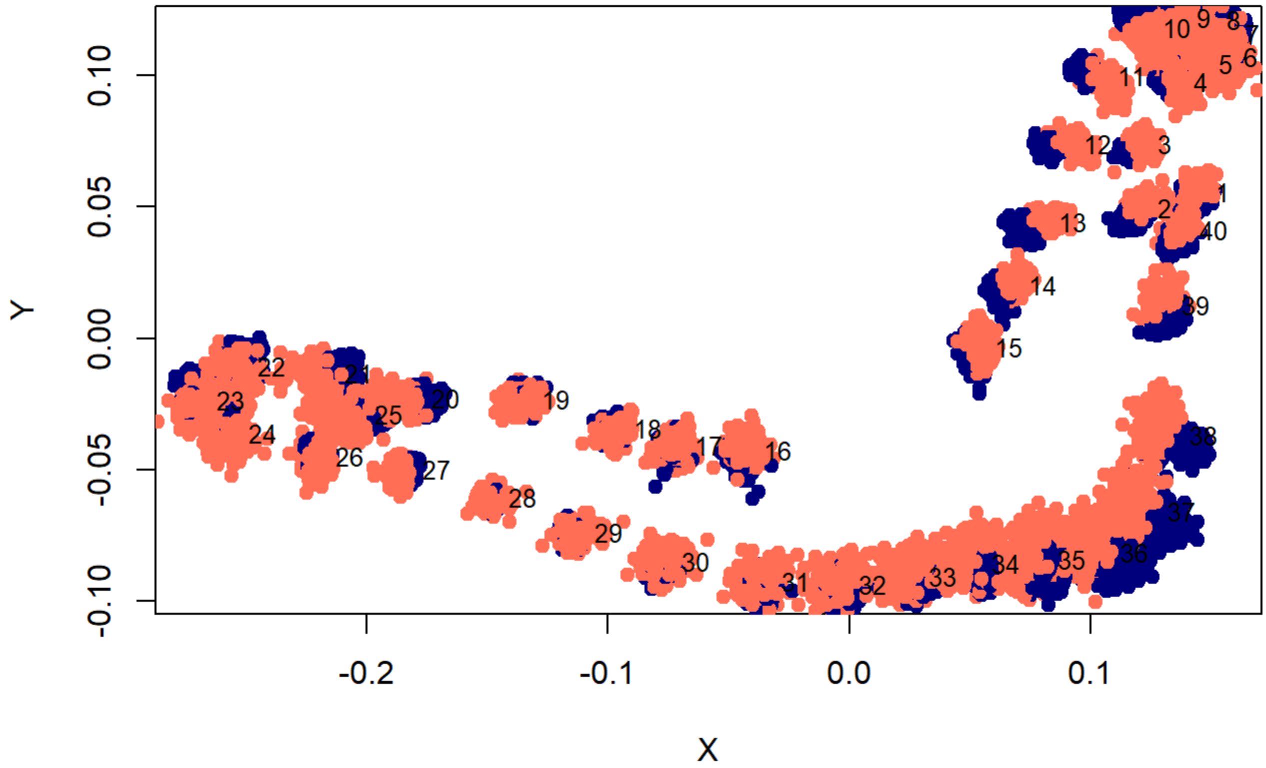
```
ALL_Cervids_species<- Descriptive_ALL_Cervids$Species
ALL_Cervids_pop <- Descriptive_ALL_Cervids$Pop
ALL_Cervids_Lat<- Descriptive_ALL_Cervids$Lat
ALL_Cervids_Long<- Descriptive_ALL_Cervids$Long
ALL_Cervids_Vegetation<- Descriptive_ALL_Cervids$Vegetation_type
ALL_Cervids_Climate<- Descriptive_ALL_Cervids$Climat
ALL_Cervids_Genetics<- Descriptive_ALL_Cervids$Genet

# morphometry-geometry data : We import in R the tps file produced with tps and Matlab :
MorphoGeom_ALL_Cervids <- readland.tps("MorphoGeom_ALL_Cervids.TPS", specID = "ID")
```

```
## 
## No curves detected; all points appear to be fixed landmarks.
```

```
# In "MorphoGeom_ALL_Cervids", no curves are detected; all points appear to be fixed landmark
s. To define and slide the semi-landmarks, we generate a matrix with gmShiny ("Matrix"):
Matrix <- as.matrix(read.csv("Matrix.csv"))

# Semi-landmarks are identified, slided and a procrust analysis is done:
Slided_MorphoGeom_ALL_Cervids <- gpagen(MorphoGeom_ALL_Cervids, PrinAxes = FALSE, print.progr
ess = FALSE, curves = Matrix)
options(max.print=1000000000)
```

1.1 Part 2 : data visualization: between species

```
Colors_ALL_Species <- c("Cervus" = "coral1", "Rusa"= "navyblue") # identify cervids by species

point_colors_Species <- Colors_ALL_Species[ALL_Cervids_species] # Color vector for species

plot(Slided_MorphoGeom_ALL_Cervids$coords[, , 1], col = point_colors_Species, pch = 19)
for (i in 2:dim(Slided_MorphoGeom_ALL_Cervids$coords)[3]) {
  points(Slided_MorphoGeom_ALL_Cervids$coords[, , i], col = point_colors_Species[i], pch = 19)
}

mean_shape <- mshape(Slided_MorphoGeom_ALL_Cervids$coords)  # Consensus shape
text(mean_shape[,1], mean_shape[,2], labels = 1:nrow(mean_shape), pos = 4, cex = 0.8, col = "black")
```



1.2 Part 3 : Analysis

1.2.1 Centroid size

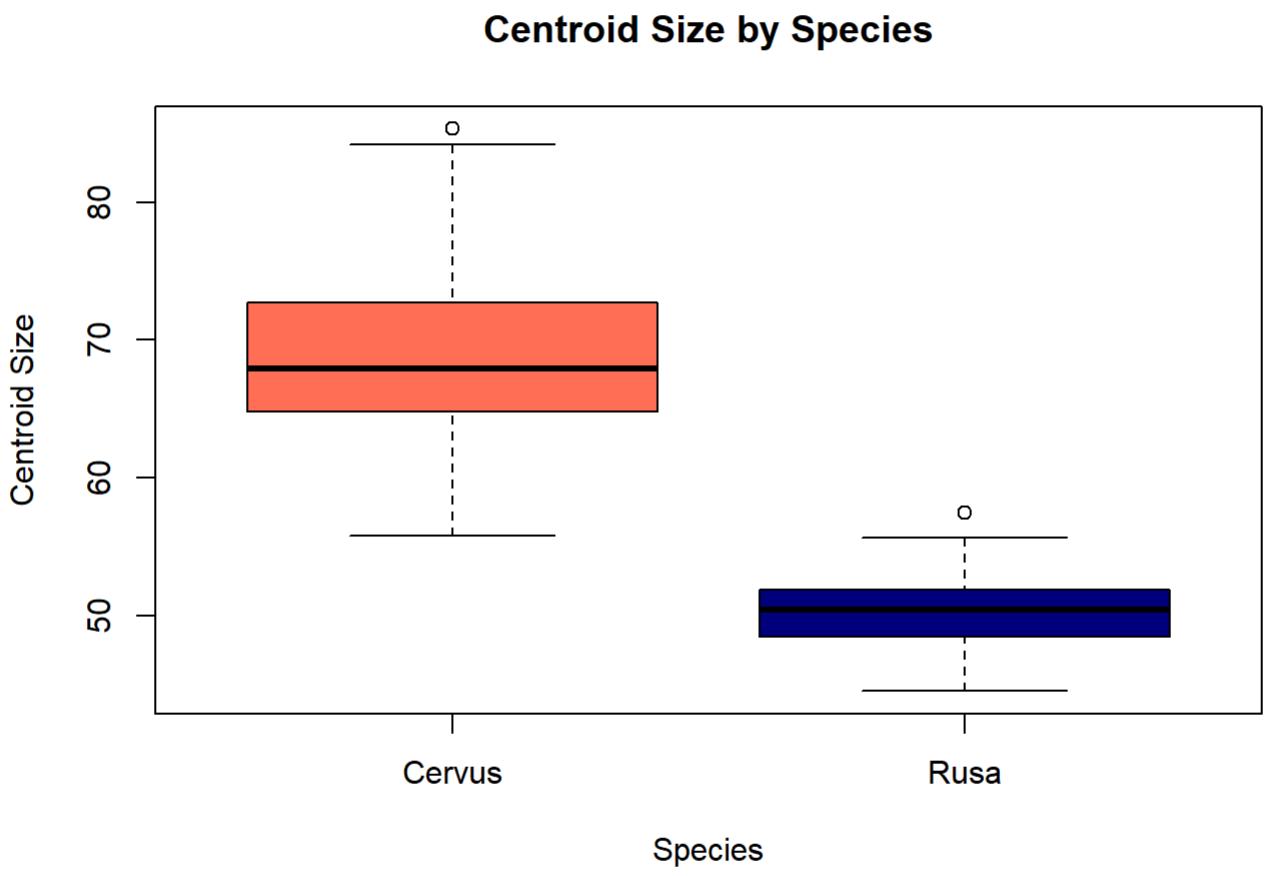
```
centroid_sizes <- Slided_MorphoGeom_ALL_Cervids$Csize
Descriptive_ALL_Cervids$Centroid_Size <- centroid_sizes
cervus_centroid_sizes <- Descriptive_ALL_Cervids$Centroid_Size[Descriptive_ALL_Cervids$Species == "Cervus"]
rusa_centroid_sizes <- Descriptive_ALL_Cervids$Centroid_Size[Descriptive_ALL_Cervids$Species == "Rusa"]

mean_se <- function(x) {
  n <- length(x)
  mean <- mean(x)
  se <- sd(x) / sqrt(n)
  return(c(mean = mean, se = se))
}
library(dplyr)
centroid_stats <- Descriptive_ALL_Cervids %>%
  group_by(Species) %>%
  summarise(
    mean_centroid_size = mean(Centroid_Size, na.rm = TRUE),
    se_centroid_size = sd(Centroid_Size, na.rm = TRUE) / sqrt(n())
  )
print(centroid_stats)
```

```
## # A tibble: 2 × 3
##   Species mean_centroid_size se_centroid_size
##   <chr>                <dbl>            <dbl>
## 1 Cervus                69.2            0.458
## 2 Rusa                  50.4            0.231
```

```
anova_result <- aov(Centroid_Size ~ Species, data = Descriptive_ALL_Cervids)
summary(anova_result)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## Species       1  27147   27147    1056 <2e-16 ***
## Residuals   313   8046      26
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
###Results ###############
# p-value < 2.2e-16 : Cervus and Rusa differ statistically in size.
##########################

boxplot(Centroid_Size ~ Species, data = Descriptive_ALL_Cervids, main = "Centroid Size by Species", xlab = "Species", ylab = "Centroid Size", col = c("coral1","navyblue"))
```



1.2.2 Principal Component Analysis (PCA):

```
PCA_ALL_Cervids <- gm.prcomp(Slided_MorphoGeom_ALL_Cervids$coords)
summary(PCA_ALL_Cervids)
```

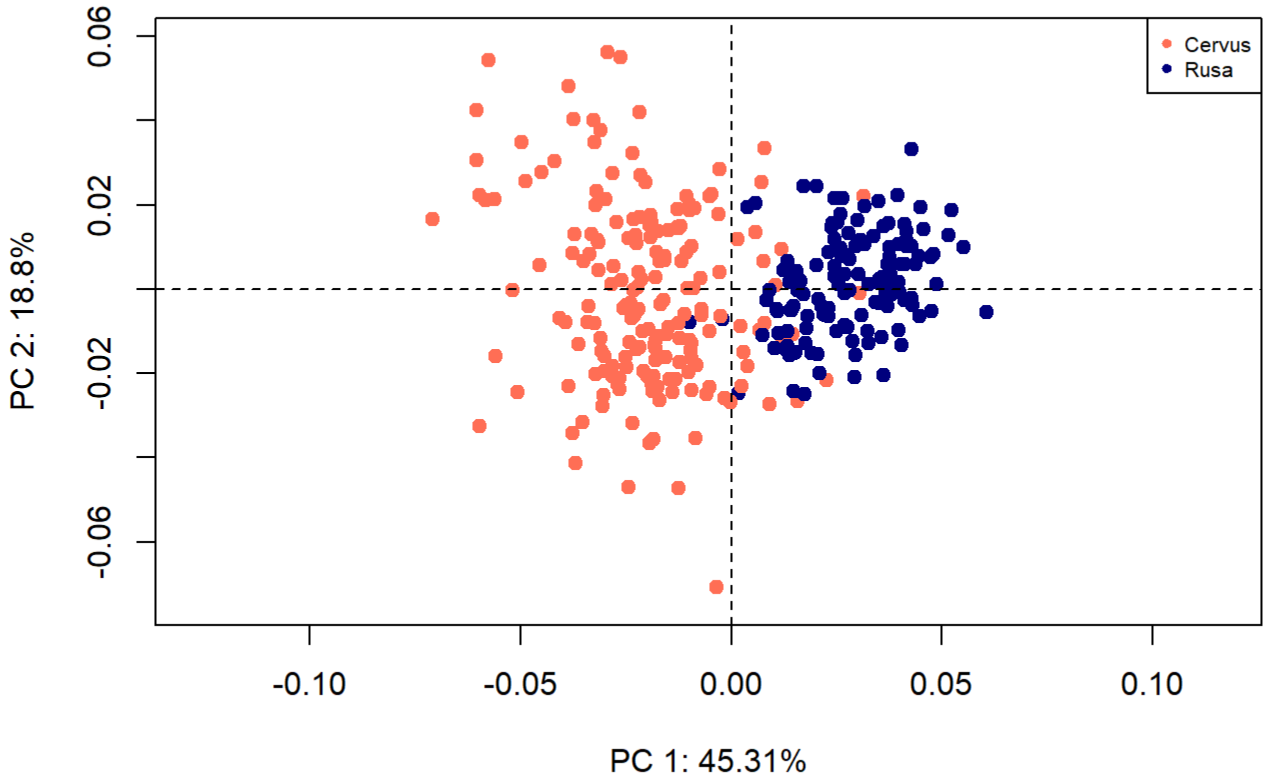
```
##
## Ordination type: Principal Component Analysis
## Centering by OLS mean
## Orthogonal projection of OLS residuals
## Number of observations: 315
## Number of vectors 79
##
## Importance of Components:
##                               Comp1        Comp2        Comp3        Comp4
## Eigenvalues            0.0008040671 0.0003336412 0.0001807615 0.0001033114
## Proportion of Variance 0.4530863671 0.1880045821 0.1018578901 0.0582152616
## Cumulative Proportion  0.4530863671 0.6410909492 0.7429488393 0.8011641010
##                               Comp5        Comp6        Comp7        Comp8
## Eigenvalues            6.829349e-05 5.227146e-05 3.285694e-05 2.736712e-05
## Proportion of Variance 3.848292e-02 2.945461e-02 1.851466e-02 1.542118e-02
## Cumulative Proportion  8.396470e-01 8.691016e-01 8.876163e-01 9.030375e-01
##                               Comp9       Comp10       Comp11       Comp12
## Eigenvalues            2.364855e-05 2.060186e-05 0.0000139751 1.315667e-05
## Proportion of Variance 1.332580e-02 1.160901e-02 0.0078748741 7.413694e-03
## Cumulative Proportion  9.163633e-01 9.279723e-01 0.9358471612 9.432609e-01
##                              Comp13       Comp14       Comp15       Comp16
## Eigenvalues            1.104484e-05 1.031427e-05 8.963337e-06 7.155288e-06
## Proportion of Variance 6.223691e-03 5.812023e-03 5.050780e-03 4.031956e-03
## Cumulative Proportion  9.494845e-01 9.552966e-01 9.603473e-01 9.643793e-01
##                              Comp17       Comp18       Comp19       Comp20
## Eigenvalues            6.712335e-06 5.464267e-06 5.257398e-06 5.139922e-06
## Proportion of Variance 3.782355e-03 3.079077e-03 2.962508e-03 2.896311e-03
## Cumulative Proportion  9.681617e-01 9.712407e-01 9.742032e-01 9.770996e-01
##                              Comp21       Comp22       Comp23       Comp24
## Eigenvalues            4.069823e-06 3.671983e-06 3.030473e-06 2.900996e-06
## Proportion of Variance 2.293317e-03 2.069137e-03 1.707651e-03 1.634692e-03
## Cumulative Proportion  9.793929e-01 9.814620e-01 9.831697e-01 9.848044e-01
##                              Comp25       Comp26       Comp27       Comp28
## Eigenvalues            2.342971e-06 2.288649e-06 2.058063e-06 1.843959e-06
## Proportion of Variance 1.320248e-03 1.289638e-03 1.159705e-03 1.039058e-03
## Cumulative Proportion  9.861246e-01 9.874142e-01 9.885739e-01 9.896130e-01
##                              Comp29       Comp30       Comp31       Comp32
## Eigenvalues            1.791771e-06 1.659545e-06 1.503549e-06 1.405169e-06
## Proportion of Variance 1.009651e-03 9.351422e-04 8.472398e-04 7.918031e-04
## Cumulative Proportion  9.906227e-01 9.915578e-01 9.924050e-01 9.931968e-01
##                              Comp33       Comp34       Comp35       Comp36
## Eigenvalues            1.231307e-06 1.063008e-06 9.887434e-07 9.572586e-07
## Proportion of Variance 6.938333e-04 5.989980e-04 5.571502e-04 5.394087e-04
## Cumulative Proportion  9.938907e-01 9.944897e-01 9.950468e-01 9.955862e-01
##                              Comp37       Comp38       Comp39       Comp40
## Eigenvalues            9.071561e-07 8.571995e-07 7.871284e-07 7.078447e-07
## Proportion of Variance 5.111763e-04 4.830261e-04 4.435415e-04 3.988657e-04
## Cumulative Proportion  9.960974e-01 9.965804e-01 9.970240e-01 9.974228e-01
##                              Comp41       Comp42       Comp43       Comp44
## Eigenvalues            6.966789e-07 6.096290e-07 5.323580e-07 5.141724e-07
## Proportion of Variance 3.925738e-04 3.435218e-04 2.999801e-04 2.897327e-04
## Cumulative Proportion  9.978154e-01 9.981589e-01 9.984589e-01 9.987486e-01
##                              Comp45       Comp46       Comp47       Comp48
## Eigenvalues            4.499520e-07 3.295972e-07 3.132330e-07 2.968679e-07
## Proportion of Variance 2.535449e-04 1.857258e-04 1.765047e-04 1.672831e-04
```

```
## Cumulative Proportion  9.990022e-01 9.991879e-01 9.993644e-01 9.995317e-01
##                               Comp49       Comp50       Comp51       Comp52
## Eigenvalues            2.174325e-07 1.381621e-07 9.929657e-08 7.856671e-08
## Proportion of Variance 1.225218e-04 7.785343e-05 5.595295e-05 4.427181e-05
## Cumulative Proportion  9.996542e-01 9.997321e-01 9.997880e-01 9.998323e-01
##                               Comp53       Comp54       Comp55       Comp56
## Eigenvalues            6.803140e-08 4.343017e-08 3.336070e-08 2.852004e-08
## Proportion of Variance 3.833524e-05 2.447261e-05 1.879853e-05 1.607085e-05
## Cumulative Proportion  9.998706e-01 9.998951e-01 9.999139e-01 9.999300e-01
##                               Comp57       Comp58       Comp59       Comp60
## Eigenvalues            2.335877e-08 1.998875e-08 1.469963e-08 1.100143e-08
## Proportion of Variance 1.316251e-05 1.126353e-05 8.283142e-06 6.199233e-06
## Cumulative Proportion  9.999431e-01 9.999544e-01 9.999627e-01 9.999689e-01
##                               Comp61       Comp62       Comp63       Comp64
## Eigenvalues            9.358134e-09 8.371836e-09 6.189029e-09 5.698767e-09
## Proportion of Variance 5.273245e-06 4.717473e-06 3.487476e-06 3.211216e-06
## Cumulative Proportion  9.999742e-01 9.999789e-01 9.999824e-01 9.999856e-01
##                               Comp65       Comp66       Comp67       Comp68
## Eigenvalues            5.141602e-09 3.379223e-09 3.068860e-09 2.625032e-09
## Proportion of Variance 2.897258e-06 1.904169e-06 1.729282e-06 1.479188e-06
## Cumulative Proportion  9.999885e-01 9.999904e-01 9.999921e-01 9.999936e-01
##                               Comp69       Comp70       Comp71       Comp72
## Eigenvalues            2.155091e-09 1.782523e-09 1.481335e-09 1.436300e-09
## Proportion of Variance 1.214379e-06 1.004439e-06 8.347220e-07 8.093455e-07
## Cumulative Proportion  9.999948e-01 9.999958e-01 9.999966e-01 9.999975e-01
##                               Comp73       Comp74       Comp75       Comp76
## Eigenvalues            1.253219e-09 1.144425e-09 9.906442e-10 5.974507e-10
## Proportion of Variance 7.061804e-07 6.448756e-07 5.582213e-07 3.366594e-07
## Cumulative Proportion  9.999982e-01 9.999988e-01 9.999994e-01 9.999997e-01
##                               Comp77       Comp78       Comp79
## Eigenvalues            3.081281e-10 2.229259e-10 2.439036e-19
## Proportion of Variance 1.736281e-07 1.256172e-07 1.374381e-16
## Cumulative Proportion  9.999999e-01 1.000000e+00 1.000000e+00
```

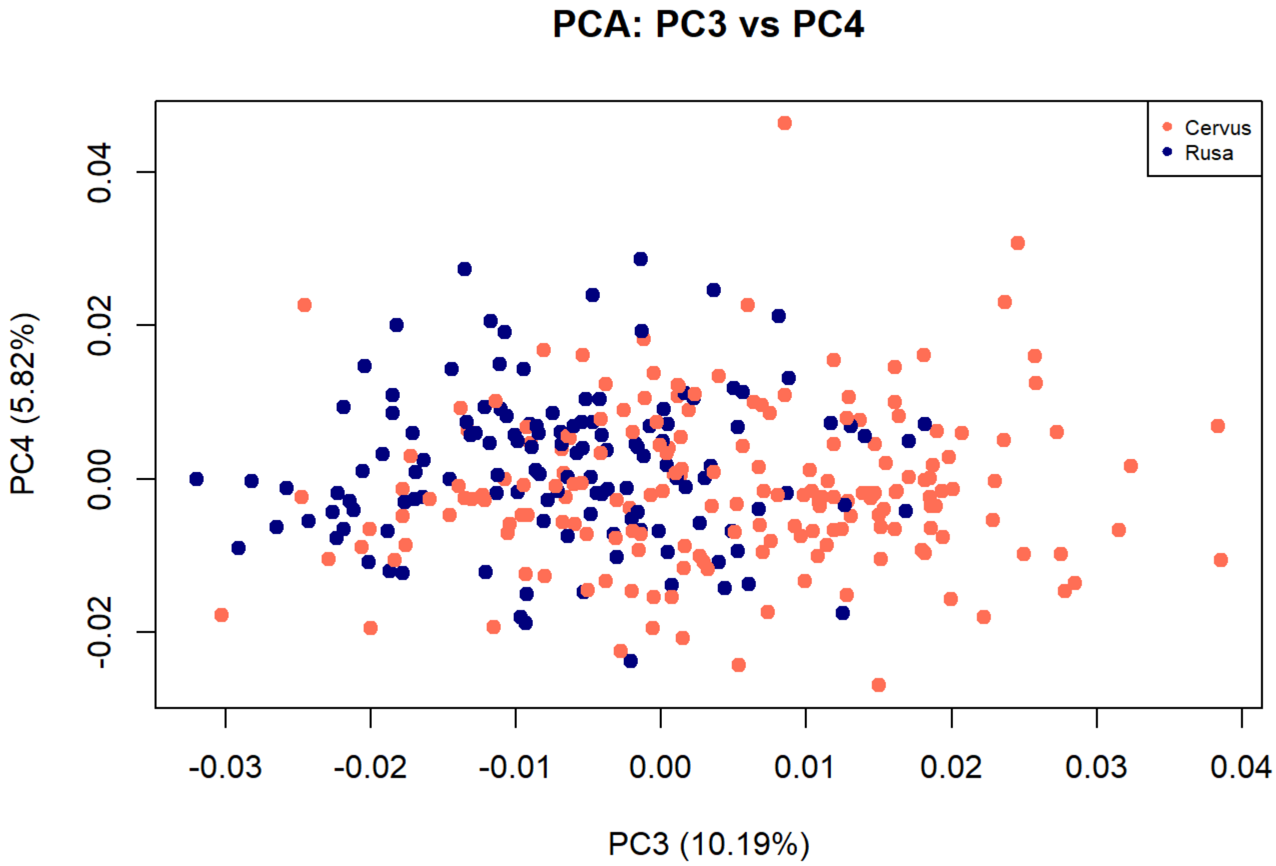
```
PC_scores_PCA_ALL_Cervids <- PCA_ALL_Cervids$x # Extract PC scores (PC 1-4 explain >80%)
view(PC_scores_PCA_ALL_Cervids)

eigenvalues <- PCA_ALL_Cervids$sdev^2
explained_variance <- eigenvalues / sum(eigenvalues) * 100 # eighenvalues in %
cumulative_variance <- cumsum(explained_variance)
cumulative_variance
```

```
##     Comp1     Comp2     Comp3     Comp4     Comp5     Comp6     Comp7     Comp8 
##  45.30864  64.10909  74.29488  80.11641  83.96470  86.91016  88.76163  90.30375 
##     Comp9    Comp10    Comp11    Comp12    Comp13    Comp14    Comp15    Comp16 
##  91.63633  92.79723  93.58472  94.32609  94.94845  95.52966  96.03473  96.43793 
##    Comp17    Comp18    Comp19    Comp20    Comp21    Comp22    Comp23    Comp24 
##  96.81617  97.12407  97.42032  97.70996  97.93929  98.14620  98.31697  98.48044 
##    Comp25    Comp26    Comp27    Comp28    Comp29    Comp30    Comp31    Comp32 
##  98.61246  98.74142  98.85739  98.96130  99.06227  99.15578  99.24050  99.31968 
##    Comp33    Comp34    Comp35    Comp36    Comp37    Comp38    Comp39    Comp40 
##  99.38907  99.44897  99.50468  99.55862  99.60974  99.65804  99.70240  99.74228 
##    Comp41    Comp42    Comp43    Comp44    Comp45    Comp46    Comp47    Comp48 
##  99.78154  99.81589  99.84589  99.87486  99.90022  99.91879  99.93644  99.95317 
##    Comp49    Comp50    Comp51    Comp52    Comp53    Comp54    Comp55    Comp56 
##  99.96542  99.97321  99.97880  99.98323  99.98706  99.98951  99.99139  99.99300 
##    Comp57    Comp58    Comp59    Comp60    Comp61    Comp62    Comp63    Comp64 
##  99.99431  99.99544  99.99627  99.99689  99.99742  99.99789  99.99824  99.99856 
##    Comp65    Comp66    Comp67    Comp68    Comp69    Comp70    Comp71    Comp72 
##  99.99885  99.99904  99.99921  99.99936  99.99948  99.99958  99.99966  99.99975 
##    Comp73    Comp74    Comp75    Comp76    Comp77    Comp78    Comp79 
##  99.99982  99.99988  99.99994  99.99997  99.99999 100.00000 100.00000
```

```
PC1<-PC_scores_PCA_ALL_Cervids[,1]
PC2<-PC_scores_PCA_ALL_Cervids[,2]
PC3<-PC_scores_PCA_ALL_Cervids[,3]
PC4<-PC_scores_PCA_ALL_Cervids[,4]

plot(PCA_ALL_Cervids, col = Colors_ALL_Species[ALL_Cervids_species], pch = 19)
legend("topright", legend = names(Colors_ALL_Species), col = Colors_ALL_Species, pch = 19, ce
x= 0.65)
```



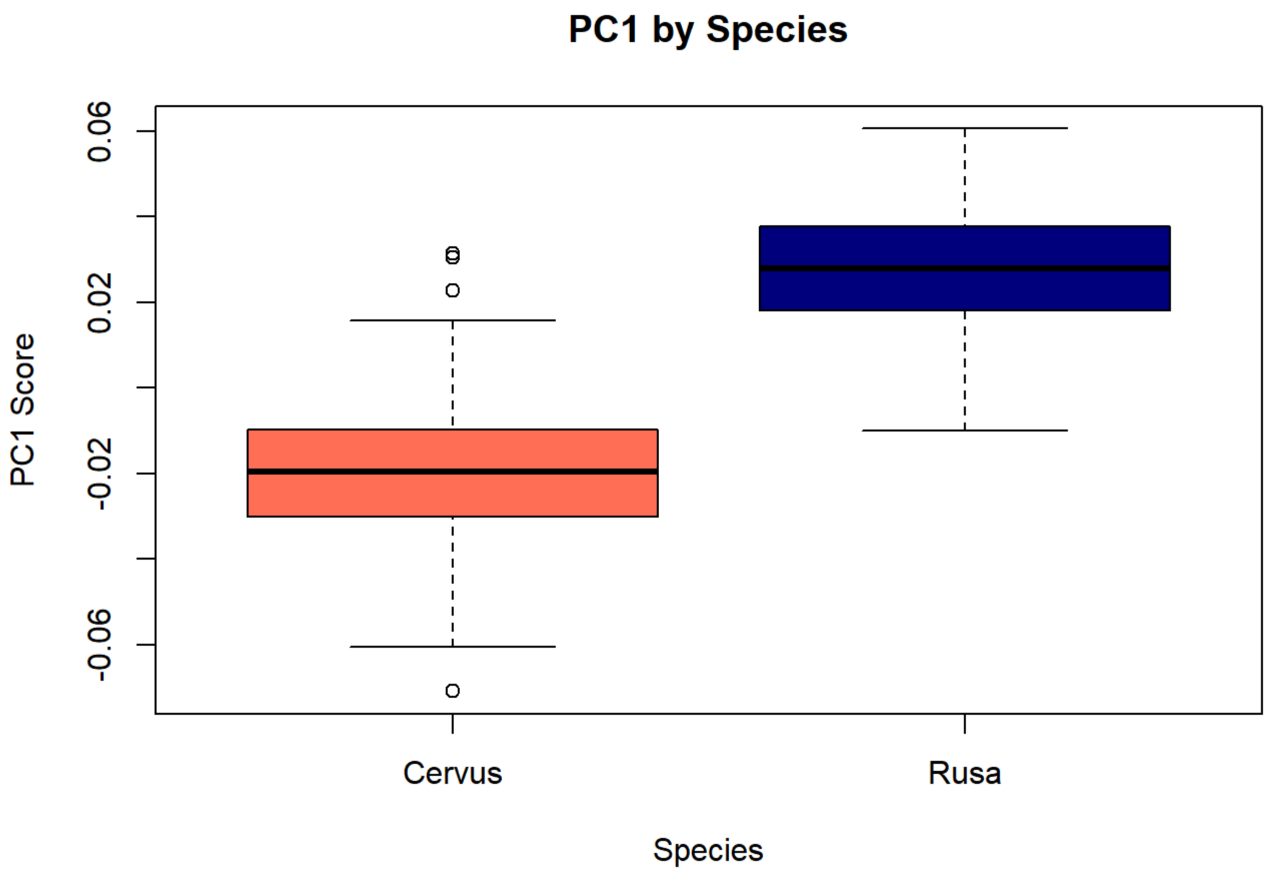
```
plot(PC3, PC4, col = Colors_ALL_Species[ALL_Cervids_species], pch = 19, xlab = paste0("PC3
(", round(explained_variance[3], 2), "%)"), ylab = paste0("PC4 (", round(explained_variance
[4], 2), "%)"), main = "PCA: PC3 vs PC4")
legend("topright", legend = names(Colors_ALL_Species), col = Colors_ALL_Species, pch = 19, ce
x= 0.65)
```



```
### test for significative differences between species :
anova_PC1 <- aov(PC1 ~ ALL_Cervids_species) # Inter-species differences on PC1
summary(anova_PC1)
```

```
##                      Df  Sum Sq Mean Sq F value Pr(>F)    
## ALL_Cervids_species   1 0.17590 0.17590     719 <2e-16 ***
## Residuals           313 0.07658 0.00024                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

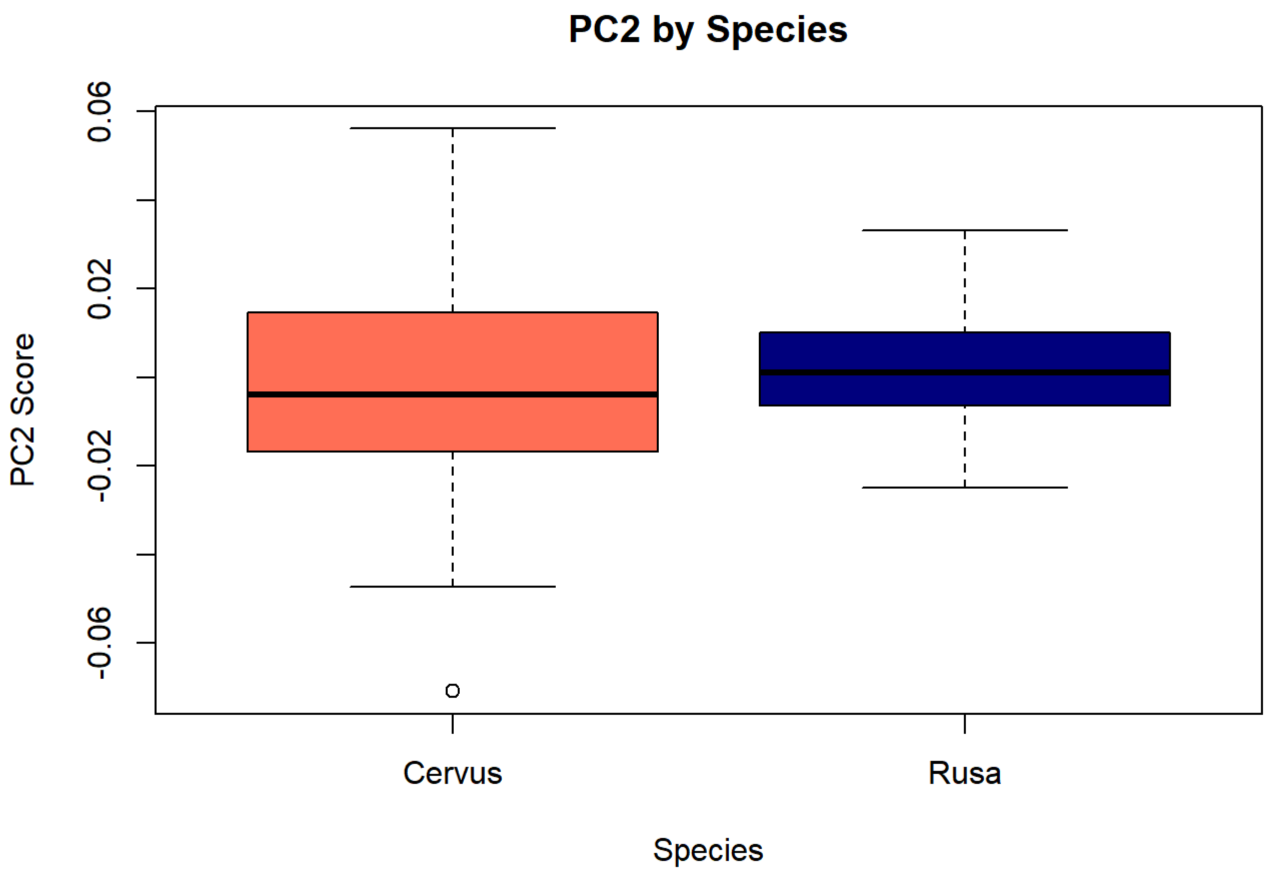
```
boxplot(PC1 ~ ALL_Cervids_species, main = "PC1 by Species", xlab = "Species", ylab = "PC1 Sco
re", col = Colors_ALL_Species)
```



```
anova_PC2 <- aov(PC2 ~ ALL_Cervids_species) # Inter-species differences on PC2
summary(anova_PC2)
```

```
##                      Df  Sum Sq   Mean Sq F value Pr(>F)
## ALL_Cervids_species   1 0.00039 0.0003877   1.163  0.282
## Residuals           313 0.10438 0.0003335
```

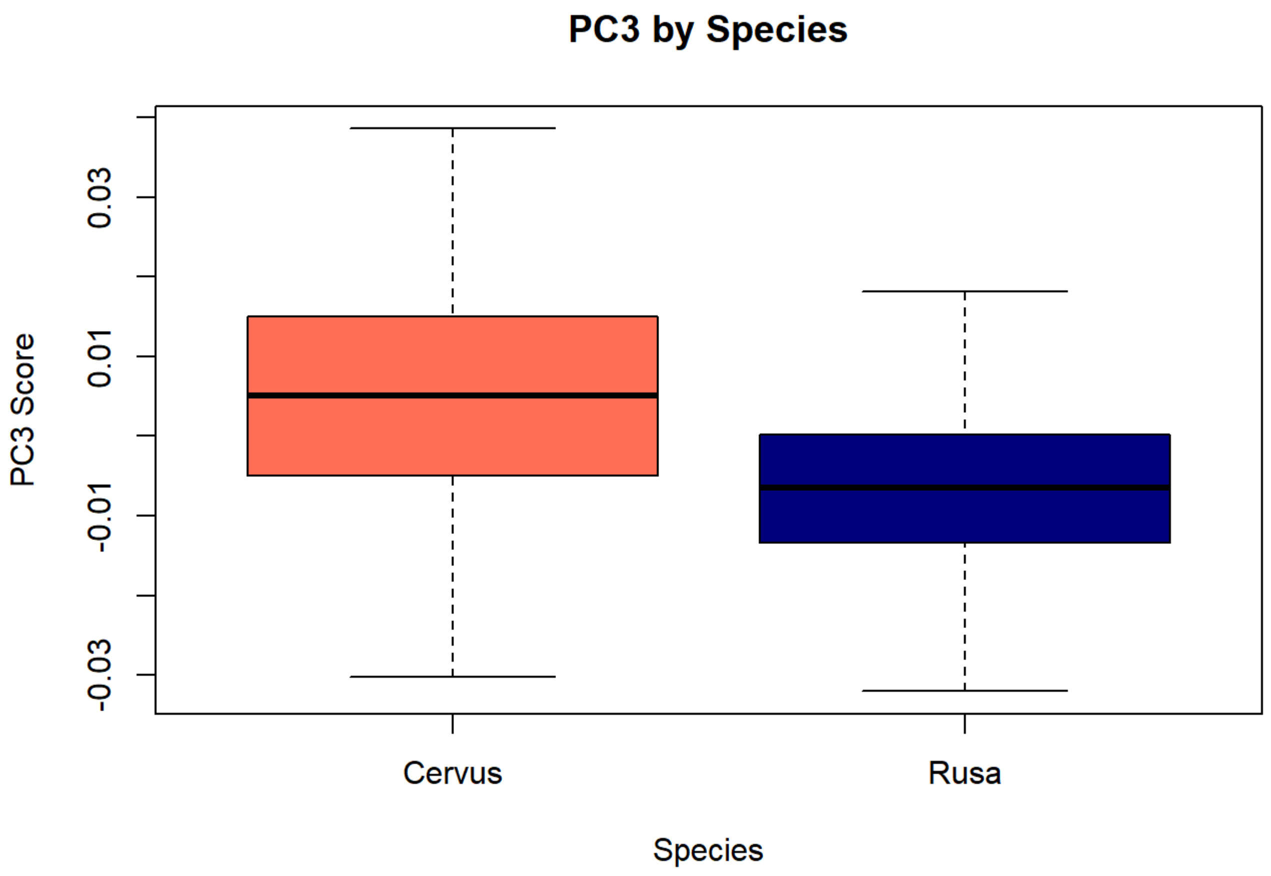
```
boxplot(PC2 ~ ALL_Cervids_species, main = "PC2 by Species", xlab = "Species", ylab = "PC2 Sco
re", col = Colors_ALL_Species)
```



```
anova_PC3 <- aov(PC3 ~ ALL_Cervids_species) # Inter-species differences on PC2
summary(anova_PC3)
```

```
##                      Df  Sum Sq  Mean Sq F value   Pr(>F)    
## ALL_Cervids_species   1 0.01000 0.010000   66.94 7.12e-15 ***
## Residuals           313 0.04676 0.000149                     
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

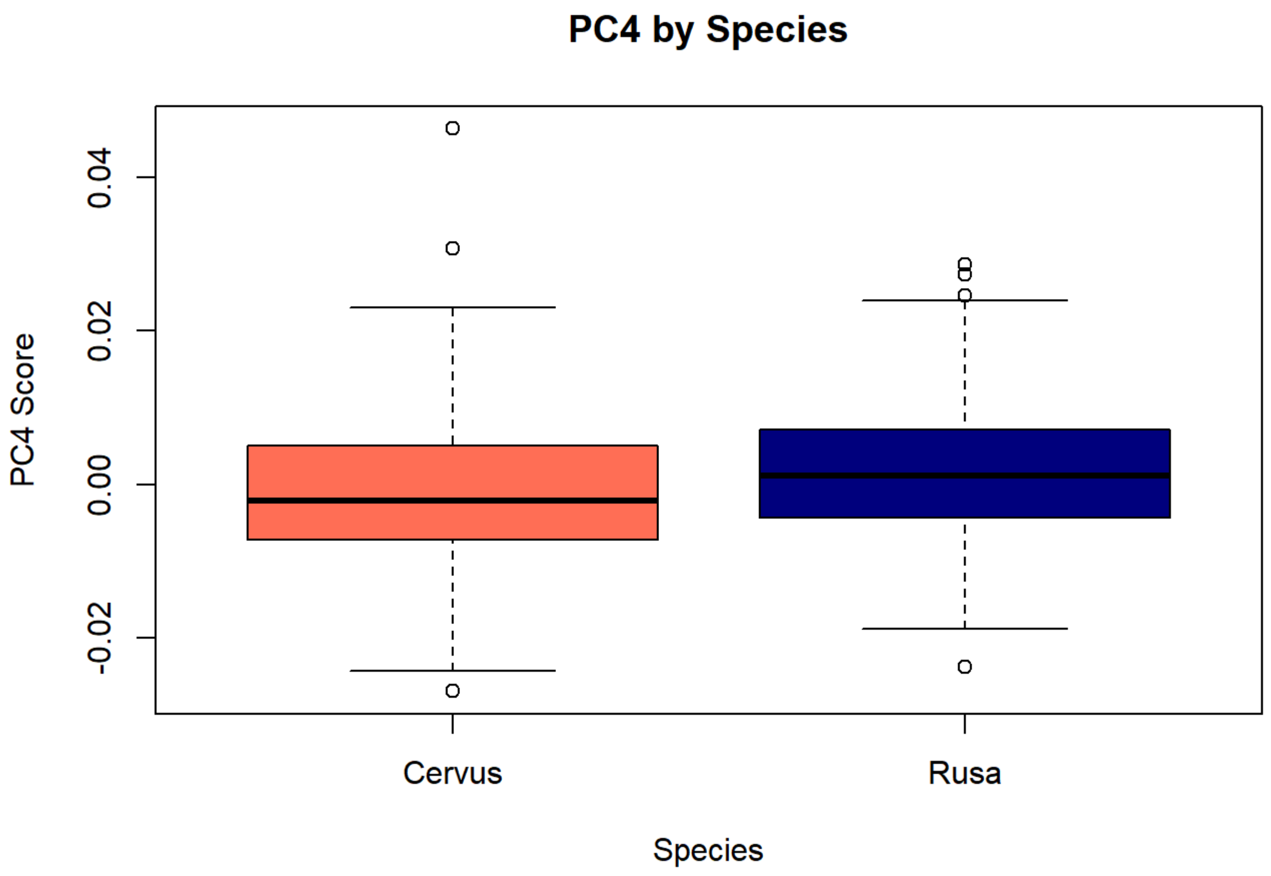
```
boxplot(PC3 ~ ALL_Cervids_species, main = "PC3 by Species", xlab = "Species", ylab = "PC3 Sco
re", col = Colors_ALL_Species)
```



```
anova_PC4 <- aov(PC4 ~ ALL_Cervids_species) # Inter-species differences on PC2
summary(anova_PC4)
```

```
##                      Df  Sum Sq   Mean Sq F value Pr(>F)  
## ALL_Cervids_species   1 0.00062 0.0006199   6.098 0.0141 *
## Residuals           313 0.03182 0.0001017                 
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

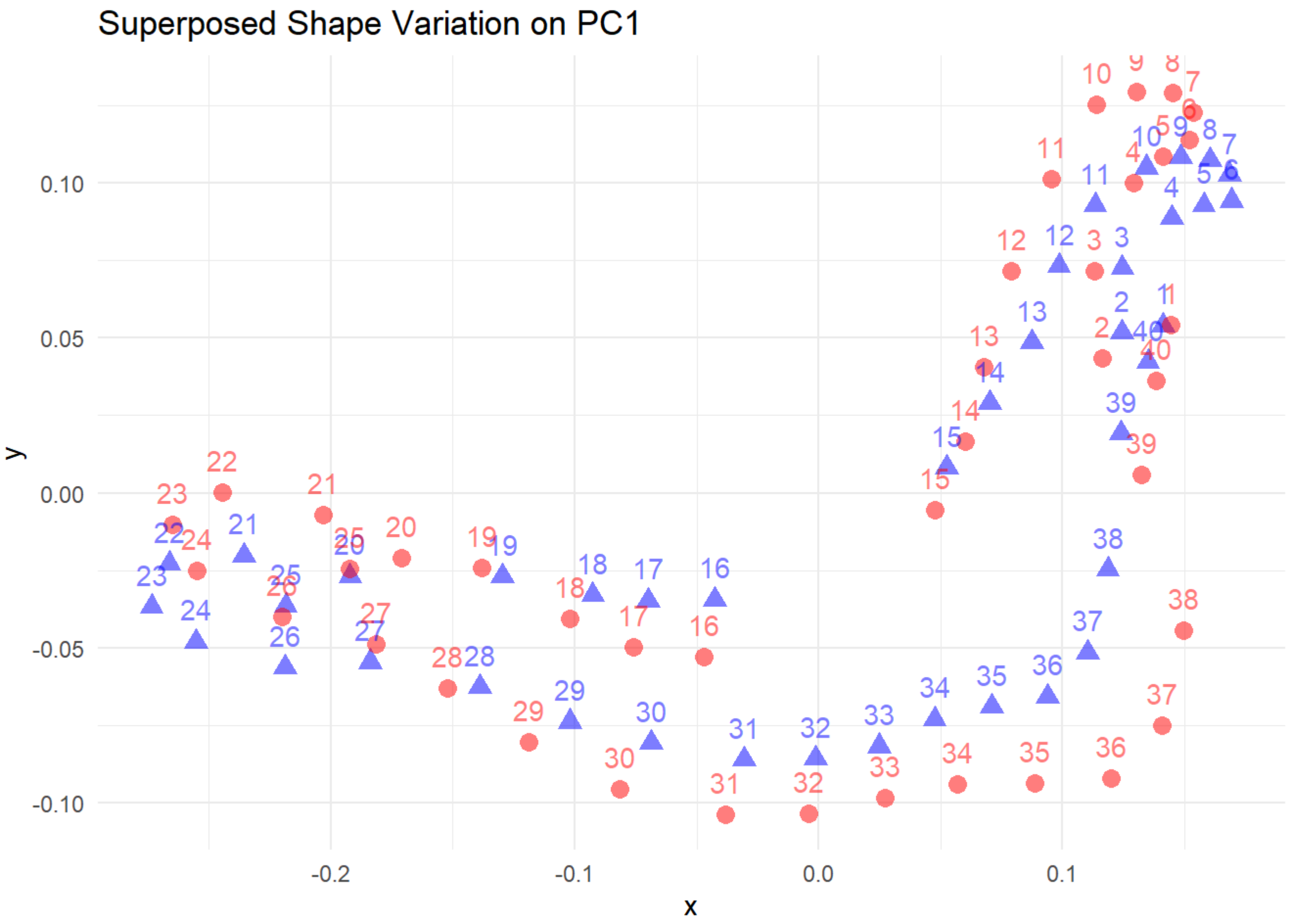
```
boxplot(PC4 ~ ALL_Cervids_species, main = "PC4 by Species", xlab = "Species", ylab = "PC4 Sco
re", col = Colors_ALL_Species)
```



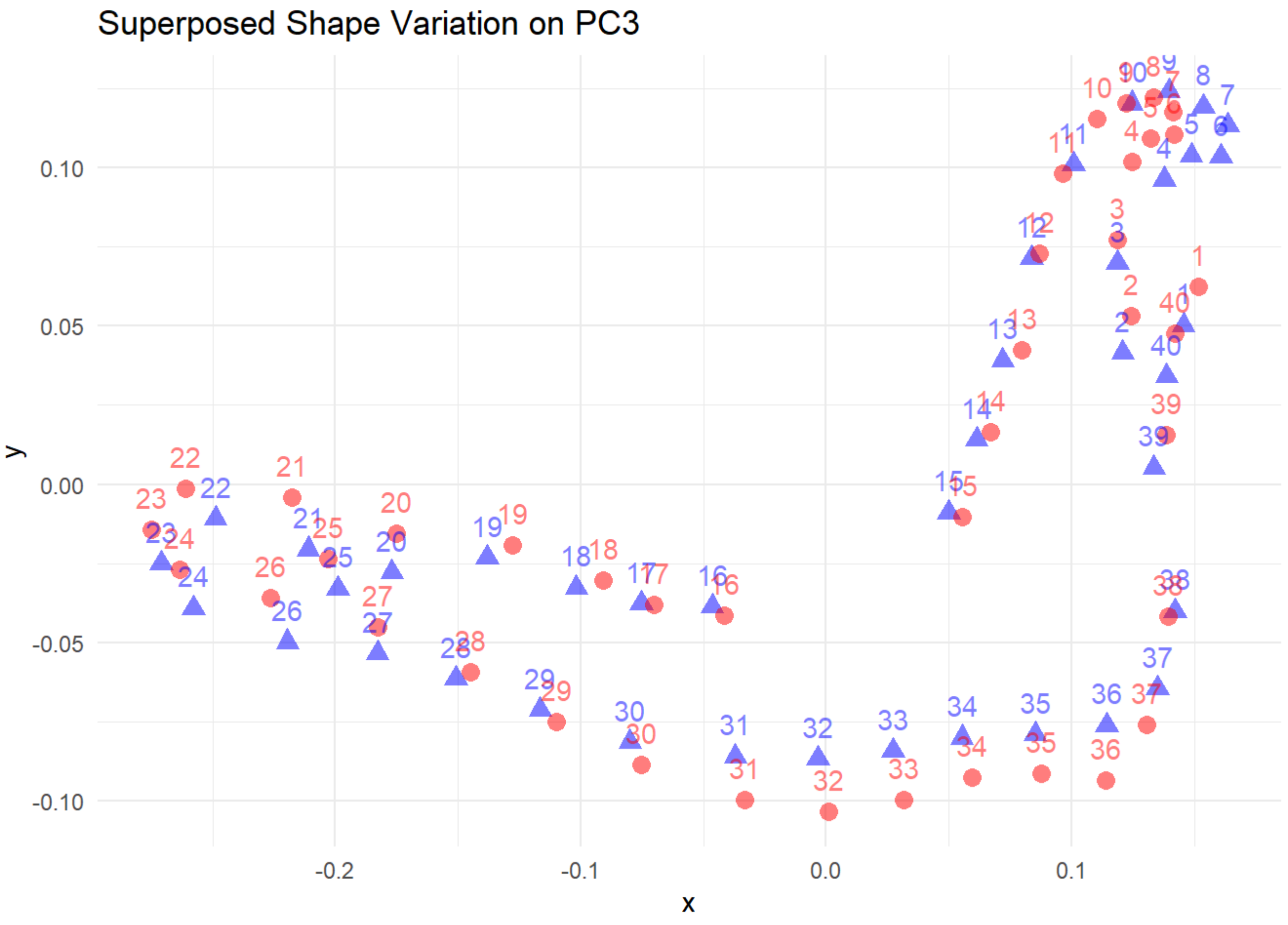
```
###Results ###############
# p-value < 2e-16 : On PC1, shape difference between the two species is significative
# p-value = 7.12e-15 : On PC3, shape difference between the two species is significative
# p-value = 0.0141 : On PC4, shape difference between the two species is significative
##########################
```

Visualize shape variation

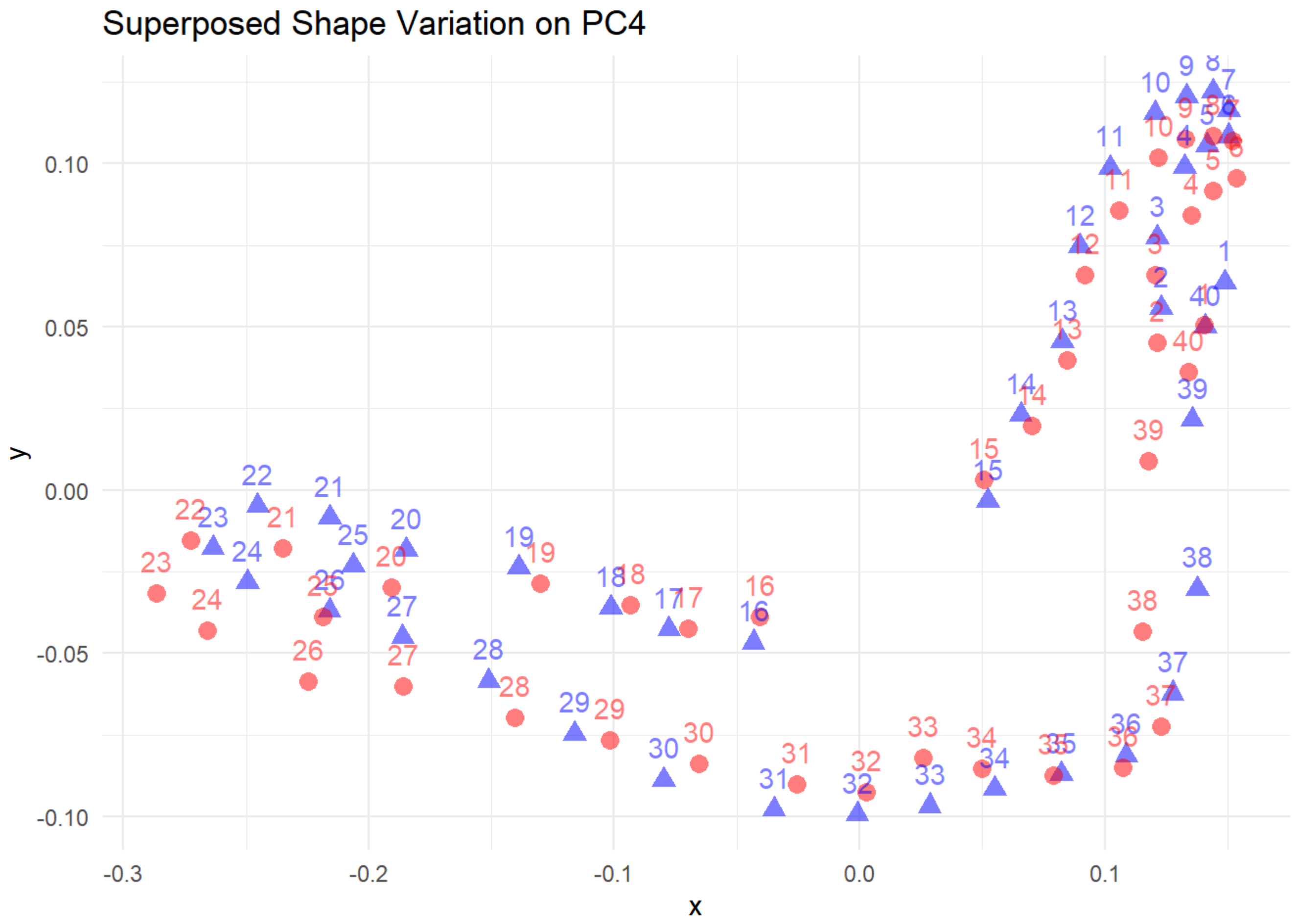
```
# Visualize shape variation on PC1
extreme_min_PC1 <- which.min(PC1)
extreme_max_PC1 <- which.max(PC1)

coords_min_PC1 <- as.data.frame(Slided_MorphoGeom_ALL_Cervids$coords[,,extreme_min_PC1])
coords_max_PC1 <- as.data.frame(Slided_MorphoGeom_ALL_Cervids$coords[,,extreme_max_PC1])
coords_min_PC1$landmark <- 1:nrow(coords_min_PC1)
coords_max_PC1$landmark <- 1:nrow(coords_max_PC1)

colnames(coords_min_PC1) <- c("x", "y", "landmark")
colnames(coords_max_PC1) <- c("x", "y", "landmark")
coords_min_PC1$group <- "Min PC1"
coords_max_PC1$group <- "Max PC1"

df_combined <- rbind(coords_min_PC1, coords_max_PC1)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on PC1") +
  scale_color_manual(values = c("Min PC1" = "blue", "Max PC1" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



```
#Visualize shape variation on PC3
extreme_min_PC3 <- which.min(PC3)
extreme_max_PC3 <- which.max(PC3)

coords_min_PC3 <- as.data.frame(Slided_MorphoGeom_ALL_Cervids$coords[,,extreme_min_PC3])
coords_max_PC3 <- as.data.frame(Slided_MorphoGeom_ALL_Cervids$coords[,,extreme_max_PC3])
coords_min_PC3$landmark <- 1:nrow(coords_min_PC3)
coords_max_PC3$landmark <- 1:nrow(coords_max_PC3)

colnames(coords_min_PC3) <- c("x", "y", "landmark")
colnames(coords_max_PC3) <- c("x", "y", "landmark")
coords_min_PC3$group <- "Min PC3"
coords_max_PC3$group <- "Max PC3"

df_combined <- rbind(coords_min_PC3, coords_max_PC3)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on PC3") +
  scale_color_manual(values = c("Min PC3" = "blue", "Max PC3" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



```
#Visualize shape variation on PC4
extreme_min_PC4 <- which.min(PC4)
extreme_max_PC4 <- which.max(PC4)

coords_min_PC4 <- as.data.frame(Slided_MorphoGeom_ALL_Cervids$coords[,,extreme_min_PC4])
coords_max_PC4 <- as.data.frame(Slided_MorphoGeom_ALL_Cervids$coords[,,extreme_max_PC4])
coords_min_PC4$landmark <- 1:nrow(coords_min_PC4)
coords_max_PC4$landmark <- 1:nrow(coords_max_PC4)

colnames(coords_min_PC4) <- c("x", "y", "landmark")
colnames(coords_max_PC4) <- c("x", "y", "landmark")
coords_min_PC4$group <- "Min PC4"
coords_max_PC4$group <- "Max PC4"

df_combined <- rbind(coords_min_PC4, coords_max_PC4)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on PC4") +
  scale_color_manual(values = c("Min PC4" = "blue", "Max PC4" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



1.2.3 Role of mandible size and the influence of the species in

these variations:

```
# Procrust regression
# evaluate how shapes ( landmark coordinates) vary as a function of explanatory variables (Cs
ize and species).
summary(Descriptive_ALL_Cervids)
```

```
##   TPS POSITION       Ref                 Length         Species         
##  Min.   :  1.0   Length:315         Min.   :18.41   Length:315        
##  1st Qu.: 79.5   Class :character   1st Qu.:21.11   Class :character  
##  Median :158.0   Mode  :character   Median :25.09   Mode  :character  
##  Mean   :158.0                      Mean   :24.83                     
##  3rd Qu.:236.5                      3rd Qu.:27.48                     
##  Max.   :315.0                      Max.   :35.88                     
##                                                                       
##      Sex                Pop                 Lat              Long        
##  Length:315         Length:315         Min.   :-34.55   Min.   :-65.298  
##  Class :character   Class :character   1st Qu.: 38.35   1st Qu.:-21.574  
##  Mode  :character   Mode  :character   Median : 63.25   Median : -4.162  
##                                        Mean   : 89.58   Mean   :-12.762  
##                                        3rd Qu.:165.20   3rd Qu.: -2.130  
##                                        Max.   :165.76   Max.   : 42.545  
##                                                                          
##  Vegetation_type       Climat             Genet           Herb_Monocots  
##  Length:315         Length:315         Length:315         Min.   :32.86  
##  Class :character   Class :character   Class :character   1st Qu.:49.14  
##  Mode  :character   Mode  :character   Mode  :character   Median :55.50  
##                                                           Mean   :51.55  
##                                                           3rd Qu.:57.10  
##                                                           Max.   :57.10  
##                                                           NA's   :158    
##  Centroid_Size  
##  Min.   :44.56  
##  1st Qu.:51.04  
##  Median :63.06  
##  Mean   :61.44  
##  3rd Qu.:69.13  
##  Max.   :85.31  
## 
```

```
gdf <- geomorph.data.frame(Slided_MorphoGeom_ALL_Cervids, Species = Descriptive_ALL_Cervids$S
pecies, Csize = Descriptive_ALL_Cervids$Centroid_Size)
fit.size <- procD.lm(coords~log(Csize) + Species, data = gdf, print.progress = FALSE)
summary(fit.size)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type I
## Effect sizes (Z) based on F distributions
##
##              Df      SS       MS     Rsq       F      Z Pr(>F)
## log(Csize)    1 0.18771 0.187714 0.33686 173.042 6.9378  0.001 ***
## Species       1 0.03107 0.031070 0.05576  28.641 6.2224  0.001 ***
## Residuals   312 0.33845 0.001085 0.60738
## Total       314 0.55724
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: procD.lm(f1 = coords ~ log(Csize) + Species, data = gdf, print.progress = FALSE)
```

```
biserial.cor(Descriptive_ALL_Cervids$Centroid_Size, Descriptive_ALL_Cervids$Species, level =
2) # test of correlation between Csize & Species
```

```
## [1] -0.8782801
```

```
###Results ###############
# p-value = 0.001 : landmark coordinates (shape) change according to the centroid size.
# p-value = 0.001 : landmark coordinates (shape) change according to the species.
# R²: 14% of the variance is explained by Log(centroid size) and 29% by the Species.

# r_pb = -0.8782801. Centroid size and species are not independent factors.  The very negativ
e r-pb value (close to -1) is due to the significant difference in centroid size between the
Rusa and Cervus species.
##########################
```

2 DATASET 2 : ALL_Cervus

1. Can we identify shape and size differences at the inter-population scale, among Cervus populations ?

2.1 Part 1 : data preparation :

```
## context data :
Descriptive_ALL_Cervus <- read_excel("Descriptive_ALL_Cervus.xlsx")
View(Descriptive_ALL_Cervus)
summary(Descriptive_ALL_Cervus)
```

```
##   TPS POSITION       Ref                Length        Species         
##  Min.   :  1.0   Length:185         Min.   :22.25   Length:185        
##  1st Qu.: 47.0   Class :character   1st Qu.:25.96   Class :character  
##  Median :203.0   Mode  :character   Median :27.03   Mode  :character  
##  Mean   :171.4                      Mean   :27.63                     
##  3rd Qu.:259.0                      3rd Qu.:28.98                     
##  Max.   :315.0                      Max.   :35.88                     
##                                                                       
##      Sex                Pop                 Lat              Long        
##  Length:185         Length:185         Min.   :-34.55   Min.   :-65.298  
##  Class :character   Class :character   1st Qu.: 38.23   1st Qu.: -4.162  
##  Mode  :character   Mode  :character   Median : 42.23   Median : -2.130  
##                                        Mean   : 36.97   Mean   : -7.262  
##                                        3rd Qu.: 48.03   3rd Qu.:  1.279  
##                                        Max.   : 63.25   Max.   :  9.020  
##                                                                          
##  Vegetation_type       Climat             Genet           Herb_Monocots  
##  Length:185         Length:185         Length:185         Min.   :32.86  
##  Class :character   Class :character   Class :character   1st Qu.:49.14  
##  Mode  :character   Mode  :character   Mode  :character   Median :55.50  
##                                                           Mean   :51.55  
##                                                           3rd Qu.:57.10  
##                                                           Max.   :57.10  
##                                                           NA's   :28
```

```
ALL_Cervus_pop <- Descriptive_ALL_Cervus$Pop
ALL_Cervus_Lat<- Descriptive_ALL_Cervus$Lat
ALL_Cervus_Long<- Descriptive_ALL_Cervus$Long
ALL_Cervus_Vegetation<- Descriptive_ALL_Cervus$Vegetation_type
ALL_Cervus_Climate<- Descriptive_ALL_Cervus$Climat
ALL_Cervus_Genetics<- Descriptive_ALL_Cervus$Genet
ALL_Cervus_Monocots<- Descriptive_ALL_Cervus$Herb_Monocots

# test for colinearity :
Descriptive_ALL_Cervus$Pop <- as.factor(Descriptive_ALL_Cervus$Pop)
Descriptive_ALL_Cervus$Lat <- as.factor(Descriptive_ALL_Cervus$Lat)
Descriptive_ALL_Cervus$Long <- as.factor(Descriptive_ALL_Cervus$Long)
Descriptive_ALL_Cervus$Vegetation_type <- as.factor(Descriptive_ALL_Cervus$Vegetation_type)
Descriptive_ALL_Cervus$Climat <- as.factor(Descriptive_ALL_Cervus$Climat)
Descriptive_ALL_Cervus$Genet <- as.factor(Descriptive_ALL_Cervus$Genet)

model <- lm(Herb_Monocots ~ Pop + Lat + Long + Vegetation_type + Climat + Genet, data = Descriptive_ALL_Cervus)
collinearity_check <- performance::check_collinearity(model)
```

```
## Model matrix is rank deficient. VIFs may not be sensible.
```

```
print(collinearity_check)
```

```
## # Check for Multicollinearity
## 
## Low Correlation
## 
##  Term  VIF      VIF  CI Increased SE Tolerance
##   Pop 1.00 [1.00, 1.00]         1.00      1.00
```

```
# The variables Lat and Long are discarded because of their high collinearity with Pop

model <- lm(Herb_Monocots ~ Pop + Vegetation_type + Climat + Genet, data = Descriptive_ALL_Ce
rvus)
collinearity_check <- performance::check_collinearity(model)
```

```
## Model matrix is rank deficient. VIFs may not be sensible.
```

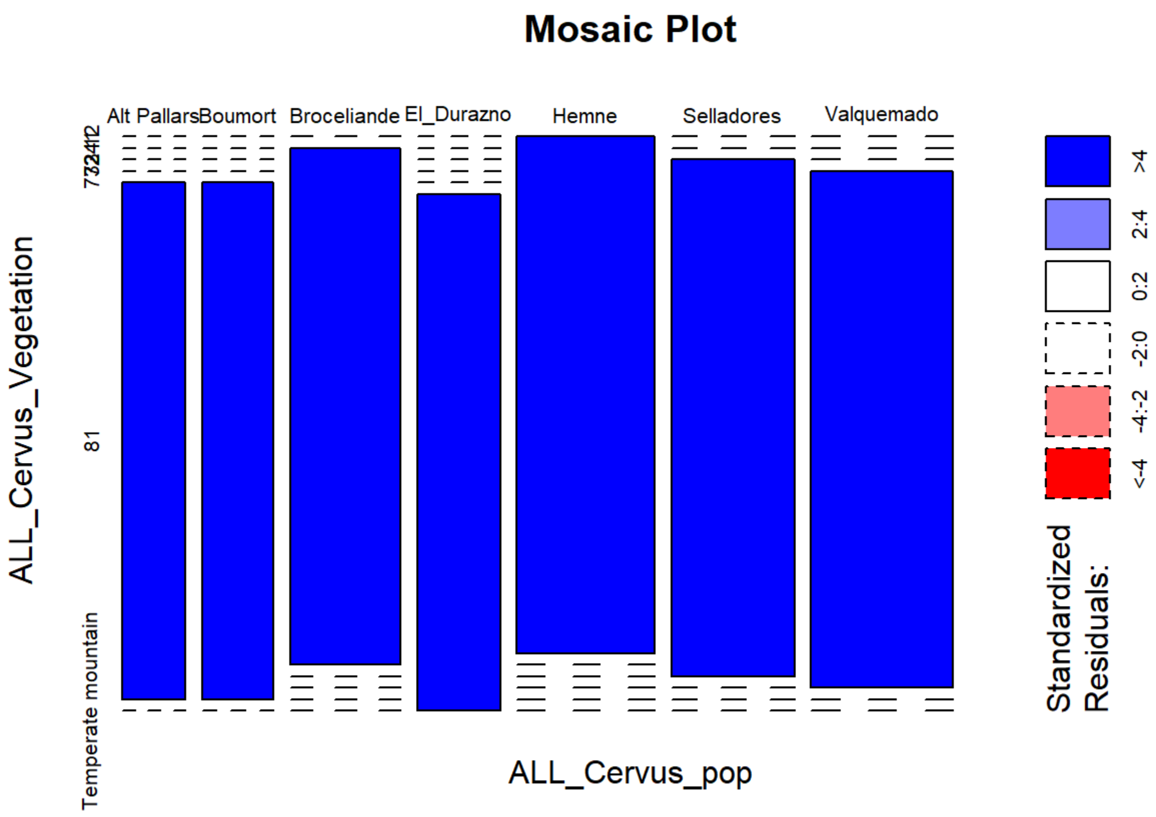
```
print(collinearity_check)
```

```
## # Check for Multicollinearity
## 
## Low Correlation
## 
##  Term  VIF      VIF  CI Increased SE Tolerance
##   Pop 1.00 [1.00, 1.00]         1.00      1.00
```

```
alias_info <- alias(lm(Herb_Monocots ~ Pop  + Vegetation_type + Climat + Genet, data = Descri
ptive_ALL_Cervus))
print(alias_info)
```

```
## Model :
## Herb_Monocots ~ Pop + Vegetation_type + Climat + Genet
##
## Complete :
##                                    (Intercept) PopBoumort PopEl_Durazno PopHemne
## Vegetation_type731                  0           0          0             0
## Vegetation_type732                  0           0          0             0
## Vegetation_type81                   1           0         -1            -1
## Vegetation_typeTemperate mountain   0           0          1             0
## ClimatBwh                           0           0          1             0
## ClimatDfb                           1           0         -1            -1
## ClimatDfc                           0           0          0             1
## GenetB                              0           0          0             1
## GenetC                              1          -1         -1            -1
## GenetD                              0           1          0             0
##                                    PopSelladores PopValquemado
## Vegetation_type731                  1             0
## Vegetation_type732                  0             1
## Vegetation_type81                  -1            -1
## Vegetation_typeTemperate mountain   0             0
## ClimatBwh                           0             0
## ClimatDfb                          -1            -1
## ClimatDfc                           0             0
## GenetB                              0             0
## GenetC                             -1            -1
## GenetD                              1             1
```

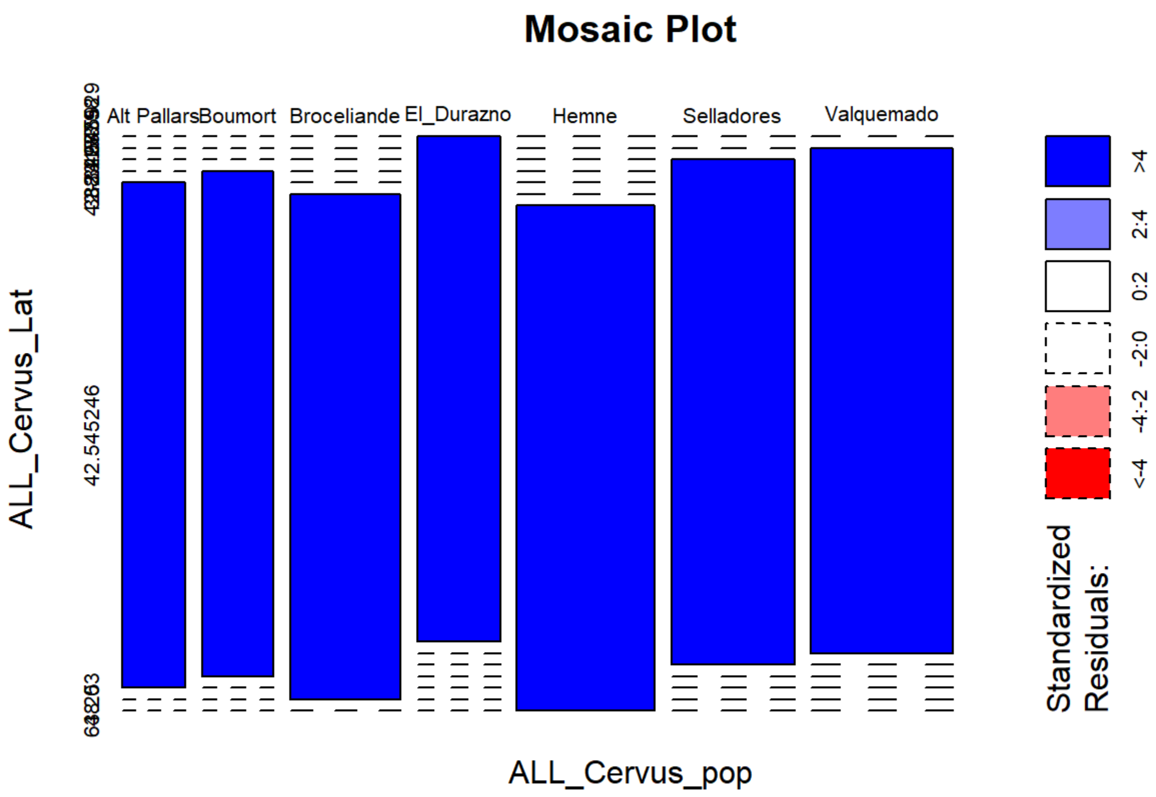
```
# Tests of independence between descriptive variables:
table_contingence <- table(ALL_Cervus_pop, ALL_Cervus_Vegetation)
mosaicplot(table_contingence, shade = TRUE, main = "Mosaic Plot")
```



```
fisher_test <- fisher.test(table_contingence, workspace = 2e8)
print(fisher_test) # statistically significant association between variables
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  table_contingence
## p-value < 2.2e-16
## alternative hypothesis: two.sided
```

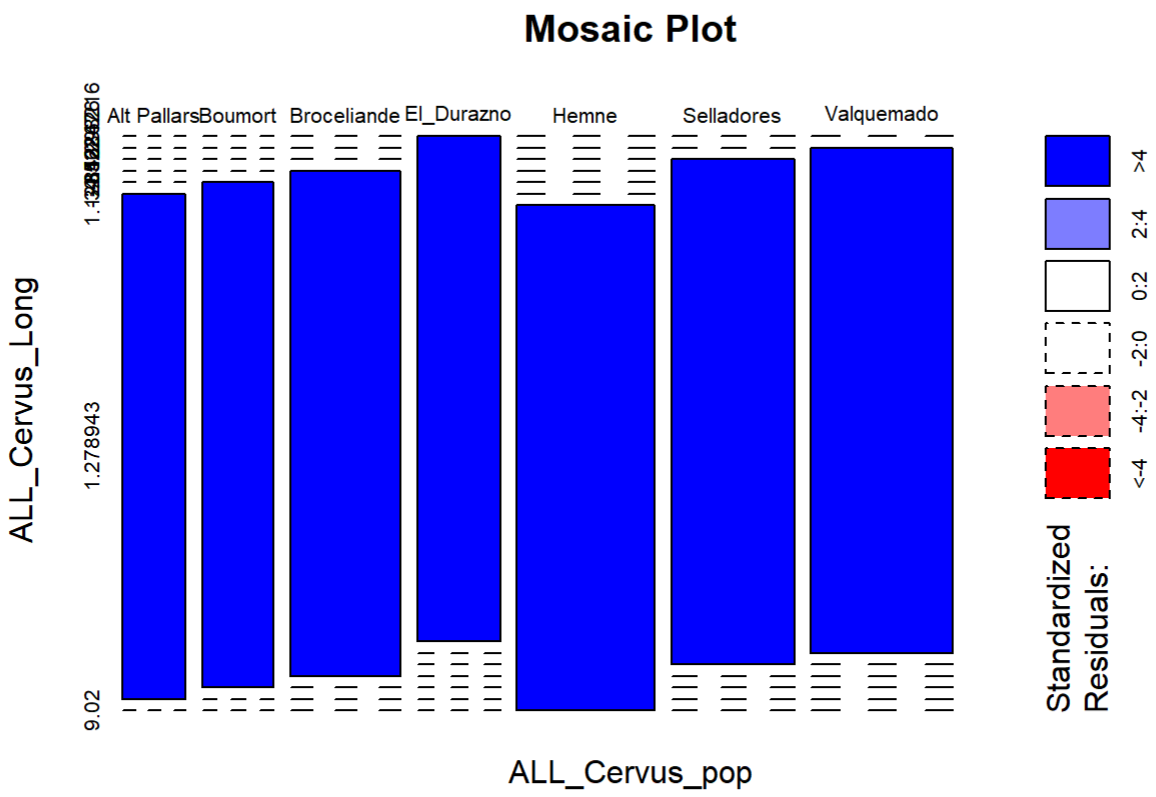
```
table_contingence <- table(ALL_Cervus_pop, ALL_Cervus_Lat)
mosaicplot(table_contingence, shade = TRUE, main = "Mosaic Plot")
```



```
fisher_test_mc <- fisher.test(table_contingence, simulate.p.value = TRUE, B = 1e7)
print(fisher_test_mc) # statistically significant association between variables
```

```
## 
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1e+07 replicates)
## 
## data:  table_contingence
## p-value = 1e-07
## alternative hypothesis: two.sided
```

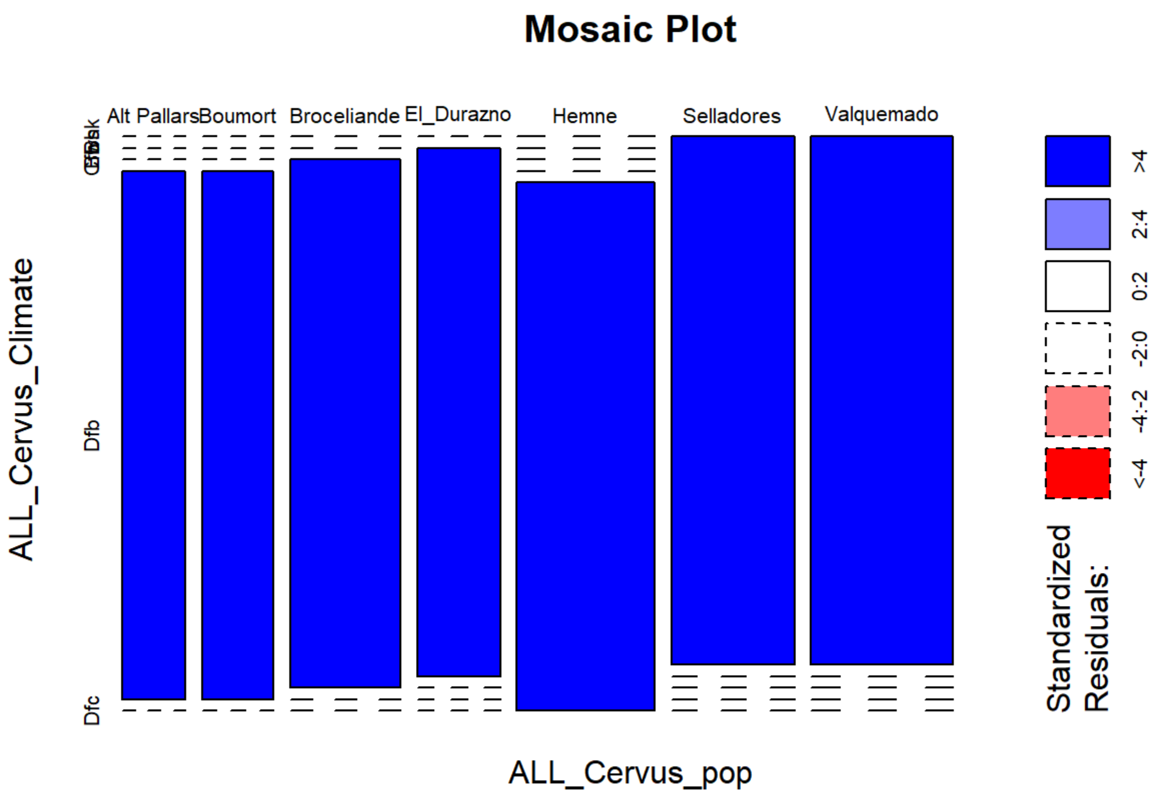
```
table_contingence <- table(ALL_Cervus_pop, ALL_Cervus_Long)
mosaicplot(table_contingence, shade = TRUE, main = "Mosaic Plot")
```



```
fisher_test_mc <- fisher.test(table_contingence, simulate.p.value = TRUE, B = 1e7)
print(fisher_test_mc)  # statistically significant association between variables
```

```
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1e+07 replicates)
##
## data:  table_contingence
## p-value = 1e-07
## alternative hypothesis: two.sided
```

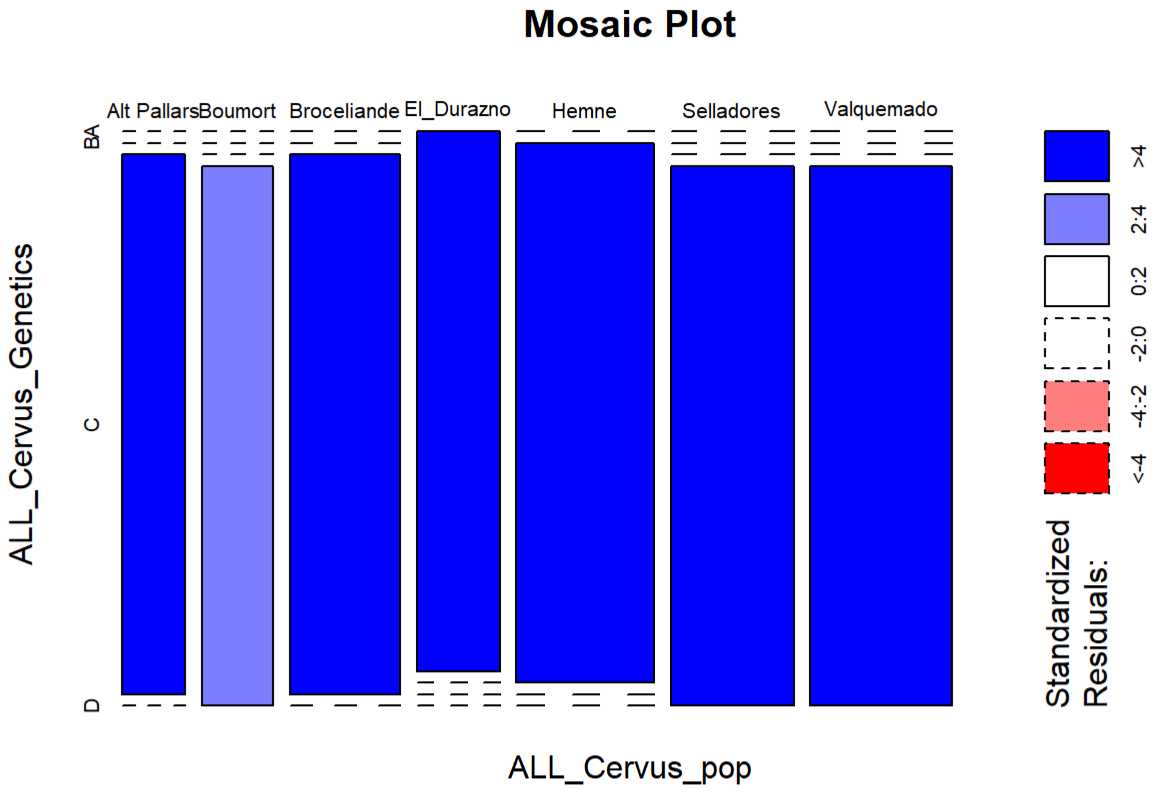
```
table_contingence <- table(ALL_Cervus_pop, ALL_Cervus_Climate)
mosaicplot(table_contingence, shade = TRUE, main = "Mosaic Plot")
```



```
fisher_test <- fisher.test(table_contingence, workspace = 2e8)
print(fisher_test) # statistically significant association between variables
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  table_contingence
## p-value < 2.2e-16
## alternative hypothesis: two.sided
```

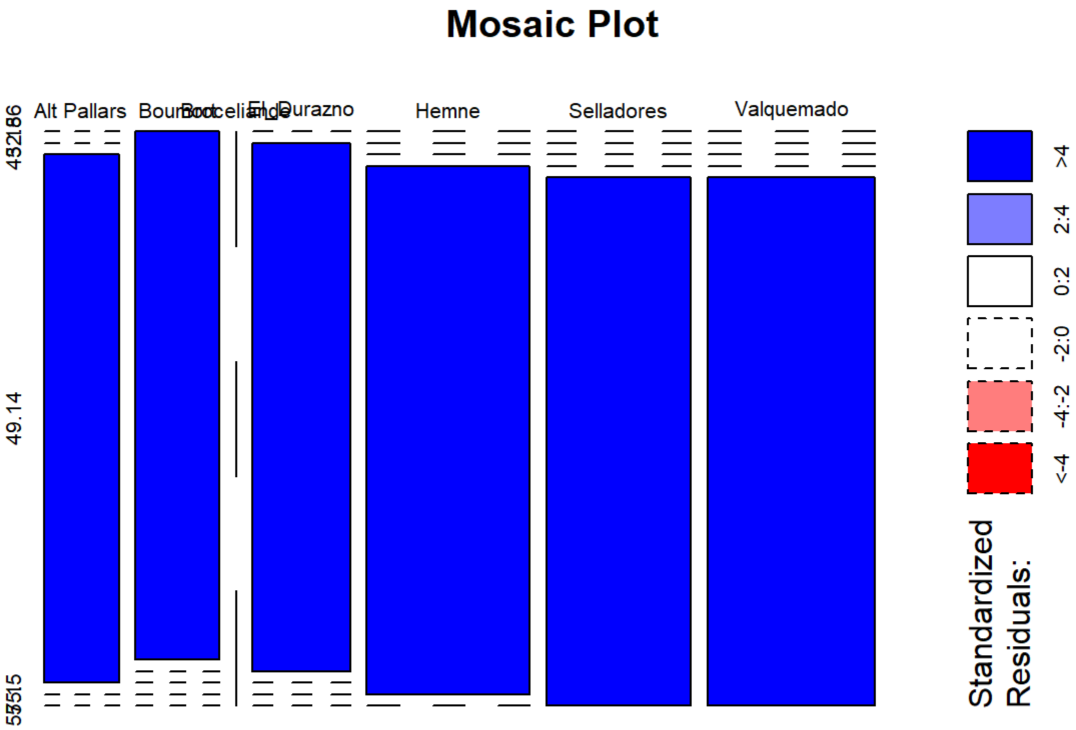
```
table_contingence <- table(ALL_Cervus_pop, ALL_Cervus_Genetics)
mosaicplot(table_contingence, shade = TRUE, main = "Mosaic Plot")
```



```
fisher_test <- fisher.test(table_contingence, workspace = 2e8)
print(fisher_test) # statistically significant association between variables
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  table_contingence
## p-value < 2.2e-16
## alternative hypothesis: two.sided
```

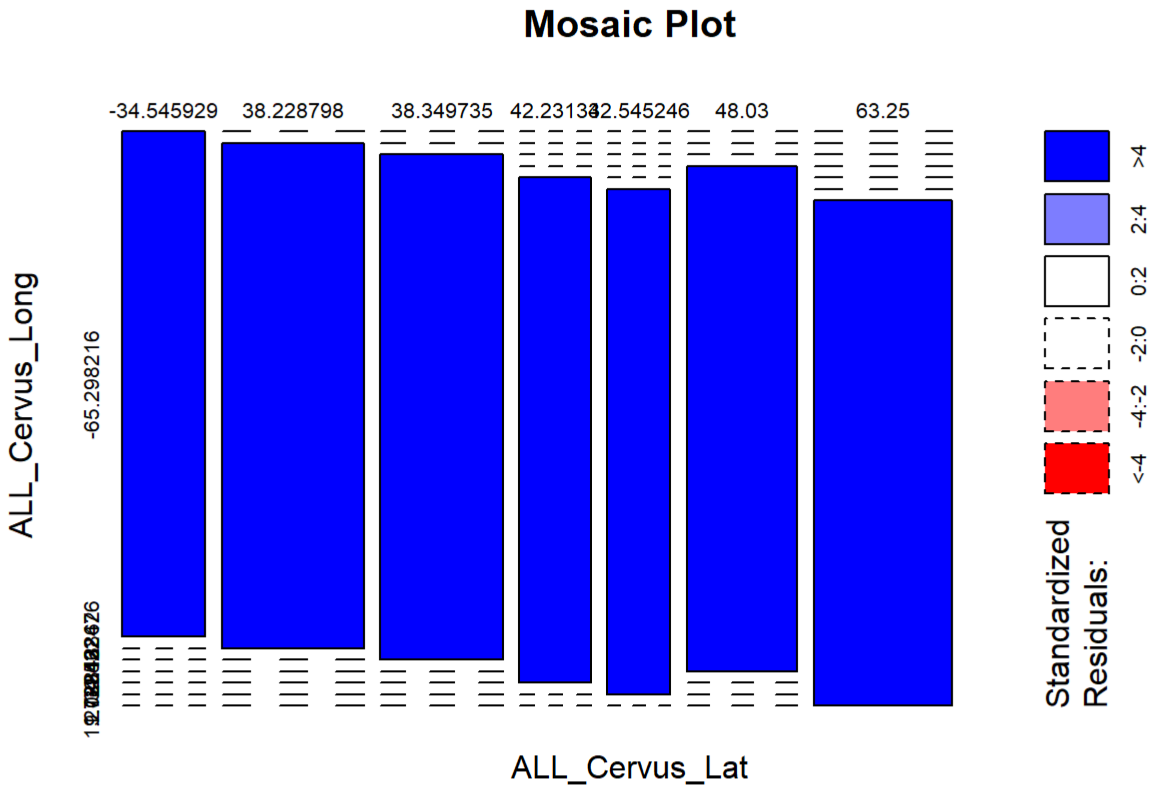
```
Descriptive_ALL_Cervus_filtered <- Descriptive_ALL_Cervus[!is.na(Descriptive_ALL_Cervus$Herb_Monocots), ]
Descriptive_ALL_Cervus_filtered <- Descriptive_ALL_Cervus_filtered[Descriptive_ALL_Cervus_filtered$Pop != "Broceliande", ]
table_contingence <- table(Descriptive_ALL_Cervus_filtered$Pop, Descriptive_ALL_Cervus_filtered$Herb_Monocots)
mosaicplot(table_contingence, shade = TRUE, main = "Mosaic Plot")
```



```
fisher_test <- fisher.test(table_contingence, workspace = 2e8)
print(fisher_test) # statistically significant association between variables
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  table_contingence
## p-value < 2.2e-16
## alternative hypothesis: two.sided
```

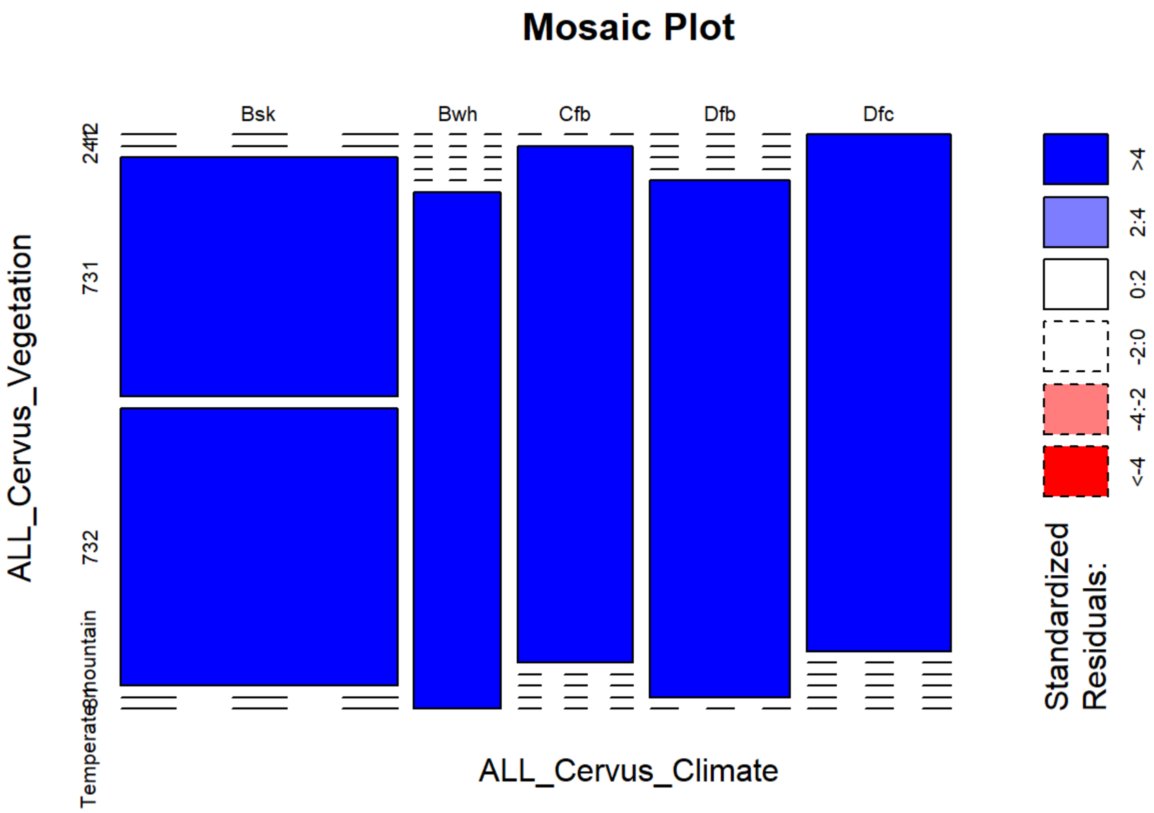
```
table_contingence <- table(ALL_Cervus_Lat, ALL_Cervus_Long)
mosaicplot(table_contingence, shade = TRUE, main = "Mosaic Plot")
```



```
fisher_test_mc <- fisher.test(table_contingence, simulate.p.value = TRUE, B = 1e7)
print(fisher_test_mc)  # statistically significant association between variables
```

```
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  1e+07 replicates)
##
## data:  table_contingence
## p-value = 1e-07
## alternative hypothesis: two.sided
```

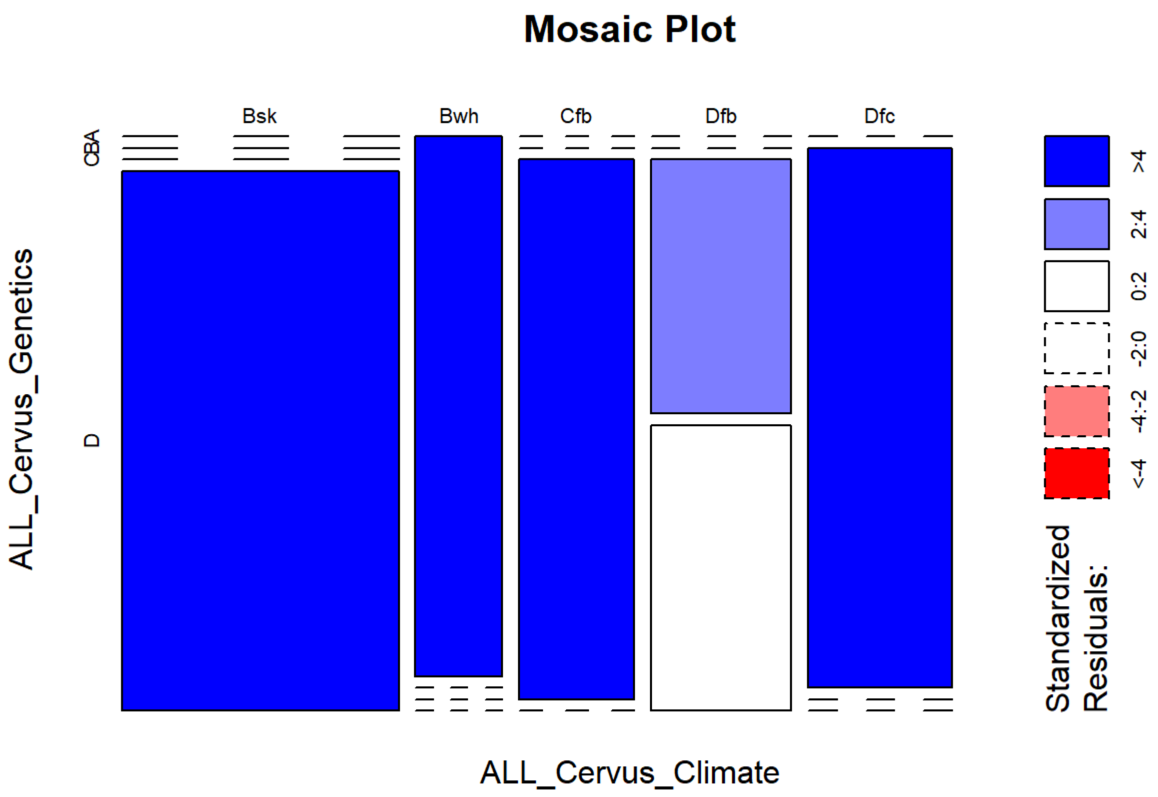
```
table_contingence <- table(ALL_Cervus_Climate, ALL_Cervus_Vegetation)
mosaicplot(table_contingence, shade = TRUE, main = "Mosaic Plot")
```



```
fisher_test <- fisher.test(table_contingence, workspace = 2e8)
print(fisher_test) # statistically significant association between variables
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  table_contingence
## p-value < 2.2e-16
## alternative hypothesis: two.sided
```

```
table_contingence <- table(ALL_Cervus_Climate, ALL_Cervus_Genetics)
mosaicplot(table_contingence, shade = TRUE, main = "Mosaic Plot")
```



```
fisher_test <- fisher.test(table_contingence, workspace = 2e8)
print(fisher_test) # statistically significant association between variables
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  table_contingence
## p-value < 2.2e-16
## alternative hypothesis: two.sided
```

```
# Vegetation-type, Climat and Genet: These variables have several categories which are linear combinations of other variables. There is a significant association between variables.
# Removing these variables reduces collinearity and redundancy.
```

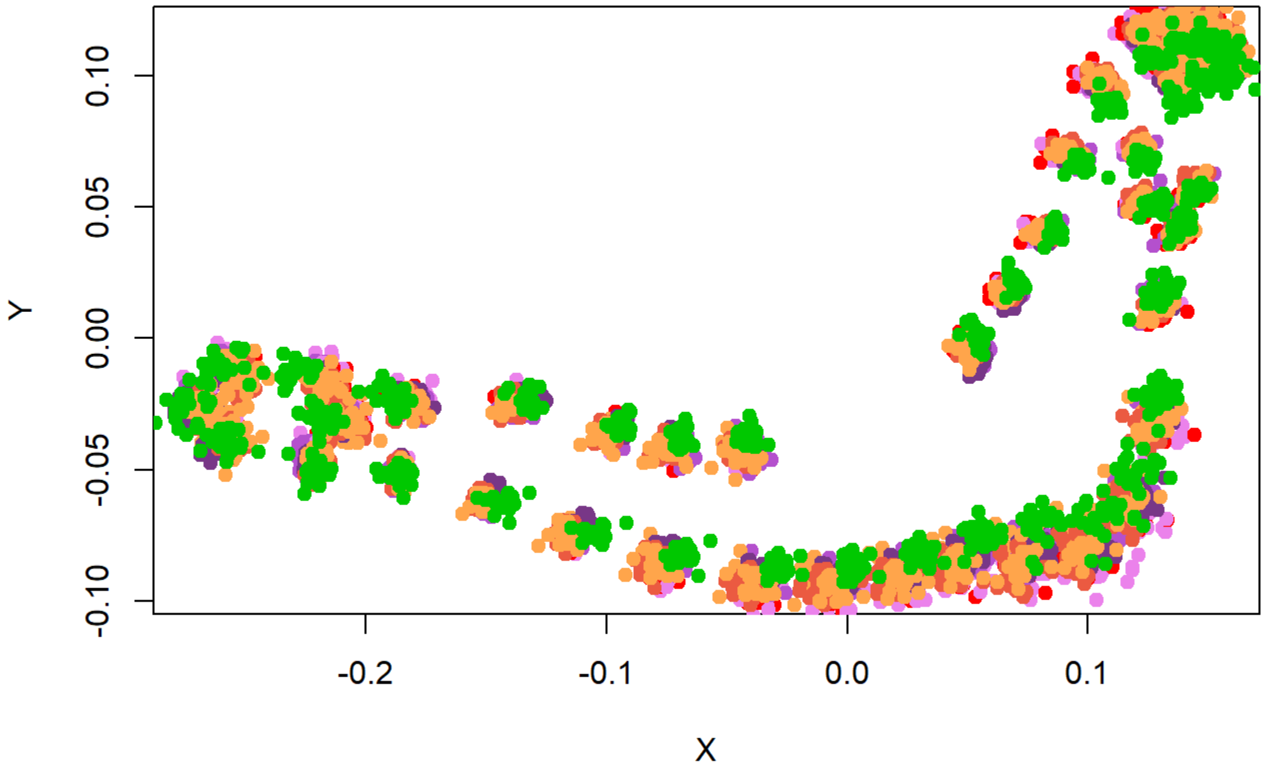
```
## morphometry-geometry data :
# We import in R the tps file produced with tps and Matlab :

MorphoGeom_ALL_Cervus <- readland.tps("MorphoGeom_ALL_Cervus.TPS", specID = "ID")
```

```
##
## No curves detected; all points appear to be fixed landmarks.
```

```
# In "MorphoGeom_ALL_Cervus", no curves are detected; all points appear to be fixed landmark
s.
# To connect the points, we generate a matrix with gmShiny ("Matrix")
Matrix <- as.matrix(read.csv("Matrix.csv"))

# Semi-landmarks are identified, slided and a procrust analysis is done:
Slided_MorphoGeom_ALL_Cervus <- gpagen(MorphoGeom_ALL_Cervus, PrinAxes = FALSE, print.progres
s = FALSE, curves = Matrix)
options(max.print=1000000000)
```

2.2 Part 2 : data visualization: between populations

```
Colors_ALL_Cervus_pop <-  c("Alt Pallars" = "violet", "Boumort" ="red",  "Broceliande" = "med
iumorchid3","El_Durazno" = "#00CC00", "Hemne" = "mediumorchid4","Selladores" ="tan1",  "Valqu
emado" = "tomato2") # identify cervids by population
point_colors_pop <- Colors_ALL_Cervus_pop[ALL_Cervus_pop] # Color vector for populations

plot(Slided_MorphoGeom_ALL_Cervus$coords[, , 1], col = point_colors_pop, pch = 19)
for (i in 2:dim(Slided_MorphoGeom_ALL_Cervus$coords)[3]) {
  points(Slided_MorphoGeom_ALL_Cervus$coords[, , i], col = point_colors_pop[i], pch = 19)
}
```



```
mean_shape <- mshape(Slided_MorphoGeom_ALL_Cervus$coords)  # Consensus shape
```

2.3 Part 3 : Analysis

2.3.1 Centroid size

```
centroid_sizes <- Slided_MorphoGeom_ALL_Cervus$Csize
Descriptive_ALL_Cervus$Centroid_Size <- centroid_sizes
AltPallars_centroid_sizes <- Descriptive_ALL_Cervus$Centroid_Size[Descriptive_ALL_Cervus$Pop
== "Alt Pallars"]
Boumort_centroid_sizes <- Descriptive_ALL_Cervus$Centroid_Size[Descriptive_ALL_Cervus$Pop ==
"Boumort"]
Selladores_centroid_sizes <- Descriptive_ALL_Cervus$Centroid_Size[Descriptive_ALL_Cervus$Pop
== "Selladores"]
Valquemado_centroid_sizes <- Descriptive_ALL_Cervus$Centroid_Size[Descriptive_ALL_Cervus$Pop
== "Valquemado"]
Broceliande_centroid_sizes <- Descriptive_ALL_Cervus$Centroid_Size[Descriptive_ALL_Cervus$Pop
== "Broceliande"]
Hemne_centroid_sizes <- Descriptive_ALL_Cervus$Centroid_Size[Descriptive_ALL_Cervus$Pop == "H
emne"]
El_Durazno_centroid_sizes <- Descriptive_ALL_Cervus$Centroid_Size[Descriptive_ALL_Cervus$Pop
== "El_Durazno"]

anova_result <- aov(Centroid_Size ~ Pop, data = Descriptive_ALL_Cervus)
summary(anova_result)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## Pop           6   3993   665.5    37.5 <2e-16 ***
## Residuals   178   3159    17.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

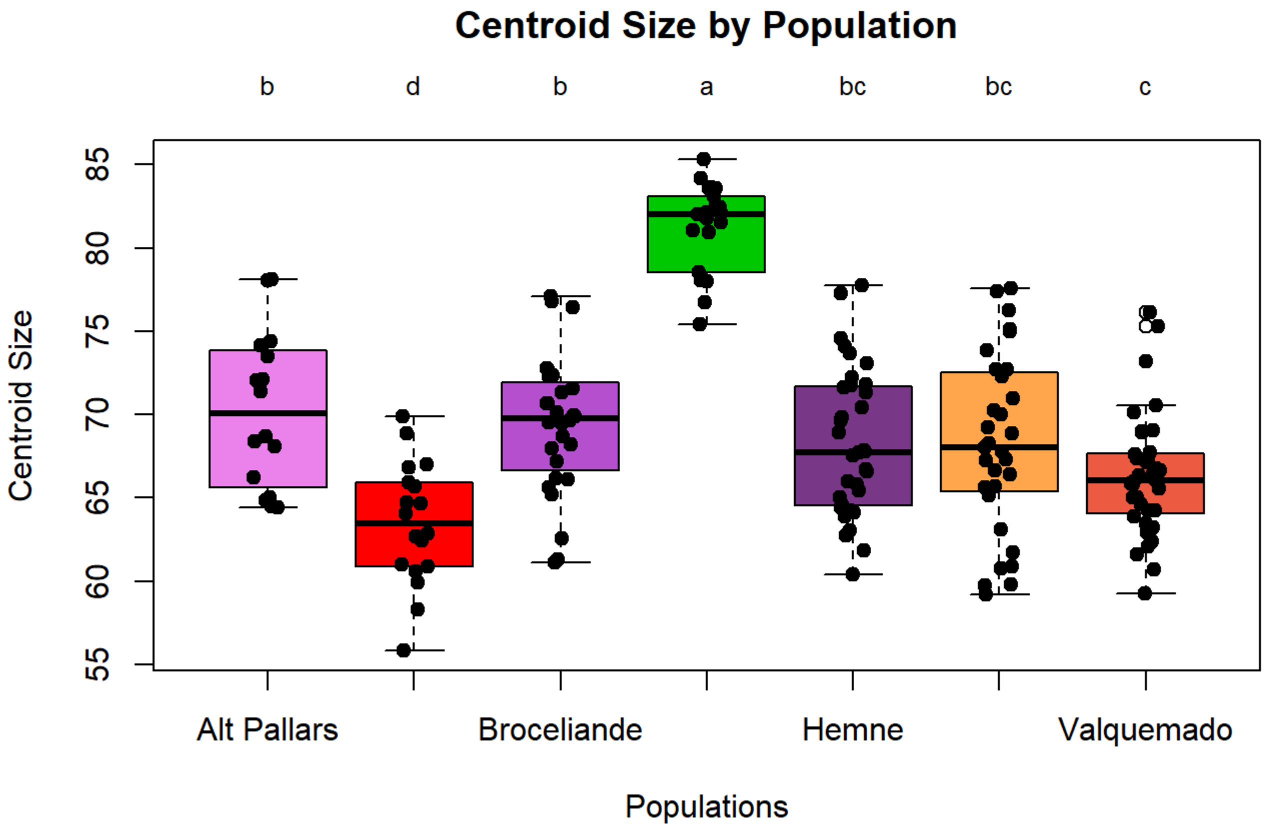
```
###Results ###############
# p-value < 2.2e-16 : Based on the anova, Cervus populations differ statistically. See detail
of the Duncan test for inter-population differences in size
##########################

# Duncan post-hoc test:
duncan_result <- duncan.test(anova_result, "Pop", console = TRUE)
```

```
##
## Study: anova_result ~ "Pop"
##
## Duncan's new multiple range test
## for Centroid_Size
##
## Mean Square Error:  17.74847
##
## Pop,  means
##
##             Centroid_Size      std  r      Min      Max
## Alt Pallars      70.25359 4.658292 16 64.44023 78.13234
## Boumort          63.45886 3.677426 18 55.83867 69.92168
## Broceliande      69.41072 4.126009 28 61.14243 77.07981
## El_Durazno       81.19731 2.665545 21 75.42802 85.30820
## Hemne            68.23121 4.412720 35 60.41402 77.76747
## Selladores       68.24847 5.377772 31 59.22152 77.55399
## Valquemado       66.32651 3.673927 36 59.26472 76.13457
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##             Centroid_Size groups
## El_Durazno       81.19731      a
## Alt Pallars      70.25359      b
## Broceliande      69.41072      b
## Selladores       68.24847     bc
## Hemne            68.23121     bc
## Valquemado       66.32651      c
## Boumort          63.45886      d
```

```
print(duncan_result)
```

```
## $statistics
##    MSerror  Df     Mean       CV
##   17.74847 178 69.22438 6.085853
## 
## $parameters
##     test name.t ntr alpha
##   Duncan    Pop   7  0.05
## 
## $duncan
## NULL
## 
## $means
##             Centroid_Size      std  r      Min      Max      Q25      Q50
## Alt Pallars      70.25359 4.658292 16 64.44023 78.13234 65.90810 70.04742
## Boumort          63.45886 3.677426 18 55.83867 69.92168 60.89049 63.46887
## Broceliande      69.41072 4.126009 28 61.14243 77.07981 66.94246 69.77760
## El_Durazno       81.19731 2.665545 21 75.42802 85.30820 78.57111 82.01785
## Hemne            68.23121 4.412720 35 60.41402 77.76747 64.53506 67.75224
## Selladores       68.24847 5.377772 31 59.22152 77.55399 65.41359 68.03278
## Valquemado       66.32651 3.673927 36 59.26472 76.13457 64.15995 66.05223
##                  Q75
## Alt Pallars 73.67352
## Boumort     65.87667
## Broceliande 71.75939
## El_Durazno  83.11226
## Hemne       71.66864
## Selladores  72.52497
## Valquemado  67.61945
## 
## $comparison
## NULL
## 
## $groups
##             Centroid_Size groups
## El_Durazno       81.19731      a
## Alt Pallars      70.25359      b
## Broceliande      69.41072      b
## Selladores       68.24847     bc
## Hemne            68.23121     bc
## Valquemado       66.32651      c
## Boumort          63.45886      d
## 
## attr(,"class")
## [1] "group"
```

```
duncan_labels <- duncan_result$groups
duncan_labels <- duncan_labels[order(rownames(duncan_labels)), ]
Descriptive_ALL_Cervus$labels <- factor(duncan_labels$groups[match(Descriptive_ALL_Cervus$Po
p, rownames(duncan_labels))])

par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(Centroid_Size ~ Pop, data = Descriptive_ALL_Cervus, main = "Centroid Size by Populati
on", xlab = "Populations", ylab = "Centroid Size", col = c("violet", "red","mediumorchid3","#
00CC00",   "mediumorchid4","tan1", "tomato2"))
stripchart(Centroid_Size ~ Pop, data = Descriptive_ALL_Cervus, vertical = TRUE, method = "jit
ter", add = TRUE, pch = 19, col = "black")
mtext(duncan_labels$groups, at = 1:length(duncan_labels$groups), side = 3, line = 1, cex = 0.
8)
```



2.3.2 Principal Component Analysis (PCA):

```
PCA_ALL_Cervus <- gm.prcomp(Slided_MorphoGeom_ALL_Cervus$coords)
summary(PCA_ALL_Cervus)
```

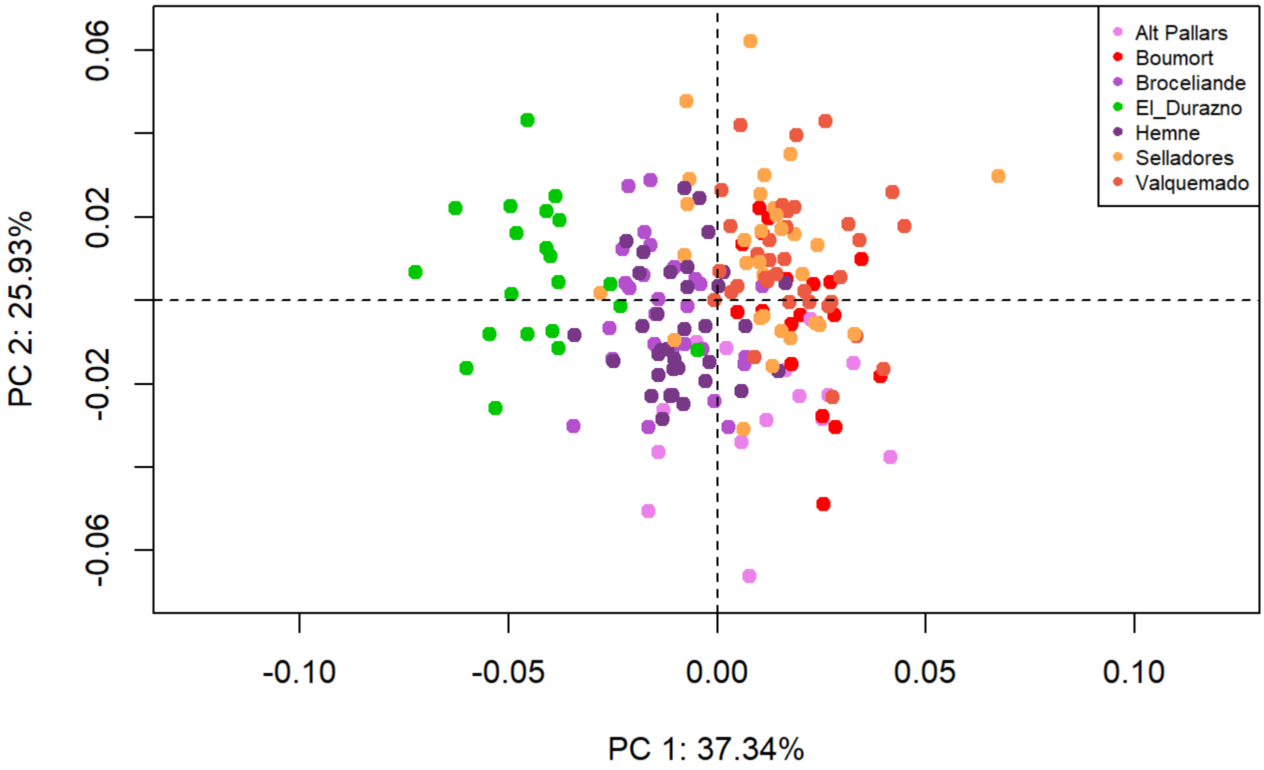
```
##
## Ordination type: Principal Component Analysis
## Centering by OLS mean
## Orthogonal projection of OLS residuals
## Number of observations: 185
## Number of vectors 78
##
## Importance of Components:
##                               Comp1        Comp2        Comp3        Comp4
## Eigenvalues            0.0005472526 0.0003800285 0.0001190682 9.024182e-05
## Proportion of Variance 0.3733940703 0.2592960019 0.0812410103 6.157260e-02
## Cumulative Proportion  0.3733940703 0.6326900723 0.7139310826 7.755037e-01
##                               Comp5        Comp6        Comp7        Comp8
## Eigenvalues            6.475048e-05 4.978996e-05 3.048686e-05 2.468868e-05
## Proportion of Variance 4.417968e-02 3.397202e-02 2.080139e-02 1.684525e-02
## Cumulative Proportion  8.196834e-01 8.536554e-01 8.744568e-01 8.913020e-01
##                               Comp9       Comp10       Comp11       Comp12
## Eigenvalues            2.200798e-05 1.901204e-05 1.431132e-05 1.319965e-05
## Proportion of Variance 1.501619e-02 1.297204e-02 9.764706e-03 9.006206e-03
## Cumulative Proportion  9.063182e-01 9.192903e-01 9.290550e-01 9.380612e-01
##                              Comp13       Comp14       Comp15       Comp16
## Eigenvalues            1.152887e-05 9.233607e-06 8.360380e-06 7.340887e-06
## Proportion of Variance 7.866228e-03 6.300151e-03 5.704343e-03 5.008736e-03
## Cumulative Proportion  9.459274e-01 9.522275e-01 9.579319e-01 9.629406e-01
##                              Comp17       Comp18       Comp19       Comp20
## Eigenvalues            6.186292e-06 5.730728e-06 4.533895e-06 3.902399e-06
## Proportion of Variance 4.220948e-03 3.910114e-03 3.093507e-03 2.662633e-03
## Cumulative Proportion  9.671616e-01 9.710717e-01 9.741652e-01 9.768278e-01
##                              Comp21       Comp22       Comp23       Comp24
## Eigenvalues            3.363330e-06 3.146377e-06 2.870025e-06 2.692483e-06
## Proportion of Variance 2.294822e-03 2.146794e-03 1.958237e-03 1.837099e-03
## Cumulative Proportion  9.791226e-01 9.812694e-01 9.832277e-01 9.850648e-01
##                              Comp25       Comp26       Comp27       Comp28
## Eigenvalues            2.088554e-06 1.860736e-06 1.748205e-06 1.590456e-06
## Proportion of Variance 1.425034e-03 1.269593e-03 1.192812e-03 1.085179e-03
## Cumulative Proportion  9.864898e-01 9.877594e-01 9.889522e-01 9.900374e-01
##                              Comp29       Comp30       Comp31       Comp32
## Eigenvalues            1.481513e-06 1.285682e-06 1.212179e-06 1.061891e-06
## Proportion of Variance 1.010846e-03 8.772293e-04 8.270779e-04 7.245351e-04
## Cumulative Proportion  9.910482e-01 9.919255e-01 9.927525e-01 9.934771e-01
##                              Comp33       Comp34       Comp35       Comp36
## Eigenvalues            1.012215e-06 9.685827e-07 8.417200e-07 7.939951e-07
## Proportion of Variance 6.906414e-04 6.608704e-04 5.743112e-04 5.417481e-04
## Cumulative Proportion  9.941677e-01 9.948286e-01 9.954029e-01 9.959447e-01
##                              Comp37       Comp38       Comp39       Comp40
## Eigenvalues            7.652677e-07 6.940383e-07 5.874119e-07 5.694417e-07
## Proportion of Variance 5.221472e-04 4.735469e-04 4.007951e-04 3.885339e-04
## Cumulative Proportion  9.964668e-01 9.969403e-01 9.973411e-01 9.977297e-01
##                              Comp41       Comp42       Comp43       Comp44
## Eigenvalues            5.010560e-07 4.851584e-07 4.069549e-07 3.517293e-07
## Proportion of Variance 3.418739e-04 3.310268e-04 2.776681e-04 2.399873e-04
## Cumulative Proportion  9.980716e-01 9.984026e-01 9.986802e-01 9.989202e-01
##                              Comp45       Comp46       Comp47       Comp48
## Eigenvalues            3.061534e-07 2.952323e-07 1.981978e-07 1.925011e-07
## Proportion of Variance 2.088905e-04 2.014390e-04 1.352317e-04 1.313448e-04
```

```
## Cumulative Proportion  9.991291e-01 9.993306e-01 9.994658e-01 9.995971e-01
##                              Comp49       Comp50       Comp51       Comp52
## Eigenvalues            1.739687e-07 1.003368e-07 6.652971e-08 4.803993e-08
## Proportion of Variance 1.187000e-04 6.846044e-05 4.539366e-05 3.277796e-05
## Cumulative Proportion  9.997158e-01 9.997843e-01 9.998297e-01 9.998625e-01
##                              Comp53       Comp54       Comp55       Comp56
## Eigenvalues            4.091358e-08 2.954851e-08 2.661500e-08 2.252210e-08
## Proportion of Variance 2.791561e-05 2.016115e-05 1.815959e-05 1.536698e-05
## Cumulative Proportion  9.998904e-01 9.999105e-01 9.999287e-01 9.999441e-01
##                              Comp57       Comp58       Comp59       Comp60
## Eigenvalues            1.482585e-08 1.277594e-08 9.391056e-09 7.885008e-09
## Proportion of Variance 1.011577e-05 8.717110e-06 6.407580e-06 5.379994e-06
## Cumulative Proportion  9.999542e-01 9.999629e-01 9.999693e-01 9.999747e-01
##                              Comp61       Comp62       Comp63       Comp64
## Eigenvalues            6.459248e-09 5.577280e-09 4.375417e-09 3.756382e-09
## Proportion of Variance 4.407188e-06 3.805415e-06 2.985376e-06 2.563004e-06
## Cumulative Proportion  9.999791e-01 9.999829e-01 9.999859e-01 9.999885e-01
##                              Comp65       Comp66       Comp67       Comp68
## Eigenvalues            3.061447e-09 2.441492e-09 2.053898e-09 1.796583e-09
## Proportion of Variance 2.088845e-06 1.665846e-06 1.401388e-06 1.225820e-06
## Cumulative Proportion  9.999905e-01 9.999922e-01 9.999936e-01 9.999948e-01
##                              Comp69       Comp70       Comp71       Comp72
## Eigenvalues            1.464655e-09 1.288876e-09 1.086801e-09 8.407087e-10
## Proportion of Variance 9.993442e-07 8.794090e-07 7.415316e-07 5.736212e-07
## Cumulative Proportion  9.999958e-01 9.999967e-01 9.999975e-01 9.999980e-01
##                              Comp73       Comp74       Comp75       Comp76
## Eigenvalues            7.859113e-10 6.889164e-10 5.628137e-10 4.175679e-10
## Proportion of Variance 5.362325e-07 4.700522e-07 3.840115e-07 2.849093e-07
## Cumulative Proportion  9.999986e-01 9.999990e-01 9.999994e-01 9.999997e-01
##                              Comp77       Comp78
## Eigenvalues            2.920180e-10 1.348681e-10
## Proportion of Variance 1.992459e-07 9.202144e-08
## Cumulative Proportion  9.999999e-01 1.000000e+00
```

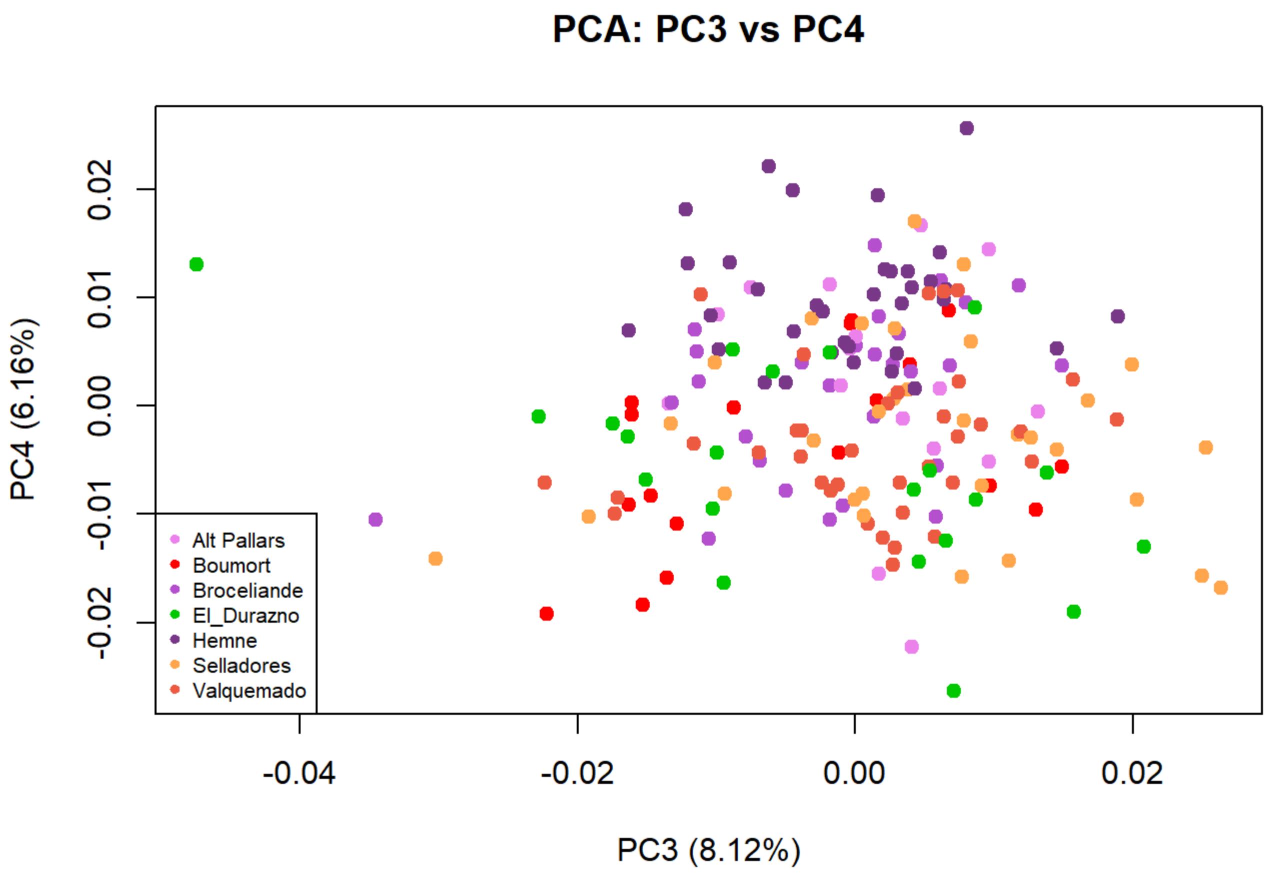
```
PC_scores_PCA_ALL_Cervus <- PCA_ALL_Cervus$x # Extract PC scores
view(PC_scores_PCA_ALL_Cervus)

eigenvalues <- PCA_ALL_Cervus$sdev^2
explained_variance <- eigenvalues / sum(eigenvalues) * 100 # eighenvalues in %
cumulative_variance <- cumsum(explained_variance)
cumulative_variance # (PC 1-5 explain >80%)
```

```
##     Comp1     Comp2     Comp3     Comp4     Comp5     Comp6     Comp7     Comp8 
##  37.33941  63.26901  71.39311  77.55037  81.96834  85.36554  87.44568  89.13020 
##     Comp9    Comp10    Comp11    Comp12    Comp13    Comp14    Comp15    Comp16 
##  90.63182  91.92903  92.90550  93.80612  94.59274  95.22275  95.79319  96.29406 
##    Comp17    Comp18    Comp19    Comp20    Comp21    Comp22    Comp23    Comp24 
##  96.71616  97.10717  97.41652  97.68278  97.91226  98.12694  98.32277  98.50648 
##    Comp25    Comp26    Comp27    Comp28    Comp29    Comp30    Comp31    Comp32 
##  98.64898  98.77594  98.89522  99.00374  99.10482  99.19255  99.27525  99.34771 
##    Comp33    Comp34    Comp35    Comp36    Comp37    Comp38    Comp39    Comp40 
##  99.41677  99.48286  99.54029  99.59447  99.64668  99.69403  99.73411  99.77297 
##    Comp41    Comp42    Comp43    Comp44    Comp45    Comp46    Comp47    Comp48 
##  99.80716  99.84026  99.86802  99.89202  99.91291  99.93306  99.94658  99.95971 
##    Comp49    Comp50    Comp51    Comp52    Comp53    Comp54    Comp55    Comp56 
##  99.97158  99.97843  99.98297  99.98625  99.98904  99.99105  99.99287  99.99441 
##    Comp57    Comp58    Comp59    Comp60    Comp61    Comp62    Comp63    Comp64 
##  99.99542  99.99629  99.99693  99.99747  99.99791  99.99829  99.99859  99.99885 
##    Comp65    Comp66    Comp67    Comp68    Comp69    Comp70    Comp71    Comp72 
##  99.99905  99.99922  99.99936  99.99948  99.99958  99.99967  99.99975  99.99980 
##    Comp73    Comp74    Comp75    Comp76    Comp77    Comp78 
##  99.99986  99.99990  99.99994  99.99997  99.99999 100.00000
```

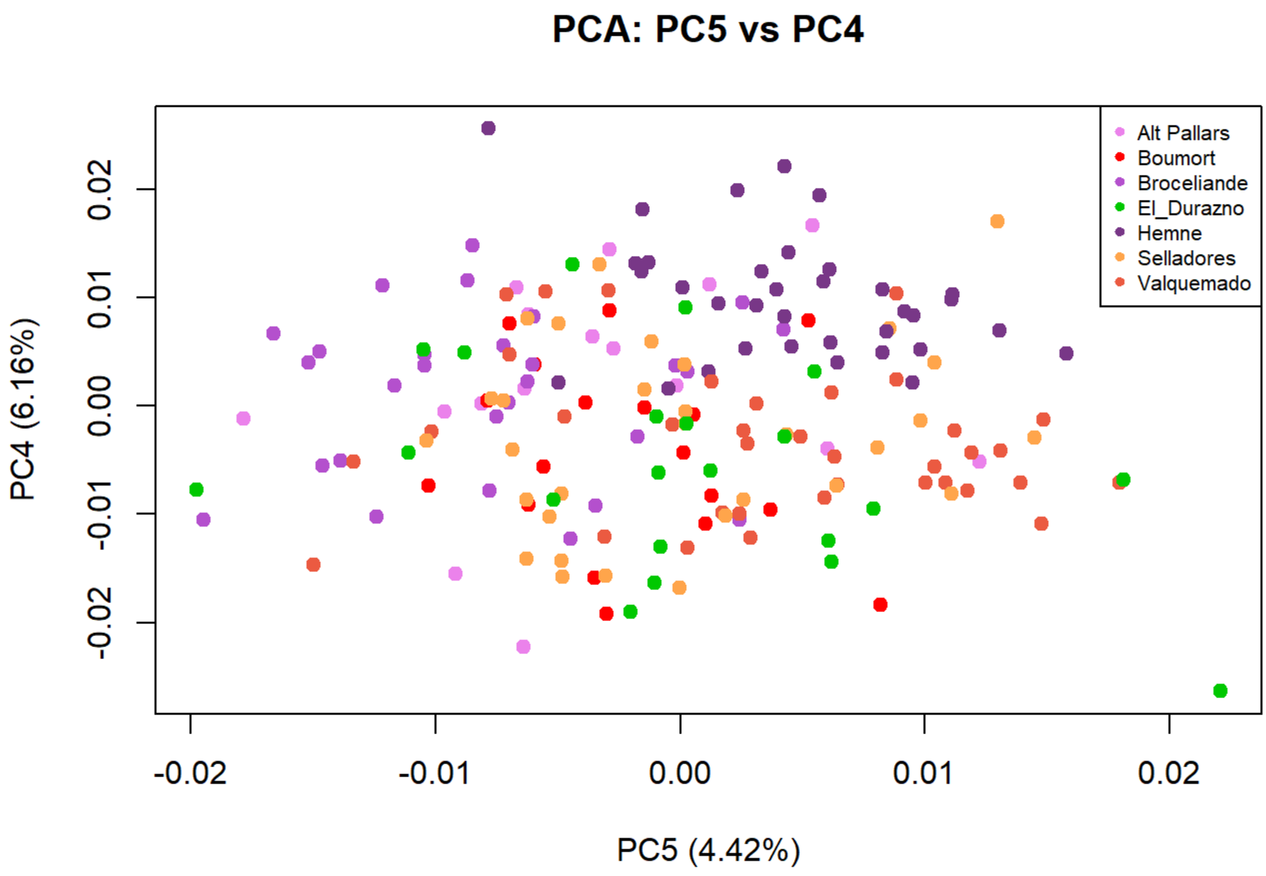
```
PC1<-PC_scores_PCA_ALL_Cervus[,1]
PC2<-PC_scores_PCA_ALL_Cervus[,2]
PC3<-PC_scores_PCA_ALL_Cervus[,3]
PC4<-PC_scores_PCA_ALL_Cervus[,4]
PC5<-PC_scores_PCA_ALL_Cervus[,5]

plot(PCA_ALL_Cervus, col = Colors_ALL_Cervus_pop[ALL_Cervus_pop], pch = 19)
legend("topright", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch = 
19, cex= 0.65)
```



```
plot(PC3, PC4, col = Colors_ALL_Cervus_pop[ALL_Cervus_pop], pch = 19, xlab = paste0("PC3 (",
round(explained_variance[3], 2), "%)"), ylab = paste0("PC4 (", round(explained_variance[4],
2), "%)"), main = "PCA: PC3 vs PC4")
legend("bottomleft", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch
= 19, cex= 0.65)
```



```
plot(PC5, PC4, col = Colors_ALL_Cervus_pop[ALL_Cervus_pop], pch = 19, xlab = paste0("PC5 (",
round(explained_variance[5], 2), "%)"), ylab = paste0("PC4 (", round(explained_variance[4],
2), "%)"), main = "PCA: PC5 vs PC4")
legend("topright", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch =
19, cex= 0.65)
```



```
### test for significative differences :
anova_PC1 <- aov(PC1 ~ ALL_Cervus_pop) # Test inter-population differences on PC1
summary(anova_PC1)
```

```
##                 Df  Sum Sq  Mean Sq F value Pr(>F)    
## ALL_Cervus_pop   6 0.07083 0.011805   70.37 <2e-16 ***
## Residuals      178 0.02986 0.000168                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_PC2 <- aov(PC2 ~ ALL_Cervus_pop) # Test inter-population differences on PC2
summary(anova_PC2)
```

```
##                 Df  Sum Sq  Mean Sq F value   Pr(>F)    
## ALL_Cervus_pop   6 0.02004 0.003339   11.91 3.17e-11 ***
## Residuals      178 0.04989 0.000280                     
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_PC3 <- aov(PC3 ~ ALL_Cervus_pop) # Test inter-population differences on PC3
summary(anova_PC3)
```

```
##                  Df   Sum Sq   Mean Sq F value Pr(>F)  
## ALL_Cervus_pop   6 0.001578 0.0002631   2.303 0.0363 *
## Residuals      178 0.020330 0.0001142                 
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_PC4 <- aov(PC4 ~ ALL_Cervus_pop) # Test inter-population differences on PC4
summary(anova_PC4)
```

```
##                  Df   Sum Sq   Mean Sq F value   Pr(>F)    
## ALL_Cervus_pop   6 0.005332 0.0008887   14.03 4.73e-13 ***
## Residuals      178 0.011272 0.0000633                     
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_PC5 <- aov(PC5 ~ ALL_Cervus_pop) # Test inter-population differences on PC5
summary(anova_PC5)
```

```
##                  Df   Sum Sq   Mean Sq F value   Pr(>F)    
## ALL_Cervus_pop   6 0.003201 0.0005335    10.9 2.53e-10 ***
## Residuals      178 0.008713 0.0000490                     
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

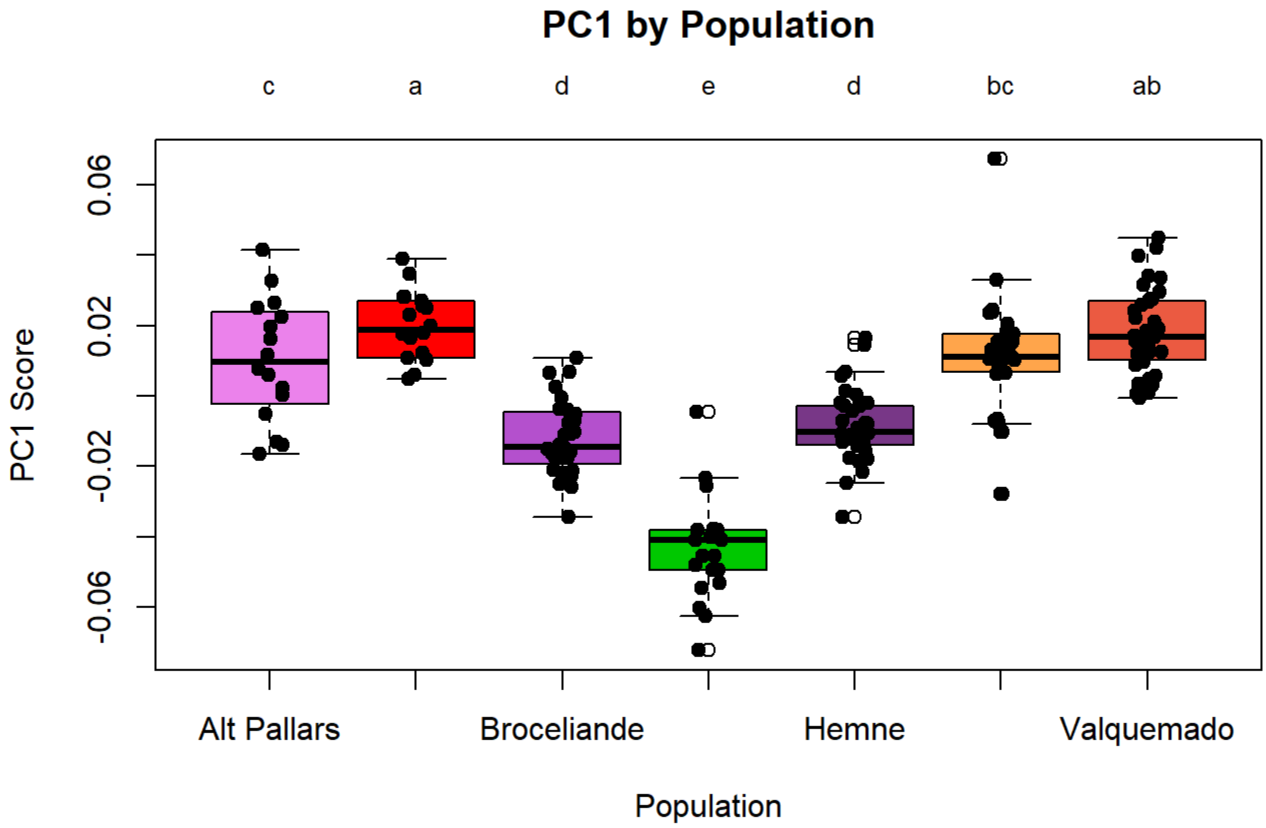
```
###Results ###############
# p-value < 2e-16 : On PC1, shape differences between the 7 populations exist. See detail of the Duncan test for inter-population differences in shape.
# p-value = 3.17e-11 : On PC2, shape differences between the 7 populations exist. See detail of the Duncan test for inter-population differences in shape.
# p-value = 0.0363 : On PC3, shape differences between the 7 populations exist. See detail of the Duncan test for inter-population differences in shape.
# p-value = 4.73e-13 : On PC4, shape differences between the 7 populations exist. See detail of the Duncan test for inter-population differences in shape.
# p-value = 2.53e-10 : On PC5, shape differences between the 7 populations exist. See detail of the Duncan test for inter-population differences in shape.
##########################

Colors_ALL_Cervus_pop <- c("Alt Pallars" = "violet", "Boumort" ="red",  "Broceliande" = "mediumorchid3","El_Durazno" = "#00CC00", "Hemne" = "mediumorchid4","Selladores" ="tan1",  "Valquemado" = "tomato2") # identify cervids by population

duncan_result <- duncan.test(anova_PC1, "ALL_Cervus_pop", console = TRUE) # post-hoc Duncan
```

```
##
## Study: anova_PC1 ~ "ALL_Cervus_pop"
##
## Duncan's new multiple range test
## for PC1
##
## Mean Square Error:  0.0001677635
##
## ALL_Cervus_pop,  means
##
##                      PC1         std  r           Min          Max
## Alt Pallars  0.010277716 0.017355439 16 -0.0165366492  0.041629670
## Boumort      0.019926284 0.009693394 18  0.0048302669  0.039059733
## Broceliande -0.011875766 0.010831360 28 -0.0344204080  0.010792770
## El_Durazno  -0.043228817 0.014448433 21 -0.0722009555 -0.004581455
## Hemne       -0.008565053 0.010225082 35 -0.0342294522  0.016468389
## Selladores   0.011457981 0.016128332 31 -0.0278887434  0.067337118
## Valquemado   0.018383040 0.012006158 36 -0.0005915064  0.044997852
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                      PC1 groups
## Boumort      0.019926284      a
## Valquemado   0.018383040     ab
## Selladores   0.011457981     bc
## Alt Pallars  0.010277716      c
## Hemne       -0.008565053      d
## Broceliande -0.011875766      d
## El_Durazno  -0.043228817      e
```

```
print(duncan_result)
```

```
## $statistics
##        MSerror  Df         Mean           CV
##   0.0001677635 178 1.179167e-17 1.098433e+17
##
## $parameters
##     test         name.t ntr alpha
##   Duncan ALL_Cervus_pop   7  0.05
##
## $duncan
## NULL
##
## $means
##                      PC1         std  r           Min          Max
## Alt Pallars  0.010277716 0.017355439 16 -0.0165366492  0.041629670
## Boumort      0.019926284 0.009693394 18  0.0048302669  0.039059733
## Broceliande -0.011875766 0.010831360 28 -0.0344204080  0.010792770
## El_Durazno  -0.043228817 0.014448433 21 -0.0722009555 -0.004581455
## Hemne       -0.008565053 0.010225082 35 -0.0342294522  0.016468389
## Selladores   0.011457981 0.016128332 31 -0.0278887434  0.067337118
## Valquemado   0.018383040 0.012006158 36 -0.0005915064  0.044997852
##                      Q25          Q50          Q75
## Alt Pallars -0.0009870613  0.009719559  0.023127577
## Boumort      0.0112528986  0.018926247  0.026773318
## Broceliande -0.0184535731 -0.014422209 -0.004803445
## El_Durazno  -0.0493921465 -0.040981702 -0.038085701
## Hemne       -0.0139867577 -0.010269834 -0.002785965
## Selladores   0.0069005925  0.011133931  0.017540589
## Valquemado   0.0107300100  0.016846719  0.026846272
##
## $comparison
## NULL
##
## $groups
##                      PC1 groups
## Boumort      0.019926284      a
## Valquemado   0.018383040     ab
## Selladores   0.011457981     bc
## Alt Pallars  0.010277716      c
## Hemne       -0.008565053      d
## Broceliande -0.011875766      d
## El_Durazno  -0.043228817      e
##
## attr(,"class")
## [1] "group"
```

```
duncan_labels <- duncan_result$groups
duncan_labels <- duncan_labels[order(rownames(duncan_labels)), ]
Descriptive_ALL_Cervus$labels <- factor(duncan_labels$groups[match(Descriptive_ALL_Cervus$Po
p, rownames(duncan_labels))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(PC1 ~ ALL_Cervus_pop, main = "PC1 by Population", xlab = "Population", ylab = "PC1 Sc
ore", col = Colors_ALL_Cervus_pop)
stripchart(PC1 ~ ALL_Cervus_pop, vertical = TRUE, method = "jitter", add = TRUE, pch = 19, co
l = "black")
mtext(duncan_labels$groups, at = 1:length(duncan_labels$groups), side = 3, line = 1, cex = 0.
8)
```



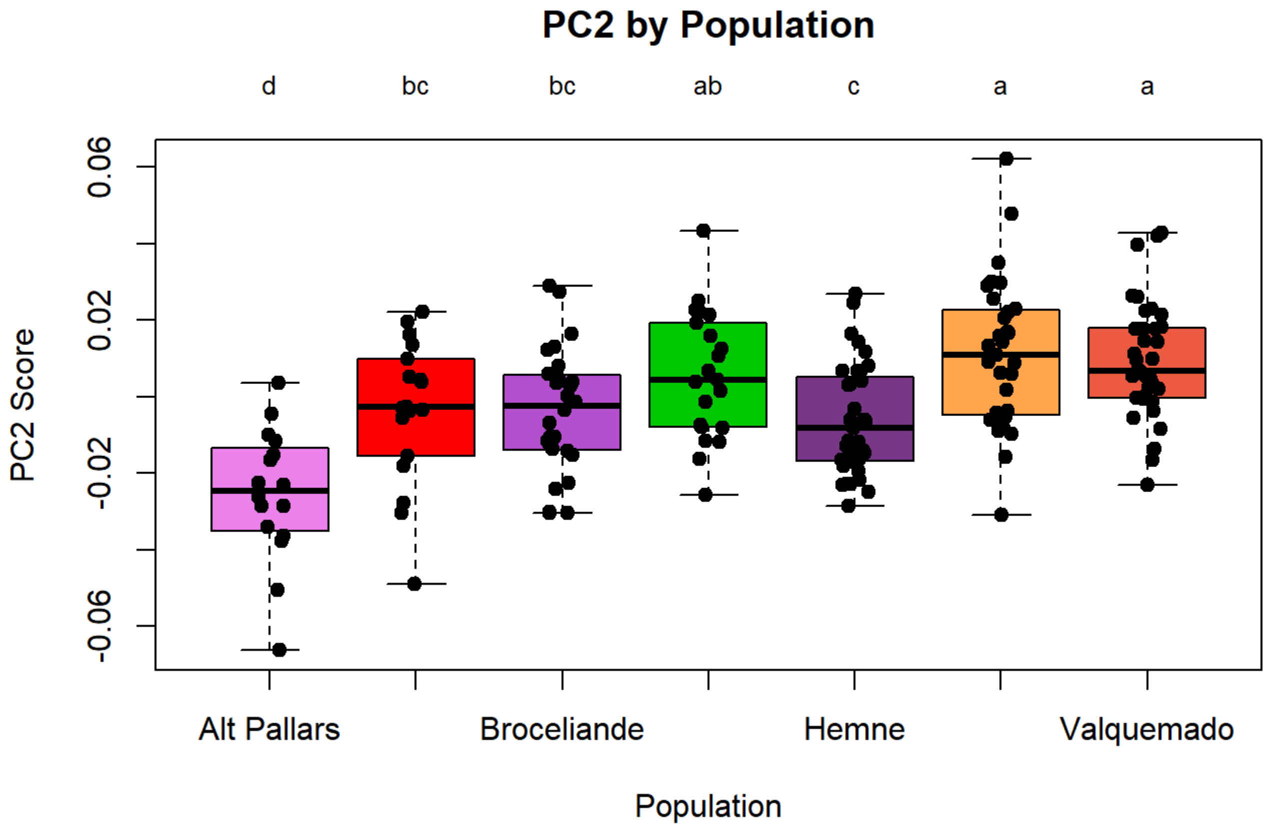
```
duncan_result <- duncan.test(anova_PC2, "ALL_Cervus_pop", console = TRUE) # post-hoc Duncan
```

```
##
## Study: anova_PC2 ~ "ALL_Cervus_pop"
##
## Duncan's new multiple range test
## for PC2
##
## Mean Square Error:  0.0002802783
##
## ALL_Cervus_pop,  means
##
##                      PC2        std  r         Min         Max
## Alt Pallars -0.025540238 0.01743777 16 -0.06622410 0.003436746
## Boumort     -0.003630122 0.01874001 18 -0.04896902 0.022167163
## Broceliande -0.003791842 0.01609668 28 -0.03042185 0.028863330
## El_Durazno   0.005615711 0.01679588 21 -0.02578172 0.043153743
## Hemne       -0.006213295 0.01451383 35 -0.02858497 0.026898510
## Selladores   0.011078975 0.01947704 31 -0.03093981 0.062001977
## Valquemado   0.009340132 0.01528546 36 -0.02315217 0.042857537
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                      PC2 groups
## Selladores   0.011078975      a
## Valquemado   0.009340132      a
## El_Durazno   0.005615711     ab
## Boumort     -0.003630122     bc
## Broceliande -0.003791842     bc
## Hemne       -0.006213295      c
## Alt Pallars -0.025540238      d
```

```
print(duncan_result)
```

```
## $statistics
##        MSerror  Df          Mean            CV
##   0.0002802783 178 -3.507302e-18 -4.773331e+17
##
## $parameters
##     test         name.t ntr alpha
##   Duncan ALL_Cervus_pop   7  0.05
##
## $duncan
## NULL
##
## $means
##                      PC2        std  r         Min         Max           Q25
## Alt Pallars -0.025540238 0.01743777 16 -0.06622410 0.003436746 -0.0346271193
## Boumort     -0.003630122 0.01874001 18 -0.04896902 0.022167163 -0.0129953921
## Broceliande -0.003791842 0.01609668 28 -0.03042185 0.028863330 -0.0137783312
## El_Durazno   0.005615711 0.01679588 21 -0.02578172 0.043153743 -0.0080387614
## Hemne       -0.006213295 0.01451383 35 -0.02858497 0.026898510 -0.0167767075
## Selladores   0.011078975 0.01947704 31 -0.03093981 0.062001977 -0.0048098289
## Valquemado   0.009340132 0.01528546 36 -0.02315217 0.042857537 -0.0004190133
##                      Q50          Q75
## Alt Pallars -0.024723614 -0.014230487
## Boumort     -0.002839599  0.008585852
## Broceliande -0.002439078  0.005345126
## El_Durazno   0.004229277  0.019301649
## Hemne       -0.008305519  0.005201223
## Selladores   0.010758407  0.022526561
## Valquemado   0.006667896  0.017831006
##
## $comparison
## NULL
##
## $groups
##                      PC2 groups
## Selladores   0.011078975      a
## Valquemado   0.009340132      a
## El_Durazno   0.005615711     ab
## Boumort     -0.003630122     bc
## Broceliande -0.003791842     bc
## Hemne       -0.006213295      c
## Alt Pallars -0.025540238      d
##
## attr(,"class")
## [1] "group"
```

```
duncan_labels <- duncan_result$groups
duncan_labels <- duncan_labels[order(rownames(duncan_labels)), ]
Descriptive_ALL_Cervus$labels <- factor(duncan_labels$groups[match(Descriptive_ALL_Cervus$Po
p, rownames(duncan_labels))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(PC2 ~ ALL_Cervus_pop, main = "PC2 by Population", xlab = "Population", ylab = "PC2 Sc
ore", col = Colors_ALL_Cervus_pop)
stripchart(PC2 ~ ALL_Cervus_pop, vertical = TRUE, method = "jitter", add = TRUE, pch = 19, co
l = "black")
mtext(duncan_labels$groups, at = 1:length(duncan_labels$groups), side = 3, line = 1, cex = 0.
8)
```



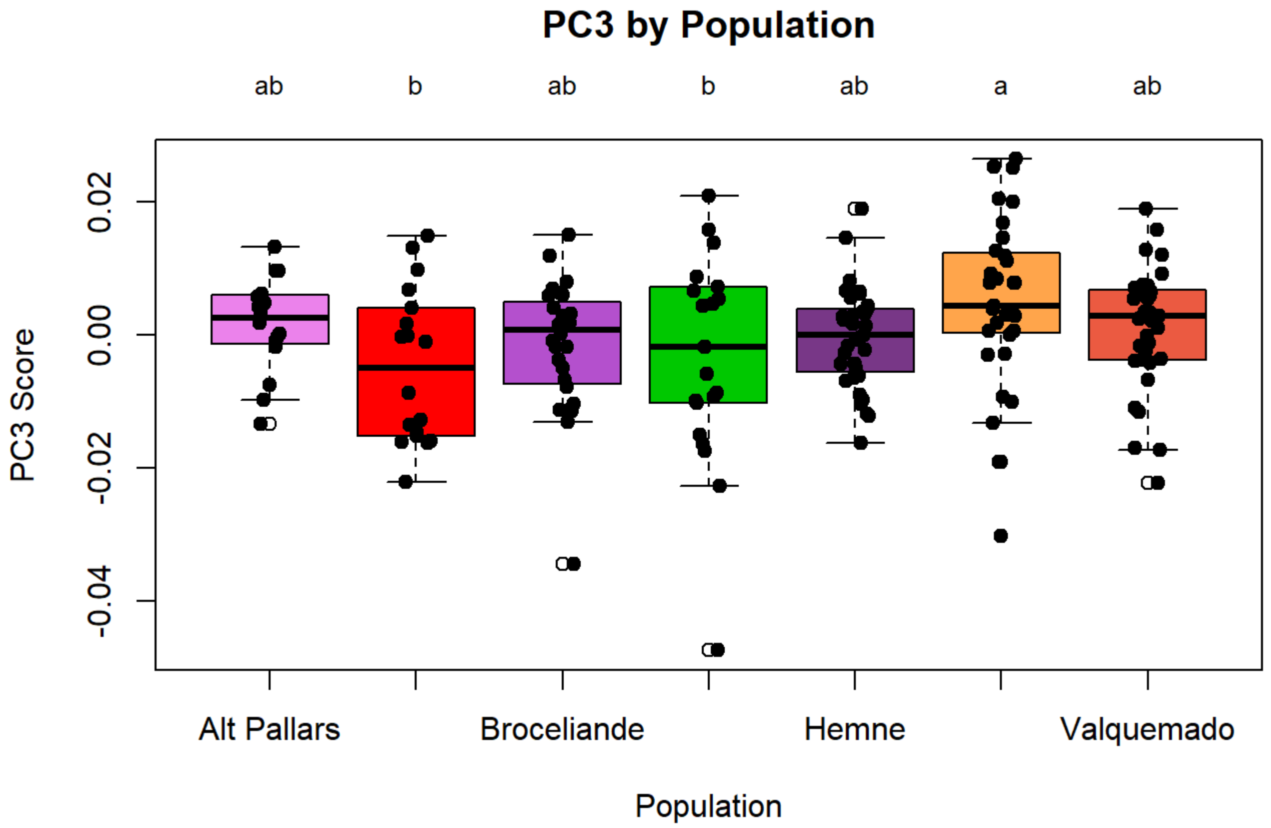
```
duncan_result <- duncan.test(anova_PC3, "ALL_Cervus_pop", console = TRUE) # post-hoc Duncan
```

```
##
## Study: anova_PC3 ~ "ALL_Cervus_pop"
##
## Duncan's new multiple range test
## for PC3
##
## Mean Square Error:  0.0001142145
##
## ALL_Cervus_pop,  means
##
##                       PC3         std  r         Min        Max
## Alt Pallars  0.0015129905 0.007233857 16 -0.01342705 0.01317342
## Boumort     -0.0048579836 0.011572678 18 -0.02220049 0.01488328
## Broceliande -0.0016099789 0.009760338 28 -0.03452755 0.01491799
## El_Durazno  -0.0033118013 0.015708075 21 -0.04743486 0.02081734
## Hemne       -0.0004565165 0.007531748 35 -0.01629552 0.01897524
## Selladores   0.0049577338 0.012876527 31 -0.03022129 0.02636572
## Valquemado   0.0011153173 0.009037409 36 -0.02238185 0.01889946
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                       PC3 groups
## Selladores   0.0049577338      a
## Alt Pallars  0.0015129905     ab
## Valquemado   0.0011153173     ab
## Hemne       -0.0004565165     ab
## Broceliande -0.0016099789     ab
## El_Durazno  -0.0033118013      b
## Boumort     -0.0048579836      b
```

```
print(duncan_result)
```

```
## $statistics
##        MSerror  Df         Mean           CV
##   0.0001142145 178 9.385562e-18 1.138677e+17
##
## $parameters
##     test         name.t ntr alpha
##   Duncan ALL_Cervus_pop   7  0.05
##
## $duncan
## NULL
##
## $means
##                       PC3         std  r         Min        Max           Q25
## Alt Pallars  0.0015129905 0.007233857 16 -0.01342705 0.01317342 -0.0012180376
## Boumort     -0.0048579836 0.011572678 18 -0.02220049 0.01488328 -0.0151194248
## Broceliande -0.0016099789 0.009760338 28 -0.03452755 0.01491799 -0.0071129500
## El_Durazno  -0.0033118013 0.015708075 21 -0.04743486 0.02081734 -0.0102295655
## Hemne       -0.0004565165 0.007531748 35 -0.01629552 0.01897524 -0.0055885046
## Selladores   0.0049577338 0.012876527 31 -0.03022129 0.02636572  0.0002374266
## Valquemado   0.0011153173 0.009037409 36 -0.02238185 0.01889946 -0.0037367371
##                       Q50         Q75
## Alt Pallars  0.0025666226 0.005795110
## Boumort     -0.0049484962 0.003368278
## Broceliande  0.0007295478 0.004462426
## El_Durazno  -0.0018421074 0.007156581
## Hemne       -0.0000673125 0.003925412
## Selladores   0.0043022228 0.012210577
## Valquemado   0.0027973793 0.006564290
##
## $comparison
## NULL
##
## $groups
##                       PC3 groups
## Selladores   0.0049577338      a
## Alt Pallars  0.0015129905     ab
## Valquemado   0.0011153173     ab
## Hemne       -0.0004565165     ab
## Broceliande -0.0016099789     ab
## El_Durazno  -0.0033118013      b
## Boumort     -0.0048579836      b
##
## attr(,"class")
## [1] "group"
```

```
duncan_labels <- duncan_result$groups
duncan_labels <- duncan_labels[order(rownames(duncan_labels)), ]
Descriptive_ALL_Cervus$labels <- factor(duncan_labels$groups[match(Descriptive_ALL_Cervus$Po
p, rownames(duncan_labels))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(PC3 ~ ALL_Cervus_pop, main = "PC3 by Population", xlab = "Population", ylab = "PC3 Sc
ore", col = Colors_ALL_Cervus_pop)
stripchart(PC3 ~ ALL_Cervus_pop, vertical = TRUE, method = "jitter", add = TRUE, pch = 19, co
l = "black")
mtext(duncan_labels$groups, at = 1:length(duncan_labels$groups), side = 3, line = 1, cex = 0.
8)
```



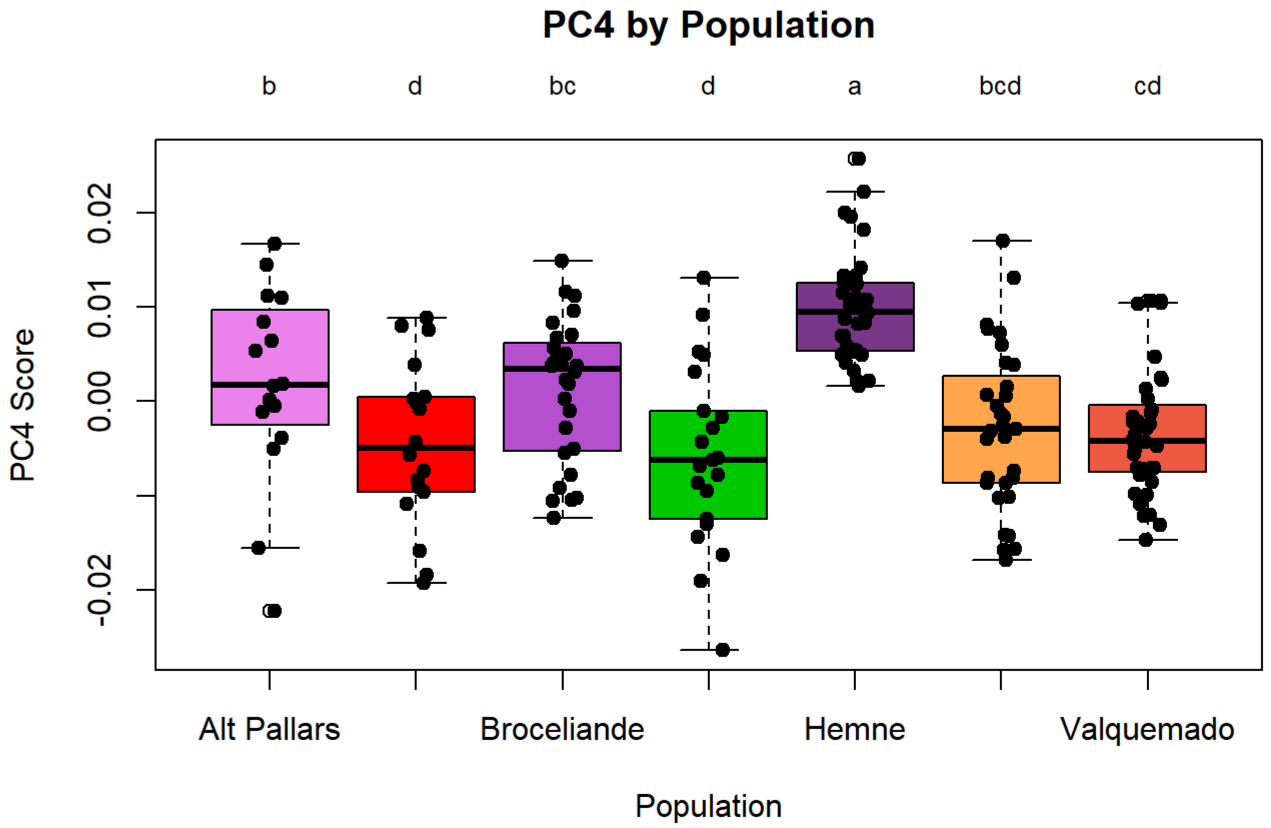
```
duncan_result <- duncan.test(anova_PC4, "ALL_Cervus_pop", console = TRUE) # post-hoc Duncan
```

```
##
## Study: anova_PC4 ~ "ALL_Cervus_pop"
##
## Duncan's new multiple range test
## for PC4
##
## Mean Square Error:  6.332674e-05
##
## ALL_Cervus_pop,  means
##
##                      PC4         std  r          Min         Max
## Alt Pallars  0.001798409 0.010357087 16 -0.022264553 0.016718133
## Boumort     -0.004489242 0.008681240 18 -0.019239739 0.008813524
## Broceliande  0.001161163 0.007557770 28 -0.012311547 0.014866783
## El_Durazno  -0.005748948 0.009626514 21 -0.026359167 0.013072031
## Hemne        0.010026366 0.005807739 35  0.001649899 0.025652950
## Selladores  -0.002847517 0.008643932 31 -0.016818014 0.017049092
## Valquemado  -0.003400072 0.006756923 36 -0.014707428 0.010684326
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                      PC4 groups
## Hemne        0.010026366      a
## Alt Pallars  0.001798409      b
## Broceliande  0.001161163     bc
## Selladores  -0.002847517    bcd
## Valquemado  -0.003400072     cd
## Boumort     -0.004489242      d
## El_Durazno  -0.005748948      d
```

```
print(duncan_result)
```

```
## $statistics
##        MSerror  Df          Mean            CV
##   6.332674e-05 178 -3.413516e-18 -2.331265e+17
##
## $parameters
##     test         name.t ntr alpha
##   Duncan ALL_Cervus_pop   7  0.05
##
## $duncan
## NULL
##
## $means
##                      PC4         std  r          Min         Max          Q25
## Alt Pallars  0.001798409 0.010357087 16 -0.022264553 0.016718133 -0.001830237
## Boumort     -0.004489242 0.008681240 18 -0.019239739 0.008813524 -0.009481209
## Broceliande  0.001161163 0.007557770 28 -0.012311547 0.014866783 -0.005138651
## El_Durazno  -0.005748948 0.009626514 21 -0.026359167 0.013072031 -0.012464072
## Hemne        0.010026366 0.005807739 35  0.001649899 0.025652950  0.005388996
## Selladores  -0.002847517 0.008643932 31 -0.016818014 0.017049092 -0.008668329
## Valquemado  -0.003400072 0.006756923 36 -0.014707428 0.010684326 -0.007365919
##                      Q50           Q75
## Alt Pallars  0.001739754  0.0090613421
## Boumort     -0.004990097  0.0004476421
## Broceliande  0.003430635  0.0058833030
## El_Durazno  -0.006176585 -0.0010003923
## Hemne        0.009476505  0.0125504718
## Selladores  -0.002877224  0.0026862883
## Valquemado  -0.004196879 -0.0006463666
##
## $comparison
## NULL
##
## $groups
##                      PC4 groups
## Hemne        0.010026366      a
## Alt Pallars  0.001798409      b
## Broceliande  0.001161163     bc
## Selladores  -0.002847517    bcd
## Valquemado  -0.003400072     cd
## Boumort     -0.004489242      d
## El_Durazno  -0.005748948      d
##
## attr(,"class")
## [1] "group"
```

```
duncan_labels <- duncan_result$groups
duncan_labels <- duncan_labels[order(rownames(duncan_labels)), ]
Descriptive_ALL_Cervus$labels <- factor(duncan_labels$groups[match(Descriptive_ALL_Cervus$Po
p, rownames(duncan_labels))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(PC4 ~ ALL_Cervus_pop, main = "PC4 by Population", xlab = "Population", ylab = "PC4 Sc
ore", col = Colors_ALL_Cervus_pop)
stripchart(PC4 ~ ALL_Cervus_pop, vertical = TRUE, method = "jitter", add = TRUE, pch = 19, co
l = "black")
mtext(duncan_labels$groups, at = 1:length(duncan_labels$groups), side = 3, line = 1, cex = 0.
8)
```



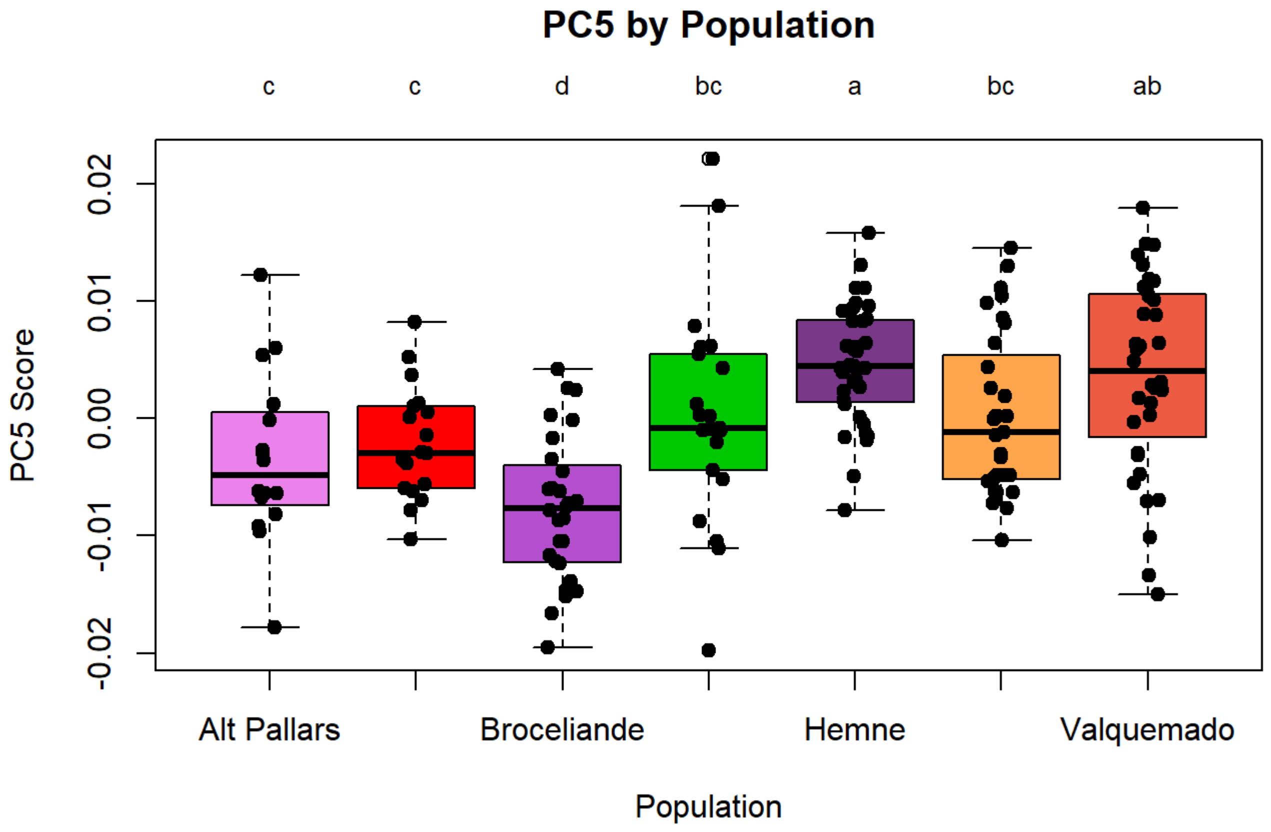
```
duncan_result <- duncan.test(anova_PC5, "ALL_Cervus_pop", console = TRUE) # post-hoc Duncan
```

```
##
## Study: anova_PC5 ~ "ALL_Cervus_pop"
##
## Duncan's new multiple range test
## for PC5
##
## Mean Square Error:  4.895077e-05
##
## ALL_Cervus_pop,  means
##
##                       PC5         std  r          Min         Max
## Alt Pallars -0.0034286710 0.007222945 16 -0.017829921 0.012231038
## Boumort     -0.0020773510 0.004858221 18 -0.010269293 0.008205072
## Broceliande -0.0077501146 0.006169438 28 -0.019490352 0.004205176
## El_Durazno   0.0003004714 0.009369778 21 -0.019768315 0.022076209
## Hemne        0.0045850010 0.005164230 35 -0.007812153 0.015773392
## Selladores   0.0002065160 0.006935819 31 -0.010381503 0.014488558
## Valquemado   0.0037796482 0.008273853 36 -0.014993326 0.017935958
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                       PC5 groups
## Hemne        0.0045850010      a
## Valquemado   0.0037796482     ab
## El_Durazno   0.0003004714     bc
## Selladores   0.0002065160     bc
## Boumort     -0.0020773510      c
## Alt Pallars -0.0034286710      c
## Broceliande -0.0077501146      d
```

```
print(duncan_result)
```

```
## $statistics
##        MSerror  Df         Mean           CV
##   4.895077e-05 178 4.162485e-18 1.680843e+17
##
## $parameters
##     test         name.t ntr alpha
##   Duncan ALL_Cervus_pop   7  0.05
##
## $duncan
## NULL
##
## $means
##                       PC5         std  r          Min         Max           Q25
## Alt Pallars -0.0034286710 0.007222945 16 -0.017829921 0.012231038 -0.0070466858
## Boumort     -0.0020773510 0.004858221 18 -0.010269293 0.008205072 -0.0058589727
## Broceliande -0.0077501146 0.006169438 28 -0.019490352 0.004205176 -0.0122156885
## El_Durazno   0.0003004714 0.009369778 21 -0.019768315 0.022076209 -0.0043983343
## Hemne        0.0045850010 0.005164230 35 -0.007812153 0.015773392  0.0013653259
## Selladores   0.0002065160 0.006935819 31 -0.010381503 0.014488558 -0.0051639047
## Valquemado   0.0037796482 0.008273853 36 -0.014993326 0.017935958 -0.0009546363
##                       Q50           Q75
## Alt Pallars -0.0048806333  0.0001888161
## Boumort     -0.0029434028  0.0009264896
## Broceliande -0.0076549563 -0.0042295373
## El_Durazno  -0.0007920092  0.0054749640
## Hemne        0.0044193076  0.0083531155
## Selladores  -0.0011804626  0.0053703341
## Valquemado   0.0040137829  0.0105219807
##
## $comparison
## NULL
##
## $groups
##                       PC5 groups
## Hemne        0.0045850010      a
## Valquemado   0.0037796482     ab
## El_Durazno   0.0003004714     bc
## Selladores   0.0002065160     bc
## Boumort     -0.0020773510      c
## Alt Pallars -0.0034286710      c
## Broceliande -0.0077501146      d
##
## attr(,"class")
## [1] "group"
```

```
duncan_labels <- duncan_result$groups
duncan_labels <- duncan_labels[order(rownames(duncan_labels)), ]
Descriptive_ALL_Cervus$labels <- factor(duncan_labels$groups[match(Descriptive_ALL_Cervus$Po
p, rownames(duncan_labels))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(PC5 ~ ALL_Cervus_pop, main = "PC5 by Population", xlab = "Population", ylab = "PC5 Sc
ore", col = Colors_ALL_Cervus_pop)
stripchart(PC5 ~ ALL_Cervus_pop, vertical = TRUE, method = "jitter", add = TRUE, pch = 19, co
l = "black")
mtext(duncan_labels$groups, at = 1:length(duncan_labels$groups), side = 3, line = 1, cex = 0.
8)
```

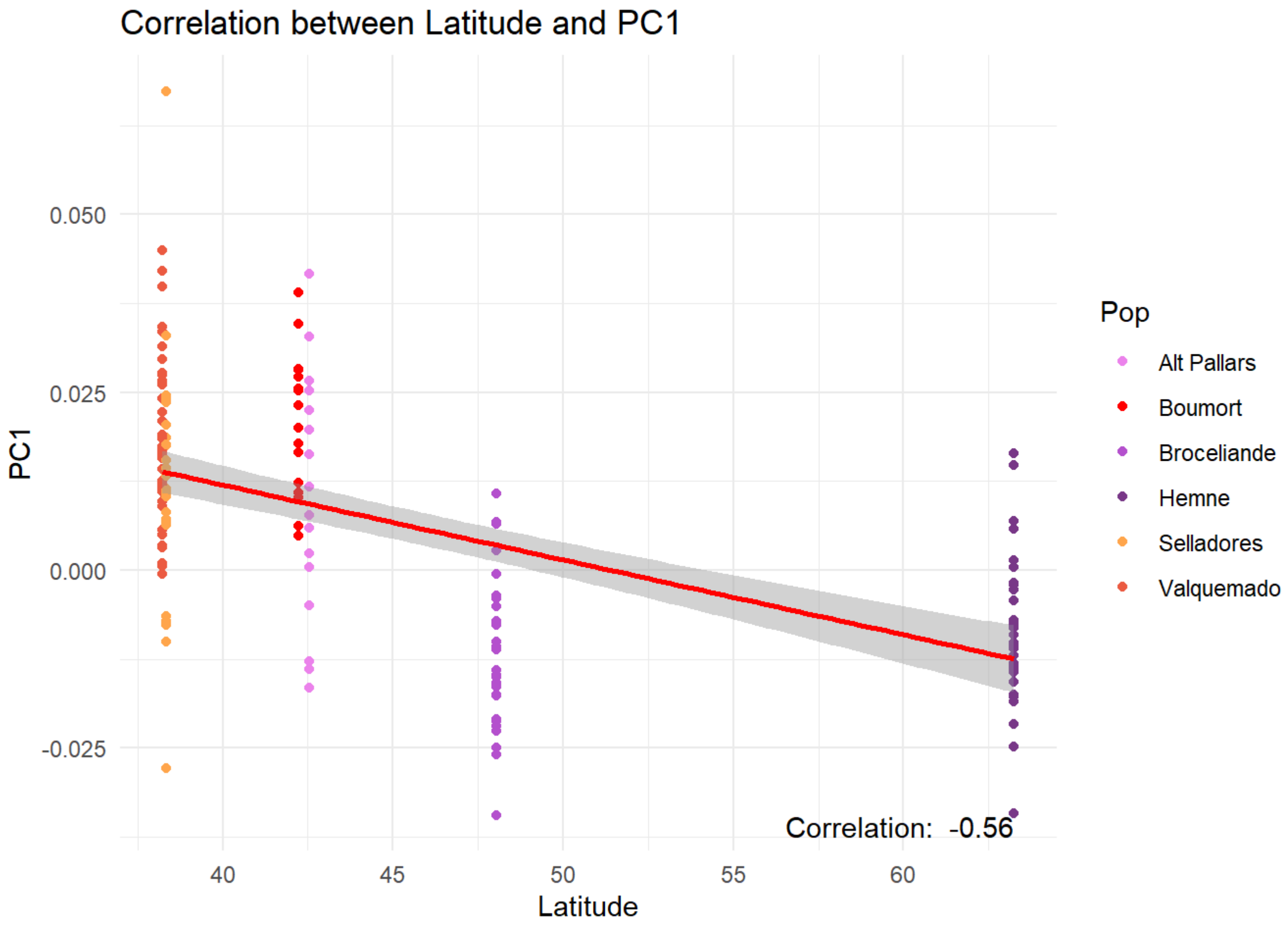


```
# test the correlation between morphological changes on PC1 and latitude :
filtered_data <- Descriptive_ALL_Cervus[Descriptive_ALL_Cervus$Pop != "El_Durazno", ]
PC1 <- PC_scores_PCA_ALL_Cervus[Descriptive_ALL_Cervus$Pop != "El_Durazno", 1]
Pop <- filtered_data$Pop
Lat <- as.numeric(as.character(filtered_data$Lat))
correlation <- cor(Lat, PC1, use = "complete.obs")
print(paste("Correlation between Latitude and PC1: ", correlation))
```

```
## [1] "Correlation between Latitude and PC1:  -0.562932561436816"
```

```
# Results :
# The correlation of -0.56 suggests a moderate relationship between latitude and PC1

Colors_ALL_Cervus_pop <- c("Alt Pallars" = "violet",
                           "Boumort" = "red",
                           "Broceliande" = "mediumorchid3",
                           "Hemne" = "mediumorchid4",
                           "Selladores" = "tan1",
                           "Valquemado" = "tomato2")
data <- data.frame(Lat = Lat, PC1 = PC1, Pop = as.factor(Pop))
ggplot(data, aes(x = Lat, y = PC1, color = Pop)) +
  geom_point() +
  geom_smooth(method = "lm", col = "red") +
  scale_color_manual(values = Colors_ALL_Cervus_pop) +
  labs(title = "Correlation between Latitude and PC1",
       x = "Latitude",
       y = "PC1") +
  theme_minimal() +
  annotate("text", x = max(data$Lat), y = min(data$PC1),
           label = paste("Correlation: ", round(cor(data$Lat, data$PC1), 2)),
           hjust = 1, vjust = 1)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

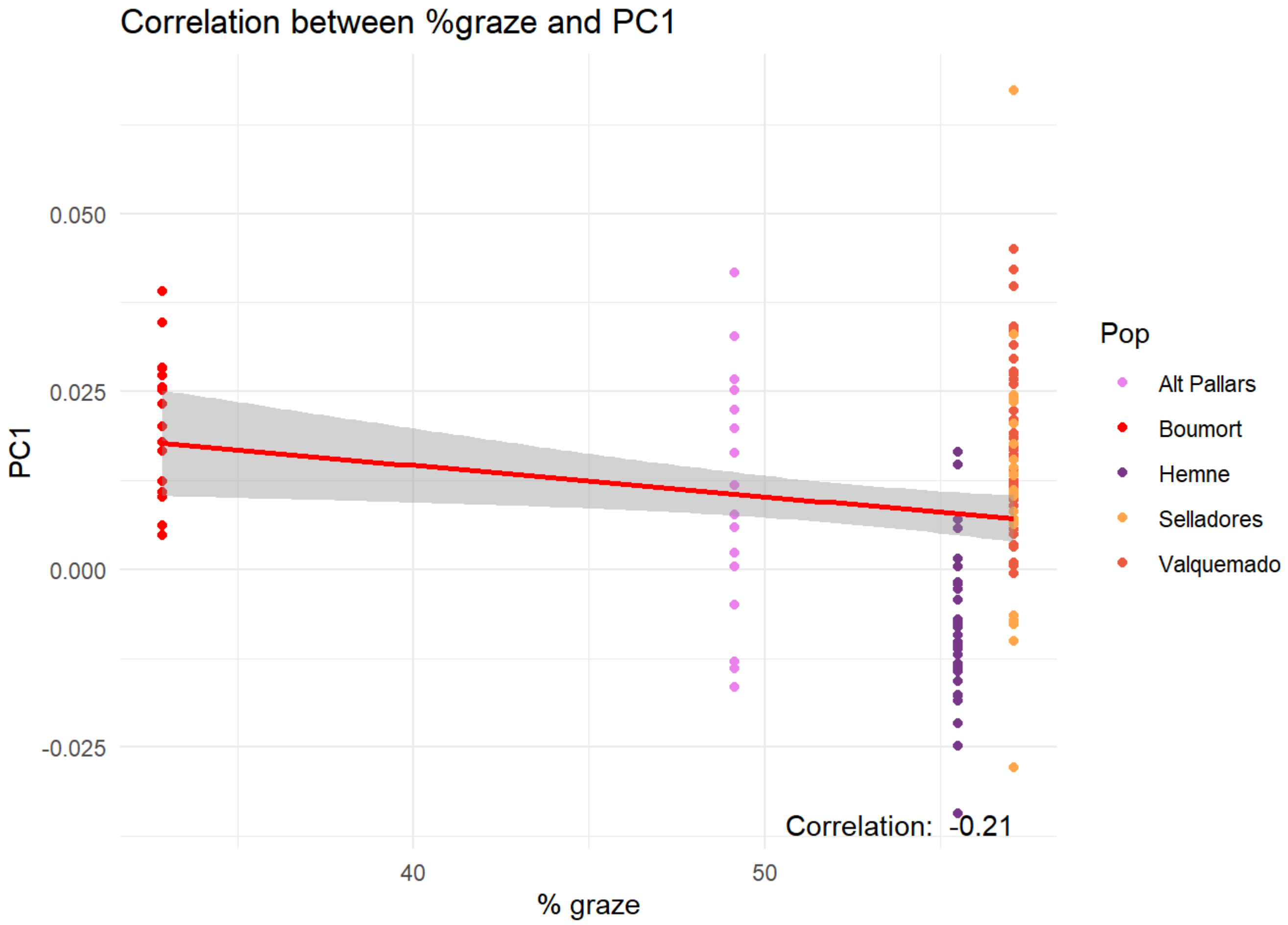


```
# test the correlation between morphological changes on PC1 and % graze :
filtered_data <- Descriptive_ALL_Cervus[!(Descriptive_ALL_Cervus$Pop %in% c("El_Durazno", "Br
oceliande")), ]
PC1 <- PC_scores_PCA_ALL_Cervus[!(Descriptive_ALL_Cervus$Pop %in% c("El_Durazno", "Broceliand
e")), 1]
Pop <- filtered_data$Pop
Graze <- as.numeric(as.character(filtered_data$Herb_Monocots))
correlation <- cor(Graze, PC1, use = "complete.obs")
print(paste("Correlation between % of graze and PC1: ", correlation))
```

```
## [1] "Correlation between % of graze and PC1:  -0.208753900464358"
```

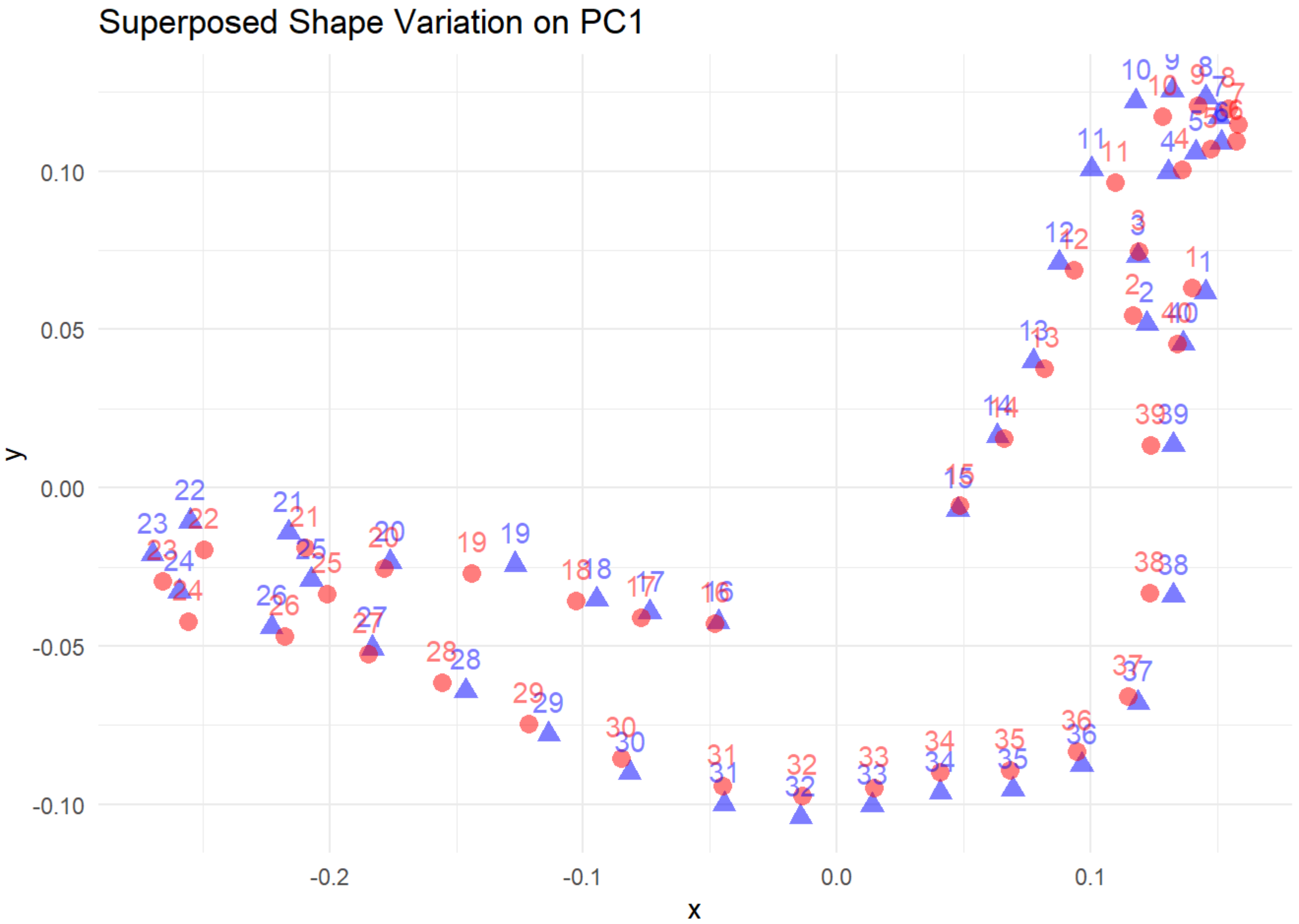
```
# Results :
# The correlation of  -0.2088 suggests a weak relationship between %graze and PC1
Colors_ALL_Cervus_pop <- c("Alt Pallars" = "violet",
                           "Boumort" = "red",
                           "Hemne" = "mediumorchid4",
                           "Selladores" = "tan1",
                           "Valquemado" = "tomato2")
data <- data.frame(Graze = Graze, PC1 = PC1, Pop = as.factor(Pop))
ggplot(data, aes(x = Graze, y = PC1, color = Pop)) +
  geom_point() +
  geom_smooth(method = "lm", col = "red") +
  scale_color_manual(values = Colors_ALL_Cervus_pop) +
  labs(title = "Correlation between %graze and PC1",
       x = "% graze",
       y = "PC1") +
  theme_minimal() +
  annotate("text", x = max(data$Graze), y = min(data$PC1),
           label = paste("Correlation: ", round(correlation, 2)),
           hjust = 1, vjust = 1)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

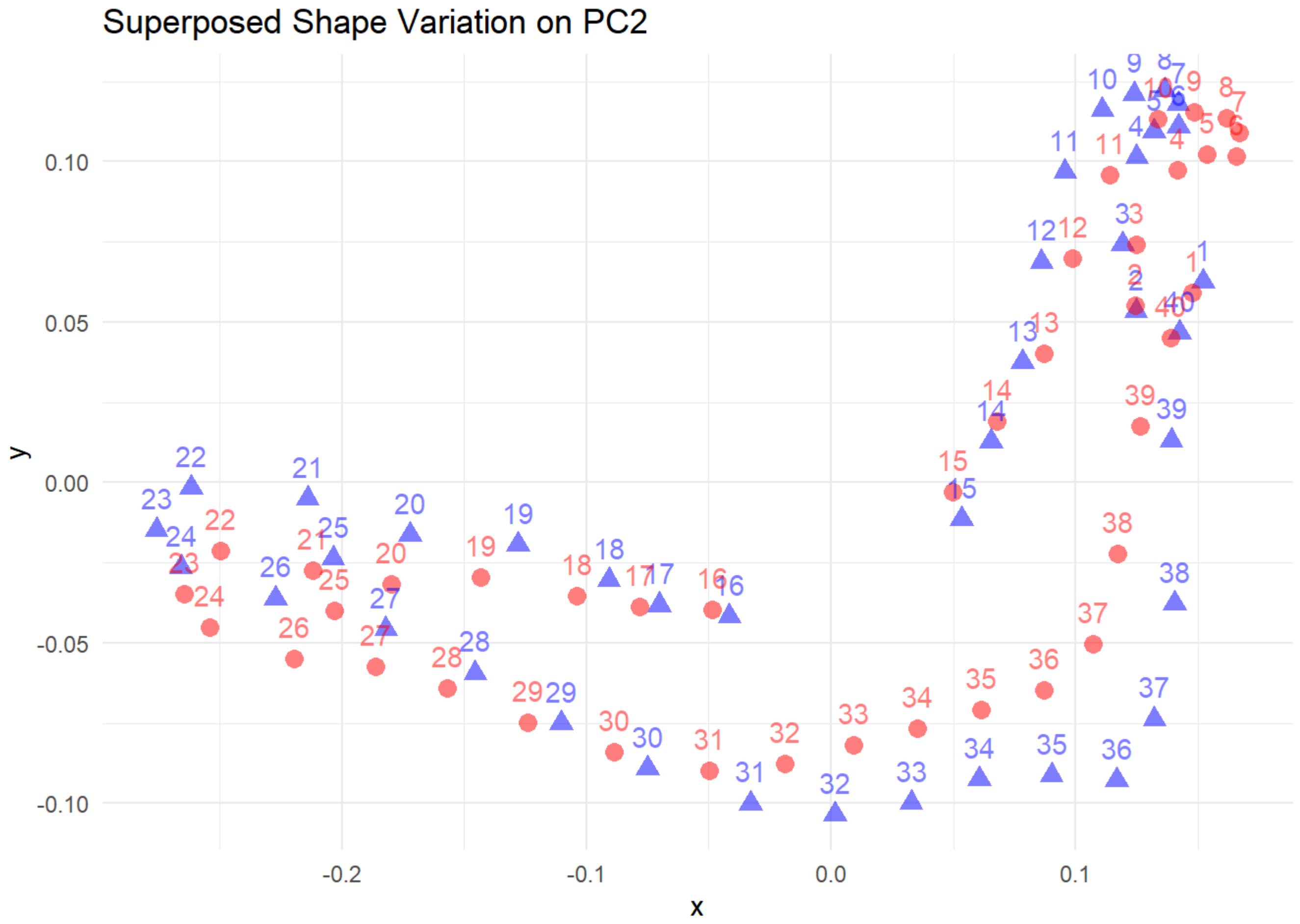


Visualize shape variation

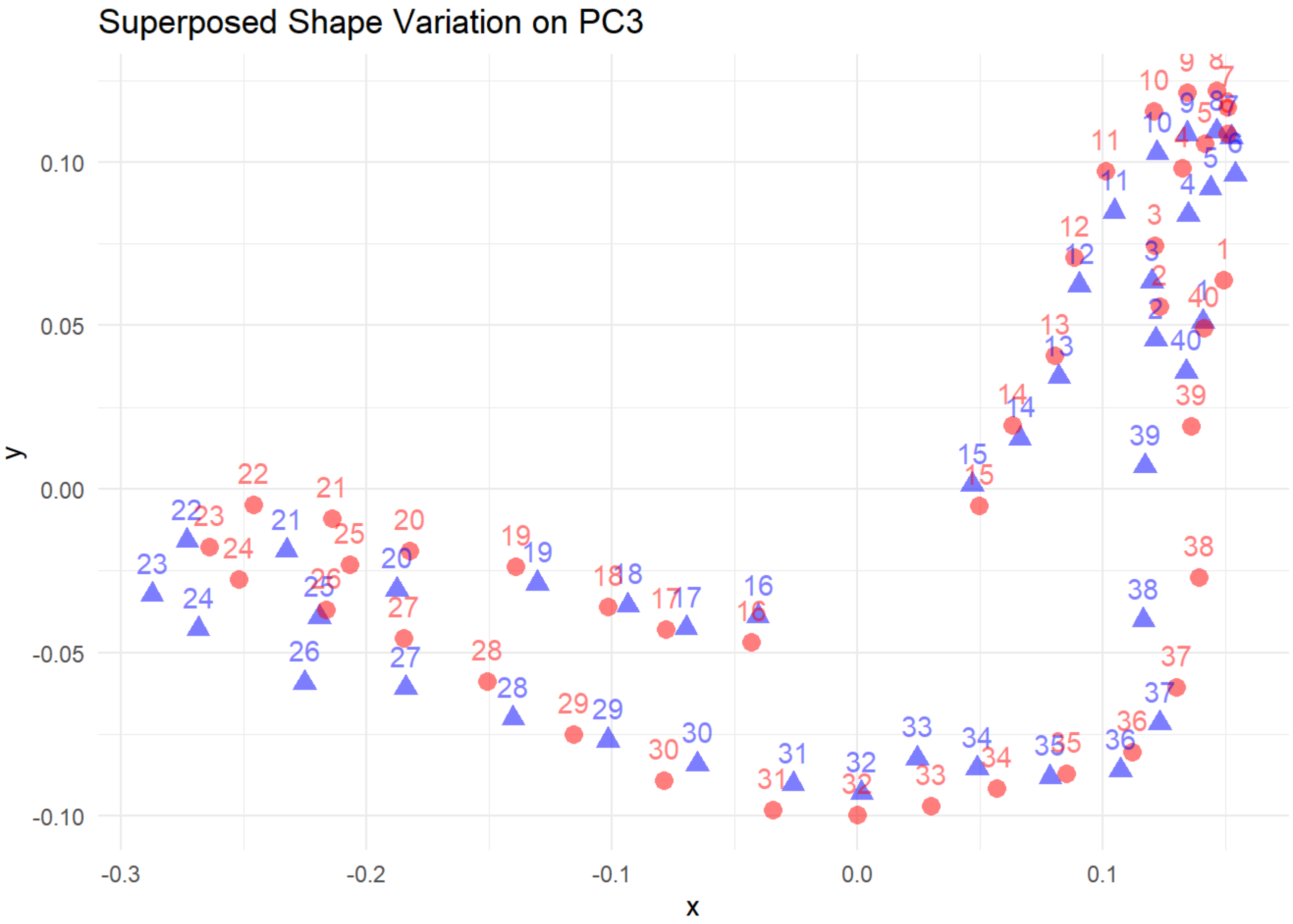
```
#Visualize shape variation on PC1
extreme_min_PC1 <- which.min(PC1)
extreme_max_PC1 <- which.max(PC1)

coords_min_PC1 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_min_PC1])
coords_max_PC1 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_max_PC1])
coords_min_PC1$landmark <- 1:nrow(coords_min_PC1)
coords_max_PC1$landmark <- 1:nrow(coords_max_PC1)

colnames(coords_min_PC1) <- c("x", "y", "landmark")
colnames(coords_max_PC1) <- c("x", "y", "landmark")
coords_min_PC1$group <- "Min PC1"
coords_max_PC1$group <- "Max PC1"

df_combined <- rbind(coords_min_PC1, coords_max_PC1)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on PC1") +
  scale_color_manual(values = c("Min PC1" = "blue", "Max PC1" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



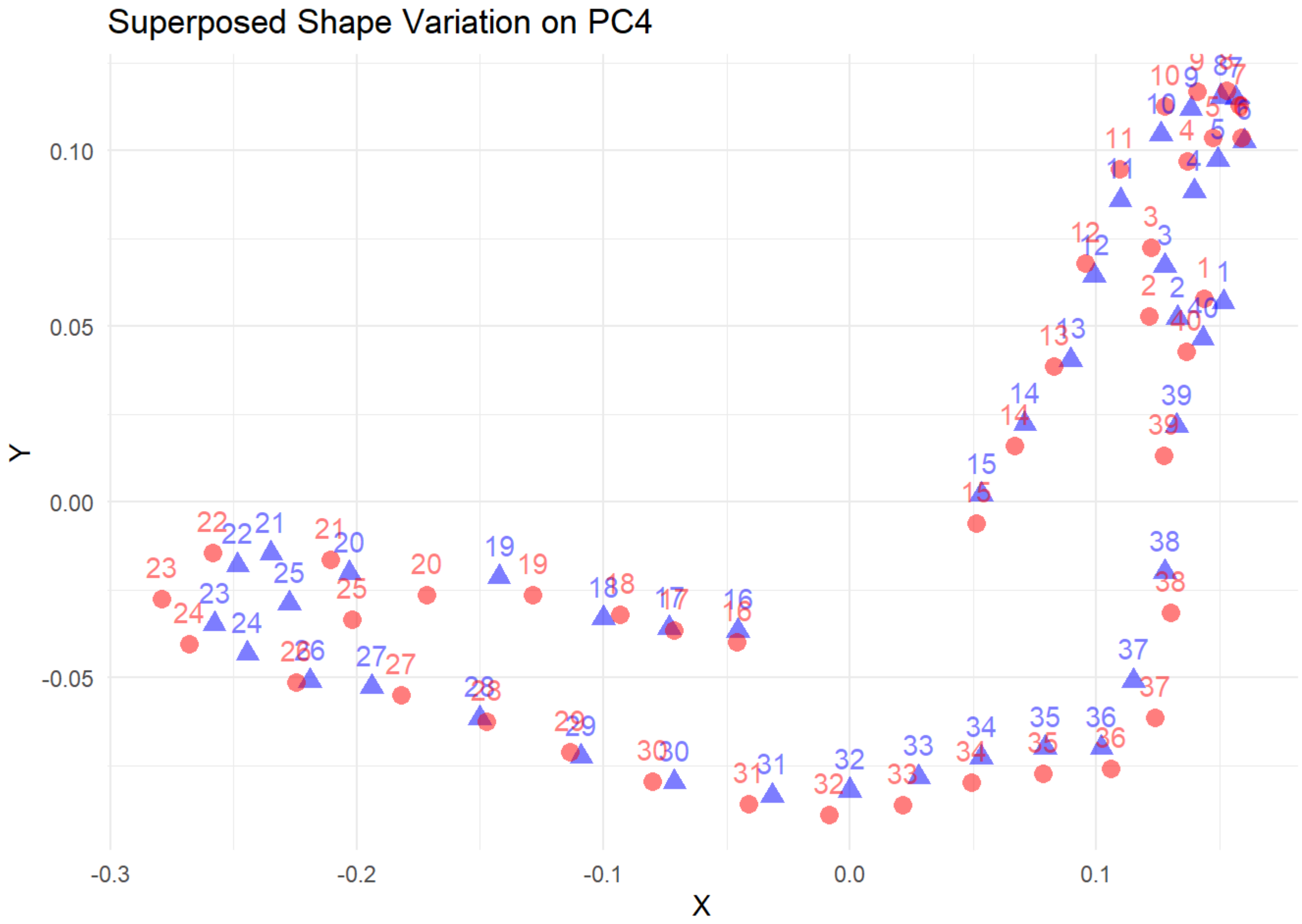
```
#Vizualize shape variation on PC2
extreme_min_PC2 <- which.min(PC2)
extreme_max_PC2 <- which.max(PC2)

coords_min_PC2 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_min_PC2])
coords_max_PC2 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_max_PC2])
coords_min_PC2$landmark <- 1:nrow(coords_min_PC2)
coords_max_PC2$landmark <- 1:nrow(coords_max_PC2)

colnames(coords_min_PC2) <- c("x", "y", "landmark")
colnames(coords_max_PC2) <- c("x", "y", "landmark")
coords_min_PC2$group <- "Min PC2"
coords_max_PC2$group <- "Max PC2"

df_combined <- rbind(coords_min_PC2, coords_max_PC2)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on PC2") +
  scale_color_manual(values = c("Min PC2" = "blue", "Max PC2" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



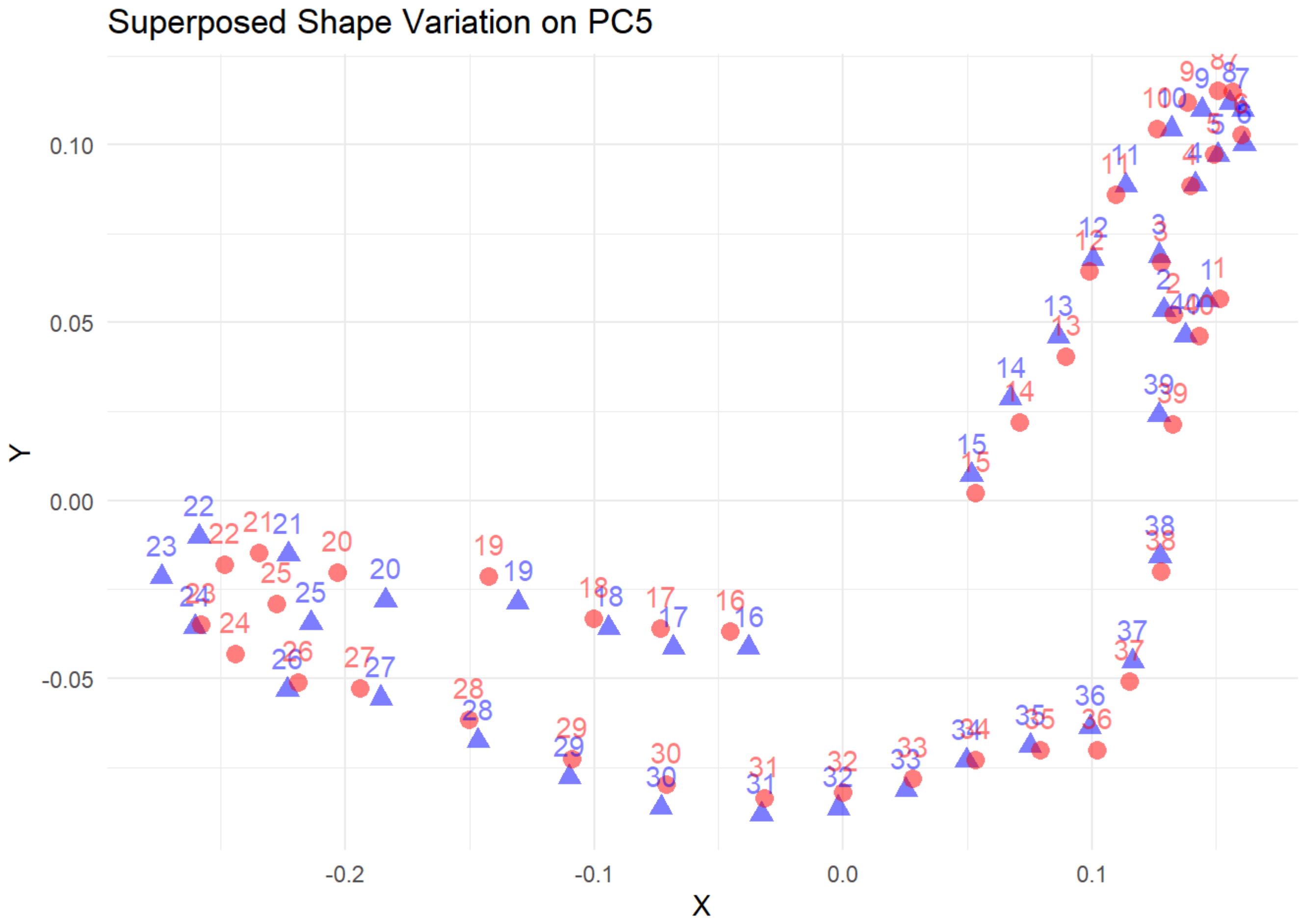
```
#Vizualize shape variation on PC3
extreme_min_PC3 <- which.min(PC3)
extreme_max_PC3 <- which.max(PC3)

coords_min_PC3 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_min_PC3])
coords_max_PC3 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_max_PC3])
coords_min_PC3$landmark <- 1:nrow(coords_min_PC3)
coords_max_PC3$landmark <- 1:nrow(coords_max_PC3)

colnames(coords_min_PC3) <- c("x", "y", "landmark")
colnames(coords_max_PC3) <- c("x", "y", "landmark")
coords_min_PC3$group <- "Min PC3"
coords_max_PC3$group <- "Max PC3"

df_combined <- rbind(coords_min_PC3, coords_max_PC3)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on PC3") +
  scale_color_manual(values = c("Min PC3" = "blue", "Max PC3" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



```
#Vizualize shape variation on PC4
extreme_min_PC4 <- which.min(PC4)
extreme_max_PC4 <- which.max(PC4)

coords_min_PC4 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_min_PC4])
coords_max_PC4 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_max_PC4])
coords_min_PC4$landmark <- 1:nrow(coords_min_PC4)
coords_max_PC4$landmark <- 1:nrow(coords_max_PC4)

colnames(coords_min_PC4) <- c("x", "y", "landmark")
colnames(coords_max_PC4) <- c("x", "y", "landmark")
coords_min_PC4$group <- "Min PC4"
coords_max_PC4$group <- "Max PC4"

df_combined <- rbind(coords_min_PC4, coords_max_PC4)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on PC4", x = "X", y = "Y") +
  scale_color_manual(values = c("Min PC4" = "blue", "Max PC4" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



```
#Vizualize shape variation on PC5
extreme_min_PC5 <- which.min(PC5)
extreme_max_PC5 <- which.max(PC5)

coords_min_PC5 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_min_PC5])
coords_max_PC5 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_max_PC5])
coords_min_PC5$landmark <- 1:nrow(coords_min_PC5)
coords_max_PC5$landmark <- 1:nrow(coords_max_PC5)

colnames(coords_min_PC5) <- c("x", "y", "landmark")
colnames(coords_max_PC5) <- c("x", "y", "landmark")
coords_min_PC5$group <- "Min PC5"
coords_max_PC5$group <- "Max PC5"

df_combined <- rbind(coords_min_PC5, coords_max_PC5)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on PC5", x = "X", y = "Y") +
  scale_color_manual(values = c("Min PC5" = "blue", "Max PC5" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```

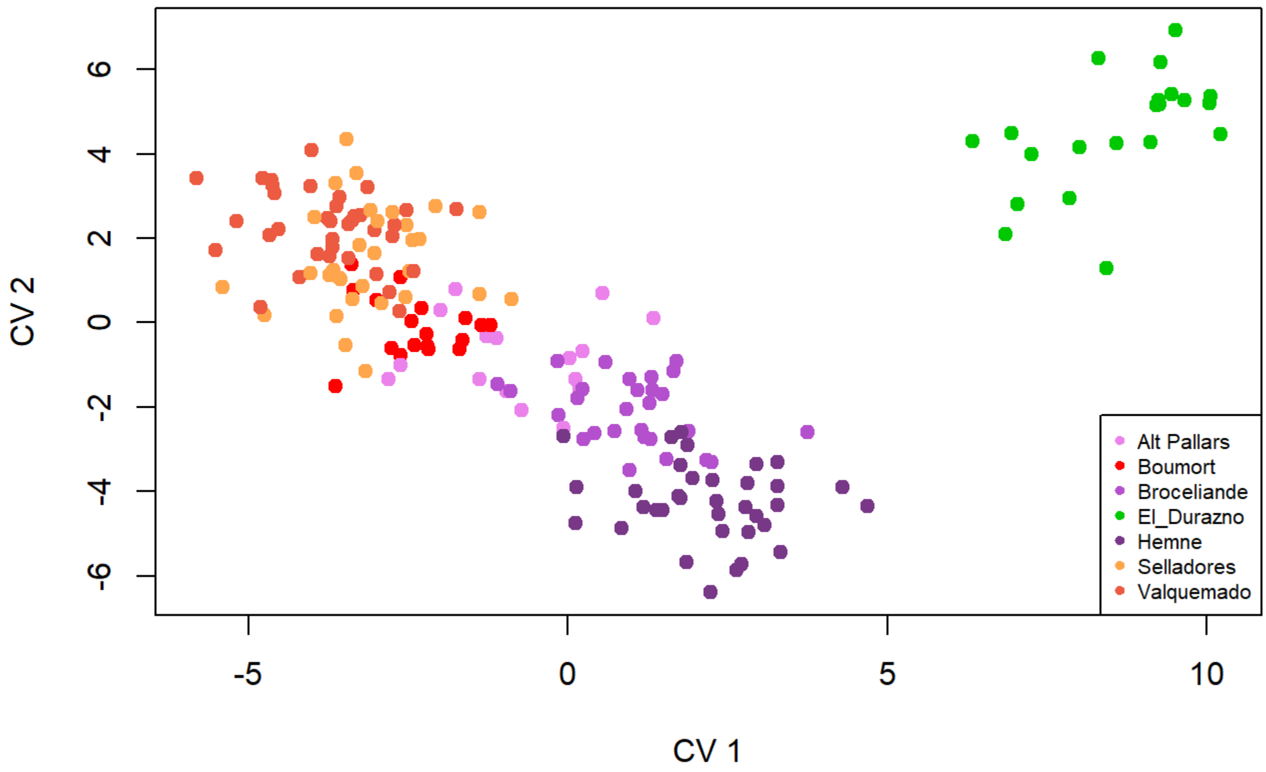


2.3.3 Canonical Variate Analysis (CVA):

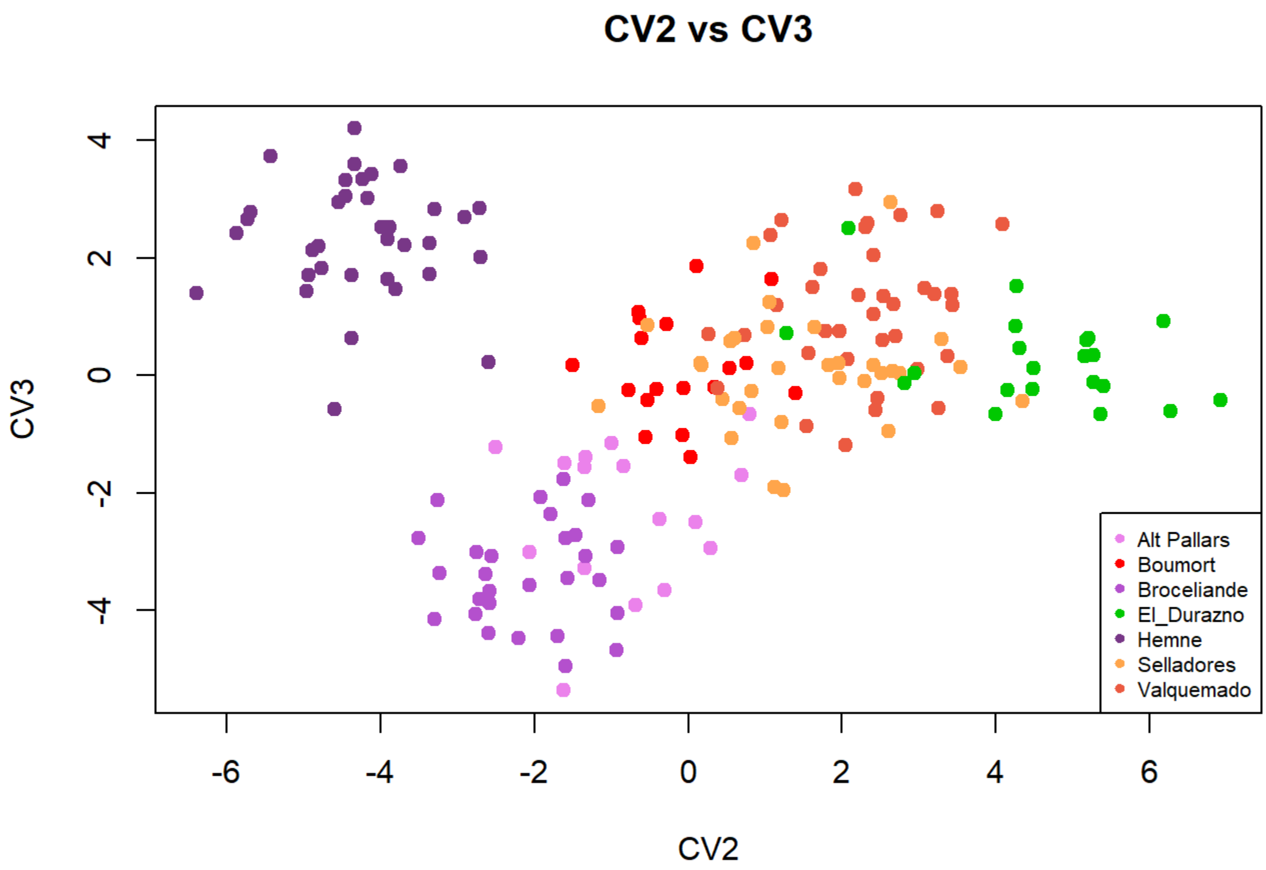
```
CVA_ALL_Cervus_pop <- CVA(Slided_MorphoGeom_ALL_Cervus$coords, ALL_Cervus_pop, rounds = 1000
0, p.adjust.method = "bonferroni")
```

```
## singular Covariance matrix: General inverse is used. Threshold for zero eigenvalue is 1e-1
0
```

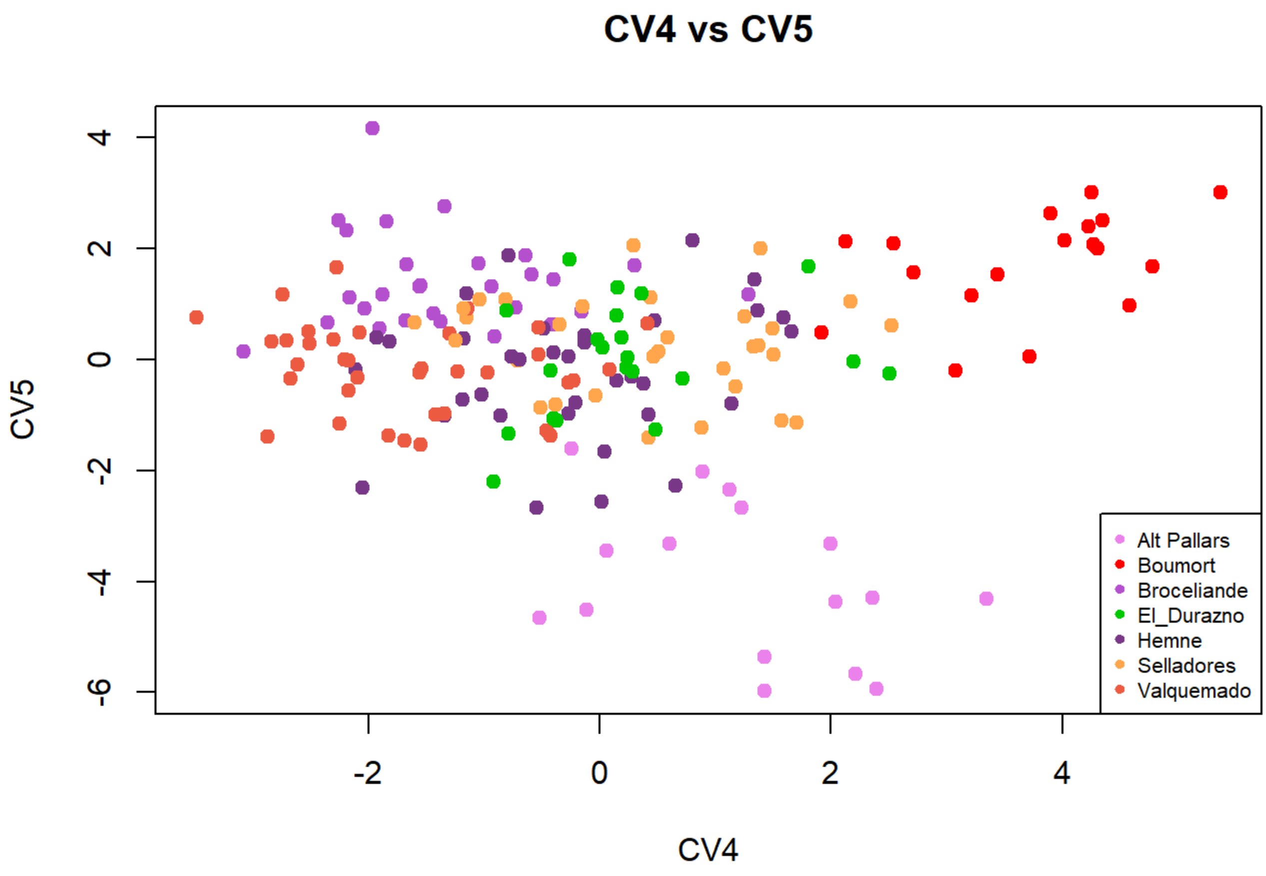
```
Colors_ALL_Cervus_pop <- c("Alt Pallars" = "violet", "Boumort" ="red",  "Broceliande" = "medi
umorchid3","El_Durazno" = "#00CC00", "Hemne" = "mediumorchid4","Selladores" ="tan1",  "Valque
mado" = "tomato2") # identify cervids by population

plot(CVA_ALL_Cervus_pop$CVscores, col = Colors_ALL_Cervus_pop[ALL_Cervus_pop], pch = 19)
legend("bottomright", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch
= 19, cex= 0.65)
```



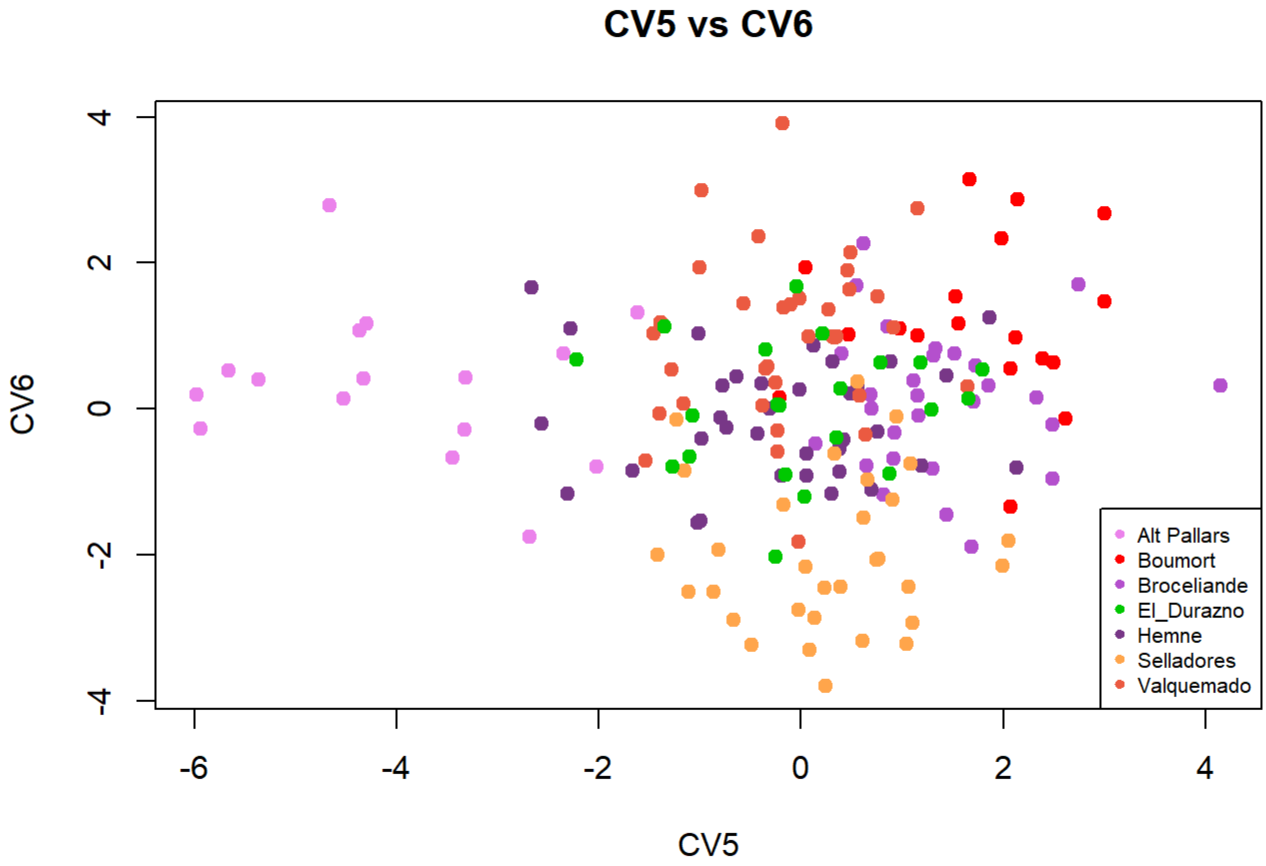
```
plot(CVA_ALL_Cervus_pop$CVscores[, 2], CVA_ALL_Cervus_pop$CVscores[, 3], col = Colors_ALL_Cervus_pop[ALL_Cervus_pop], pch = 19, xlab = "CV2", ylab = "CV3", main = "CV2 vs CV3")
legend("bottomright", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch = 19, cex = 0.65)
```



```
plot(CVA_ALL_Cervus_pop$CVscores[, 4], CVA_ALL_Cervus_pop$CVscores[, 5], col = Colors_ALL_Cervus_pop[ALL_Cervus_pop], pch = 19, xlab = "CV4", ylab = "CV5", main = "CV4 vs CV5")
legend("bottomright", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch = 19, cex = 0.65)
```



```
plot(CVA_ALL_Cervus_pop$CVscores[, 5], CVA_ALL_Cervus_pop$CVscores[, 6], col = Colors_ALL_Cer
vus_pop[ALL_Cervus_pop], pch = 19, xlab = "CV5", ylab = "CV6", main = "CV5 vs CV6")
legend("bottomright", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch
= 19, cex = 0.65)
```



```
CVA_ALL_Cervus_pop$Dist
```

```
## $GroupdistMaha
##             Alt Pallars   Boumort Broceliande El_Durazno     Hemne Selladores
## Boumort        6.983313                                                      
## Broceliande    6.426130  7.356153                                            
## El_Durazno    11.859980 12.573874   10.927054                                
## Hemne          7.717362  8.028752    6.526656  11.096325                     
## Selladores     6.401524  5.134595    7.102090  12.258207  8.386696           
## Valquemado     7.340559  6.399409    8.047958  12.761230  9.088418   3.924374
## 
## $GroupdistEuclid
##             Alt Pallars    Boumort Broceliande El_Durazno      Hemne Selladores
## Boumort      0.02724981                                                        
## Broceliande  0.03322852 0.03445544                                             
## El_Durazno   0.06297466 0.06453169  0.03613667                                 
## Hemne        0.03100907 0.03401471  0.01731893 0.04137734                      
## Selladores   0.03782210 0.02084816  0.03045885 0.05612440 0.03102700           
## Valquemado   0.03816263 0.01859471  0.03585875 0.06256169 0.03459698 0.01161137
## 
## $probsMaha
##             Alt Pallars    Boumort Broceliande El_Durazno      Hemne Selladores
## Boumort      0.00209979                                                        
## Broceliande  0.00209979 0.00209979                                             
## El_Durazno   0.00209979 0.00209979  0.00209979                                 
## Hemne        0.00209979 0.00209979  0.00209979 0.00209979                      
## Selladores   0.00209979 0.01049895  0.00209979 0.00209979 0.00209979           
## Valquemado   0.00209979 0.00209979  0.00209979 0.00209979 0.00209979 0.02099790
## 
## $probsEuclid
##             Alt Pallars    Boumort Broceliande El_Durazno      Hemne Selladores
## Boumort      0.03569643                                                        
## Broceliande  0.00209979 0.00209979                                             
## El_Durazno   0.00209979 0.00209979  0.00209979                                 
## Hemne        0.00209979 0.00209979  0.27297270 0.00209979                      
## Selladores   0.00209979 0.19528047  0.00209979 0.00209979 0.00209979           
## Valquemado   0.00209979 0.49345065  0.00209979 0.00209979 0.00209979 1.00000000
## 
## $p.adjust.method
## [1] "bonferroni"
```

```
CV_scores <- as.data.frame(CVA_ALL_Cervus_pop$CVscores)
CV_scores
```

```
##                       CV 1        CV 2        CV 3        CV 4        CV 5
## Alt.Pallars     1.33951382  0.09552410 -2.50443900 -0.23875631 -1.61631180
## Boumort        -3.63568346 -1.50321090  0.17370499  4.22883802  2.39079826
## Alt.Pallars.1   0.12379009 -1.35022075 -1.55974613  1.12714225 -2.34355853
## Boumort.1      -2.99810011  0.53312057  0.11680331  4.34869881  2.49716176
## Alt.Pallars.2  -0.72289750 -2.06924651 -3.01196917  2.39635027 -5.93721572
## Boumort.2      -2.61365317 -0.77804693 -0.25488956  3.07752098 -0.20937652
## Alt.Pallars.3   0.53783343  0.69772801 -1.69661407 -0.11203435 -4.51896616
## Alt.Pallars.4  -2.62568643 -0.99770310 -1.16433692 -0.52202700 -4.66072928
## Alt.Pallars.5  -2.81303321 -1.35025371 -3.27706468  1.42241030 -5.36694522
## Boumort.3      -2.19758922 -0.54816863 -1.04964818  1.91624604  0.47235969
## Alt.Pallars.6   0.22116232 -0.68338874 -3.91311711  2.36112388 -4.29337836
## Alt.Pallars.7  -1.27236191 -0.31354713 -3.66214305  1.42596376 -5.97666207
## Alt.Pallars.8  -1.38907325 -1.33186036 -1.39666792  0.06250579 -3.44140907
## Boumort.4      -2.29674957  0.34140595 -0.21162282  5.36901695  3.00689955
## Alt.Pallars.9   0.02502601 -0.83958499 -1.54857431  0.89316780 -2.02043541
## Boumort.5      -2.39978579 -0.52720749 -0.41901763  4.02221610  2.13774278
## Alt.Pallars.10  0.17707798 -1.60997912 -1.50528234  0.60178533 -3.31657810
## Boumort.6      -1.65354152 -0.41557892 -0.24398287  3.71702103  0.05079482
## Alt.Pallars.11 -0.95491416 -1.62539131 -5.36536439  2.21249720 -5.65886217
## Boumort.7      -2.21151843 -0.28551036  0.87124358  3.89765254  2.61682084
## Boumort.8      -1.68963860 -0.64126625  1.06631152  2.12332679  2.12161762
## Boumort.9      -2.17801101 -0.62713194  0.97316922  4.26829540  2.07276974
## Alt.Pallars.12 -1.12170933 -0.36879213 -2.45386204  1.22848279 -2.67927993
## Boumort.10     -3.39411172  1.39582583 -0.29752573  4.77955686  1.66601813
## Boumort.11     -1.35910577 -0.05930471 -0.21932537  4.58669432  0.97173543
## Boumort.12     -3.34848616  0.76539239  0.20107714  4.30544512  1.98876514
## Boumort.13     -1.20558506 -0.06975798 -1.01911446  3.21412548  1.15476572
## Boumort.14     -2.44927319  0.03391873 -1.39276394  2.53913915  2.07651865
## Boumort.15     -2.75417956 -0.61072552  0.62699741  3.44472136  1.52517415
## Boumort.16     -2.62505353  1.07792595  1.62860732  2.71626724  1.56216697
## Boumort.17     -1.60119073  0.11317031  1.86266460  4.25595264  2.99767888
## Broceliande     1.32354409 -1.59173079 -4.95337723 -2.03143832  0.91424451
## Broceliande.1  -1.10578957 -1.46931050 -2.71755799 -0.41492606  0.62115977
## Broceliande.2   1.65454309 -1.15520367 -3.48707090  0.30197872  1.68451454
## Broceliande.3  -0.16365286 -0.92059243 -4.04435197 -0.72429546  0.92836598
## Broceliande.4   0.23967932 -2.75871017 -4.06227270 -1.96143263  4.14854610
## Broceliande.5   0.23133359 -1.57340874 -3.45111430 -1.34509376  2.74350361
## Broceliande.6   1.30576675 -1.29903359 -2.12928762 -1.37862867  0.68619393
## Broceliande.7   1.48017408 -1.70421410 -4.44218968 -0.15987847  0.85904298
## Broceliande.8   1.69394505 -0.91856303 -2.93213149 -1.89955649  0.54649971
## Broceliande.9  -0.90159280 -1.62045684 -1.76509859 -0.64392221  1.85884270
## Broceliande.10  1.54468259 -3.23297432 -3.37589565 -1.04450775  1.72901507
## Broceliande.11  0.14721765 -1.79329405 -2.36959416  1.28974527  1.15570001
## Broceliande.12  0.58899473 -0.93459074 -4.68283986 -1.54490793  1.33441165
## Broceliande.13  1.19402708 -2.70855238 -3.80482847 -1.66692493  1.71183842
## Broceliande.14  2.25066517 -3.30265720 -4.14806589 -0.93753453  1.31018666
## Broceliande.15  1.09623902 -1.59273397 -2.77583894 -2.18858827  2.32535069
## Broceliande.16  0.96730761 -1.33399000 -3.08583992 -1.67818220  0.69977356
## Broceliande.17  1.15370887 -2.55701288 -3.07255468 -2.25576408  2.48966069
## Broceliande.18  0.41673503 -2.63056095 -3.38062339 -1.43632057  0.81495909
## Broceliande.19  1.29219234 -2.75569963 -3.00728828 -0.90767768  0.40520257
## Broceliande.20  1.28468819 -1.91863425 -2.08392873 -0.59006301  1.52071945
## Broceliande.21  0.96785129 -3.49994005 -2.77891368 -0.40106740  1.43761765
## Broceliande.22  1.87974209 -2.58442516 -3.87468561 -1.88082191  1.15975833
```

```
## Broceliande.23 -0.15336720 -2.19956229 -4.47658585 -2.35184217  0.65213598
## Broceliande.24  3.75209012 -2.59864989 -4.39542674 -1.55443664  1.29987473
## Broceliande.25  2.17210084 -3.25559452 -2.12861870 -3.07802899  0.14033650
## Broceliande.26  0.73414903 -2.58438112 -3.67960373 -2.16043370  1.11044891
## Broceliande.27  0.90970401 -2.06345969 -3.56638777 -1.84164930  2.48846217
## Selladores     -1.38768777  2.62717856  2.95309399  1.50493998  0.08611460
## Selladores.1   -2.52286786  2.29933941 -0.09520127  1.57723306 -1.10931348
## Selladores.2   -0.87964556  0.55849601 -1.07708567  1.38913557  1.99646408
## Selladores.3   -4.74554075  0.17095720  0.16783072  0.51311238  0.13222365
## Selladores.4   -2.48249589  1.22010362 -0.80319161  1.07289291 -0.17234532
## Selladores.5   -2.91485798  0.44916255 -0.40061255 -0.51449670 -0.86667007
## Selladores.6   -3.30655065  3.53886598  0.13111712 -0.71351342 -0.02736511
## Selladores.7   -3.36615396  0.55004174  0.58160988  2.16855622  1.04352783
## Selladores.8   -3.63666645  3.29807961  0.60703861 -1.15178267  0.74368835
## Alt.Pallars.13 -1.99564937  0.29686990 -2.94211391  1.99578870 -3.32357701
## Alt.Pallars.14 -1.75810426  0.79426476 -0.65994739  3.34213459 -4.32229105
## Alt.Pallars.15 -0.07574087 -2.50036577 -1.21946861  2.04423938 -4.36063335
## Hemne           1.77771198 -2.60051468  0.21867981  0.01496985 -2.56465497
## Hemne.1         2.94395160 -3.36670986  1.72013038 -1.92683754  0.38465130
## Hemne.2         1.85093375 -5.68883453  2.77707039 -0.85453732 -1.01363301
## Hemne.3         2.83147137 -4.96602057  1.43026566 -0.78888236  1.86073407
## Hemne.4         4.29008030 -3.90458706  2.31959823 -0.40112118  0.12437391
## Hemne.5         1.75486743 -4.16551728  3.01134670 -0.26570262  0.05437170
## Hemne.6         0.11755097 -4.76587912  1.82731587  1.59395196  0.75501087
## Hemne.7         1.72897917 -4.12355021  3.41879964 -0.76039922  0.05487652
## Hemne.8         3.33451876 -5.43506176  3.73274438  0.42214492 -0.99545041
## Hemne.9         2.33322978 -4.23890157  3.33645923 -2.05083818 -2.30567580
## Hemne.10        1.05223469 -3.99086831  2.52591887 -0.13133113  0.42267398
## Hemne.11        2.25925463 -3.74052714  3.56460801 -0.69084820 -0.01063997
## Hemne.12        3.08370303 -4.81156700  2.20500975 -0.54761041 -2.66786035
## Hemne.13        1.47360126 -4.44929856  3.04139796 -1.17859128  0.37792108
## Hemne.14        3.27526897 -4.33771666  4.19861820 -0.26722238 -0.98652006
## Hemne.15        3.28010982 -3.87836229  2.51998748 -0.13223287  0.30520921
## Hemne.16        1.86472054 -2.91096168  2.69284566 -0.48045960  0.55556617
## Hemne.17        1.95129841 -3.68395505  2.21490920  1.14045069 -0.79749641
## Hemne.18       -0.07065486 -2.70301983  2.01614239  1.36906729  0.88342554
## Hemne.19        2.71110432 -5.72525353  2.65812461  1.66117376  0.48927607
## Hemne.20        2.77885097 -4.37343099  0.62447573  0.65873905 -2.27768564
## Hemne.21        1.18346850 -4.38193327  1.70321909 -2.11092440 -0.18824871
## Hemne.22        0.84665569 -4.87925467  2.12174828 -1.02246569 -0.63383338
## Hemne.23        2.42604306 -4.93614565  1.69792672  0.27686589 -0.31363947
## Hemne.24        2.23341813 -6.39411298  1.39681041 -1.14865642  1.18900431
## Hemne.25        1.62518887 -2.71316935  2.84864215  0.14435939 -0.38738453
## Hemne.26        1.38580300 -4.45601283  3.32805925 -1.34193360 -1.01816397
## Hemne.27        2.81062281 -3.81053744  1.46387934 -1.81933061  0.31516057
## Hemne.28        2.95565765 -4.59424643 -0.57932542 -1.18754294 -0.73127304
## Hemne.29        2.64153450 -5.86626436  2.42570198  0.47915154  0.70021287
## Hemne.30        3.28260135 -3.29717592  2.83508660  0.04183977 -1.66677019
## Hemne.31        4.69575980 -4.34045055  3.60119296  1.33705787  1.44100121
## Hemne.32        2.35461474 -4.54419607  2.95015857 -0.20885633 -0.77669151
## Hemne.33        0.12930900 -3.90587351  1.63609771  0.80196845  2.12913734
## Hemne.34        1.76453700 -3.36800204  2.25375971  0.38235570 -0.43304982
## Valquemado     -3.00298446  1.15428207  1.19767544 -0.52587288  0.57733937
## Valquemado.1   -3.72741655  1.56969102  0.37363953 -2.09435309 -0.32594478
## Valquemado.2   -3.72061416  2.41059448  1.03694628 -2.83560847  0.31404478
## Valquemado.3   -3.02415861  2.18250480  3.16769603 -0.45625808 -1.28146759
```

```
## Valquemado.4   -4.63540125  3.37527994  0.31983791 -2.27099222  1.65061207
## Valquemado.5   -3.43602014  2.33031306  2.58345618 -1.29397279  0.46363084
## Valquemado.6   -4.80709745  0.37565667 -0.22879021 -2.50865256  0.27819872
## Valquemado.7   -3.33695736  2.52963796  0.59104794 -0.26428882 -0.42106114
## Valquemado.8   -2.52940562  2.66936636  1.21685858 -1.53690291 -0.16681478
## Valquemado.9   -4.20357072  1.07212461  2.37710439 -2.61627857 -0.10072662
## Valquemado.10  -2.74759986  2.05055901 -1.19440108 -2.17179316 -0.56751944
## Valquemado.11  -2.78637327  0.72899442  0.68242984 -1.13953150  0.91885635
## Valquemado.12  -4.78310943  3.41917270  1.38239959 -2.17296516 -0.01861516
## Valquemado.13  -3.57867792  2.98020215  0.10784649 -0.52795483  0.07394714
## Valquemado.14  -4.53517154  2.21362657  1.36480038 -2.66955524 -0.34855870
## Valquemado.15  -3.36970143  2.43574517 -0.59032417 -0.22877904 -0.38113089
## Valquemado.16  -3.62773712  2.76633256  2.72818202 -2.86840695 -1.40250512
## Valquemado.17  -3.76496484  2.46786673 -0.38927536 -1.22441688 -0.23179138
## Valquemado.18  -3.44043931  1.53281616 -0.86241591 -1.82626779 -1.37798865
## Valquemado.19  -3.91748075  1.61257115  1.49035319 -2.24483897 -1.15639235
## Valquemado.20  -5.18242182  2.40656119  2.04258492 -1.54740045 -1.53639351
## Valquemado.21  -3.24778831  2.54145433  1.34728743 -2.30000966  0.35440741
## Valquemado.22  -3.14377992  3.20667583  1.38061524 -2.70324866  0.33010051
## Valquemado.23  -2.41501907  1.21560411  2.63332913 -3.48640729  0.75346348
## Valquemado.24  -2.70686511  2.30444622  2.51618743 -0.96945056 -0.24764868
## Valquemado.25  -5.81358141  3.43221508  1.19190230 -2.20284420 -0.01278462
## Valquemado.26  -3.68929122  1.78367292  0.75441589 -2.51765161  0.49541358
## Valquemado.27  -4.59741219  3.07504516  1.48255456 -2.07697069  0.47857413
## Valquemado.28  -1.73889892  2.69854111  0.66306702  0.41060451  0.63666525
## Valquemado.29  -4.02235681  3.23935735  2.79390030 -1.41858345 -0.99732683
## Valquemado.30  -4.66825864  2.07698085  0.28048747 -1.55645646 -0.23300525
## Valquemado.31  -2.64197049  0.26138841  0.69995163 -0.42321006 -1.38577219
## Valquemado.32  -4.00794862  4.08835096  2.56600829 -1.68638621 -1.45854289
## Valquemado.33  -3.67657662  1.96688273  0.75259384 -1.33755175 -0.98077980
## Valquemado.34  -4.61803093  3.25157753 -0.55944054 -2.74086738  1.15636712
## Valquemado.35  -5.51052203  1.71464928  1.79968182  0.08496304 -0.18412207
## Selladores.9   -3.09245138  2.65626344  0.07644851 -1.17518607  0.90781348
## Selladores.10  -3.95936127  2.51007289  0.04189148  2.52109465  0.60653537
## Selladores.11  -2.07103489  2.75072729  0.03391438 -1.03817932  1.06834230
## Selladores.12  -1.37792224  0.66716597 -0.55292066  0.87885026 -1.23073769
## Selladores.13  -3.02128752  1.64137014  0.81150775 -0.80953255  1.08078641
## Selladores.14  -2.32884052  1.96587944 -0.05378289 -0.34545559  0.61924632
## Selladores.15  -3.46103407  4.34588174 -0.44497254  1.17320077 -0.48830283
## Selladores.16  -3.25867318  1.82655786  0.16500377 -1.59753831  0.66131898
## Selladores.17  -3.16799631 -1.16031373 -0.52520500  0.58563706  0.39266621
## Selladores.18  -3.47601231 -0.53379354  0.85841615  1.37661089  0.23911717
## Selladores.19  -2.54725079  0.60144162  0.63813929  1.49741951  0.55645296
## Selladores.20  -5.40390220  0.82850188 -0.27822231  0.46672630  0.04874954
## Selladores.21  -2.73802820  2.60827913 -0.95962939 -0.37669369 -0.81067214
## Selladores.22  -3.66151278  1.24353178 -1.96133805  0.44068019  1.10269332
## Selladores.23  -3.56029650  1.02661046  0.81824081 -0.03826529 -0.66240787
## Selladores.24  -3.22104051  0.85507177  2.24669677 -1.24144362  0.33317940
## Selladores.25  -2.97930760  2.40956639  0.16561927  1.33464173  0.23376835
## Selladores.26  -4.02953140  1.17100430  0.11634947  0.29563977  2.05597855
## Selladores.27  -3.61868255  0.16019295  0.20318865  1.24995027  0.76534459
## Selladores.28  -2.43579965  1.95565225  0.19771514  1.70205574 -1.14901898
## Selladores.29  -3.73250885  1.12371434 -1.91362273 -0.14409485  0.94319438
## Selladores.30  -3.57686610  1.05945970  1.24190785  0.42382738 -1.41547336
## El_Durazno      9.21670204  5.15195285  0.32925412 -0.42741925 -0.20910227
## El_Durazno.1    6.33932221  4.30698324  0.45924396  0.23883350  0.03325439
```

```
## El_Durazno.2    9.44653991  5.40272978 -0.18361784 -0.40235223 -1.07568987
## El_Durazno.3    7.84553747  2.94071992  0.04226987  0.48059964 -1.26907217
## El_Durazno.4    8.43348209  1.28358327  0.71772009  0.35983655  1.18029035
## El_Durazno.5    6.94678202  4.49586699  0.11484240  0.71402663 -0.35215155
## El_Durazno.6    7.25939185  3.99432155 -0.66877539 -0.26256976  1.79831769
## El_Durazno.7    9.50118768  6.92108305 -0.42271810 -0.01385915  0.35706298
## El_Durazno.8    8.58395305  4.25230118  0.82639752  1.80303742  1.65985780
## El_Durazno.9    9.64672009  5.27434863 -0.11988458  0.02439156  0.21724330
## El_Durazno.10   9.11068681  4.26686279  1.51445826 -0.78906066 -1.34884154
## El_Durazno.11   8.29956143  6.27475274 -0.60995122 -0.37073632 -1.10449741
## El_Durazno.12   8.01224336  4.15735218 -0.24891455  0.15357831  1.29196344
## El_Durazno.13  10.04942883  5.36245364 -0.67096094 -0.80571457  0.87785802
## El_Durazno.14   9.27611184  6.17857848  0.92551632  2.19661471 -0.04423576
## El_Durazno.15  10.04637948  5.21124419  0.62680515  2.50805581 -0.25139258
## El_Durazno.16  10.21104998  4.47595338 -0.24198339  0.28539214 -0.23082996
## El_Durazno.17   9.24872578  5.26454208  0.34092661  0.19307542  0.38922855
## El_Durazno.18   9.25675871  5.18426829  0.60297594  0.14747810  0.78386631
## El_Durazno.19   7.03281657  2.81191923 -0.13279902  0.23028905 -0.15237011
## El_Durazno.20   6.85537349  2.08932562  2.51164562 -0.91344060 -2.21426682
##                         CV 6
## Alt.Pallars     1.3161587228
## Boumort         0.6925142666
## Alt.Pallars.1   0.7634589449
## Boumort.1       0.6345277812
## Alt.Pallars.2  -0.2692674834
## Boumort.2       0.1533894424
## Alt.Pallars.3   0.1401580605
## Alt.Pallars.4   2.7891176088
## Alt.Pallars.5   0.4020339408
## Boumort.3       1.0193623947
## Alt.Pallars.6   1.1678093714
## Alt.Pallars.7   0.1982517980
## Alt.Pallars.8  -0.6665174608
## Boumort.4       2.6810541624
## Alt.Pallars.9  -0.7877562988
## Boumort.5       2.8722480681
## Alt.Pallars.10  0.4324373063
## Boumort.6       1.9346438178
## Alt.Pallars.11  0.5277995441
## Boumort.7      -0.1263495536
## Boumort.8       0.9753246716
## Boumort.9       0.5498401768
## Alt.Pallars.12 -1.7467772600
## Boumort.10      3.1403917952
## Boumort.11      1.1019232092
## Boumort.12      2.3383160353
## Boumort.13      1.0108417516
## Boumort.14     -1.3416009130
## Boumort.15      1.5429399997
## Boumort.16      1.1766301137
## Boumort.17      1.4690421639
## Broceliande    -0.6849962365
## Broceliande.1   2.2699806869
## Broceliande.2  -1.8851719207
## Broceliande.3  -0.3272145812
## Broceliande.4   0.3139651286
```

```
## Broceliande.5   1.7026031914
## Broceliande.6   0.1972474271
## Broceliande.7   1.1348925715
## Broceliande.8   1.6921962931
## Broceliande.9   0.3213100104
## Broceliande.10  0.5921372388
## Broceliande.11  0.1799016410
## Broceliande.12  0.8295257676
## Broceliande.13  0.0971297051
## Broceliande.14  0.7318299249
## Broceliande.15  0.1547023876
## Broceliande.16  0.0116990825
## Broceliande.17 -0.9584683184
## Broceliande.18 -1.1698416217
## Broceliande.19  0.7552059764
## Broceliande.20  0.7524164052
## Broceliande.21 -1.4417285521
## Broceliande.22 -0.0848929156
## Broceliande.23 -0.7805156082
## Broceliande.24 -0.8196293319
## Broceliande.25 -0.4700202172
## Broceliande.26  0.3956367787
## Broceliande.27 -0.2095889232
## Selladores     -3.3013149713
## Selladores.1   -2.5027875598
## Selladores.2   -2.1484952308
## Selladores.3   -2.8627074726
## Selladores.4   -1.3093072986
## Selladores.5   -2.5020365409
## Selladores.6   -2.7501843400
## Selladores.7   -3.2111300609
## Selladores.8   -2.0596337717
## Alt.Pallars.13 -0.2770979584
## Alt.Pallars.14  0.4184260627
## Alt.Pallars.15  1.0799308661
## Hemne          -0.1938331266
## Hemne.1        -0.8614080430
## Hemne.2         1.0289853956
## Hemne.3         1.2566798143
## Hemne.4         0.8646459612
## Hemne.5        -0.9163177043
## Hemne.6        -0.3081879092
## Hemne.7        -0.6169957259
## Hemne.8        -1.5364213962
## Hemne.9        -1.1539285141
## Hemne.10       -0.4206053537
## Hemne.11        0.2613443875
## Hemne.12        1.6611945165
## Hemne.13       -0.5384955666
## Hemne.14       -0.4128470181
## Hemne.15       -1.1613033957
## Hemne.16        0.3132680524
## Hemne.17       -0.1227422048
## Hemne.18        0.6478615350
## Hemne.19        0.2154502961
## Hemne.20        1.1080053310
```

```
## Hemne.21       -0.9193699831
## Hemne.22        0.4471711293
## Hemne.23        0.0007468155
## Hemne.24       -0.7772147216
## Hemne.25        0.3425306234
## Hemne.26       -1.5601843419
## Hemne.27        0.6535037574
## Hemne.28       -0.2508247853
## Hemne.29       -1.1063041562
## Hemne.30       -0.8445880021
## Hemne.31        0.4641361637
## Hemne.32        0.3210158483
## Hemne.33       -0.8056977153
## Hemne.34       -0.3345714104
## Valquemado      0.1778255282
## Valquemado.1    0.5839568964
## Valquemado.2    0.9880093757
## Valquemado.3    0.5442258245
## Valquemado.4    0.3035554812
## Valquemado.5    1.8919683817
## Valquemado.6    1.3625439372
## Valquemado.7    2.3666404849
## Valquemado.8    1.3942726661
## Valquemado.9    1.4375110503
## Valquemado.10   1.4462548858
## Valquemado.11   1.1143646078
## Valquemado.12  -1.8205004498
## Valquemado.13   0.9866287485
## Valquemado.14   0.5524211106
## Valquemado.15   0.0496689647
## Valquemado.16  -0.0574647688
## Valquemado.17  -0.2969922790
## Valquemado.18   1.1684921632
## Valquemado.19   0.0755551059
## Valquemado.20  -0.7094553950
## Valquemado.21   0.9916962138
## Valquemado.22   0.9796347345
## Valquemado.23   1.5401924325
## Valquemado.24   0.3613748609
## Valquemado.25   1.5089249641
## Valquemado.26   2.1469631328
## Valquemado.27   1.6298426986
## Valquemado.28  -0.3535009406
## Valquemado.29   1.9375629437
## Valquemado.30  -0.5838319442
## Valquemado.31   1.1901499152
## Valquemado.32   1.0299641139
## Valquemado.33   3.0006215756
## Valquemado.34   2.7453749942
## Valquemado.35   3.9067113527
## Selladores.9   -1.2412920964
## Selladores.10  -3.1789900731
## Selladores.11  -2.4341342462
## Selladores.12  -0.1490028584
## Selladores.13  -0.7444144538
## Selladores.14  -1.4900969289
```

```
## Selladores.15  -3.2360215659
## Selladores.16  -0.9644627459
## Selladores.17  -2.4370688558
## Selladores.18  -3.7949972178
## Selladores.19   0.3773975651
## Selladores.20  -2.1610114375
## Selladores.21  -1.9259531311
## Selladores.22  -2.9220543629
## Selladores.23  -2.8820107509
## Selladores.24  -0.6069095901
## Selladores.25  -2.4531145875
## Selladores.26  -1.8019566840
## Selladores.27  -2.0490581264
## Selladores.28  -0.8398761087
## Selladores.29  -0.1026383976
## Selladores.30  -1.9995579674
## El_Durazno      0.0478799859
## El_Durazno.1   -1.2075742979
## El_Durazno.2   -0.0893174431
## El_Durazno.3   -0.7859018724
## El_Durazno.4    0.6374702023
## El_Durazno.5    0.8106281779
## El_Durazno.6    0.5443067465
## El_Durazno.7   -0.3976439470
## El_Durazno.8    0.1413765938
## El_Durazno.9    1.0338316258
## El_Durazno.10   1.1337611919
## El_Durazno.11  -0.6465122126
## El_Durazno.12  -0.0131938682
## El_Durazno.13  -0.8846416716
## El_Durazno.14   1.6804942897
## El_Durazno.15  -2.0232429157
## El_Durazno.16   0.0588797562
## El_Durazno.17   0.2824009259
## El_Durazno.18   0.6336380656
## El_Durazno.19  -0.9022599195
## El_Durazno.20   0.6810633945
```

```
CV_scores$Pop <- ALL_Cervus_pop
CV1 <- CV_scores[,1]
CV2 <- CV_scores[,2]
CV3 <- CV_scores[,3]
CV4 <- CV_scores[,4]
CV5 <- CV_scores[,5]
CV6 <- CV_scores[,6]

anova_result_CV1 <- aov(CV1 ~ Pop, data = CV_scores)
summary(anova_result_CV1)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## Pop           6   2662   443.6   443.6 <2e-16 ***
## Residuals   178    178     1.0
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_result_CV2 <- aov(CV2 ~ Pop, data = CV_scores)
summary(anova_result_CV2)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)    
## Pop           6   1456   242.6   242.6 <2e-16 ***
## Residuals   178    178     1.0                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_result_CV3 <- aov(CV3 ~ Pop, data = CV_scores)
summary(anova_result_CV3)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)    
## Pop           6  646.6   107.8   107.8 <2e-16 ***
## Residuals   178  178.0     1.0                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_result_CV4 <- aov(CV4 ~ Pop, data = CV_scores)
summary(anova_result_CV4)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)    
## Pop           6  430.1   71.68   71.69 <2e-16 ***
## Residuals   178  178.0    1.00                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_result_CV5 <- aov(CV5 ~ Pop, data = CV_scores)
summary(anova_result_CV5)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)    
## Pop           6  366.9   61.14   61.14 <2e-16 ***
## Residuals   178  178.0    1.00                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_result_CV6 <- aov(CV6 ~ Pop, data = CV_scores)
summary(anova_result_CV6)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)    
## Pop           6  187.5   31.25   31.25 <2e-16 ***
## Residuals   178  178.0    1.00                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
###Results ###############
# p-value <2e-16 : For PC1-6, shape differences between the 7 populations are significative
##########################
duncan_result_CV1 <- duncan.test(anova_result_CV1, "Pop", console = TRUE)
```

```
##
## Study: anova_result_CV1 ~ "Pop"
##
## Duncan's new multiple range test
## for CV1
##
## Mean Square Error:  1
##
## Pop,  means
##
##                    CV1       std  r         Min        Max
## Alt Pallars -0.7690479 1.1788299 16 -2.81303321  1.3395138
## Boumort     -2.3672920 0.6997422 18 -3.63568346 -1.2055851
## Broceliande  0.9984528 0.9884370 28 -1.10578957  3.7520901
## El_Durazno   8.6008931 1.1733898 21  6.33932221 10.2110500
## Hemne        2.1988000 1.0780208 35 -0.07065486  4.6957598
## Selladores  -3.0955422 0.9289286 31 -5.40390220 -0.8796456
## Valquemado  -3.7404334 0.9183188 36 -5.81358141 -1.7388989
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                    CV1 groups
## El_Durazno   8.6008931      a
## Hemne        2.1988000      b
## Broceliande  0.9984528      c
## Alt Pallars -0.7690479      d
## Boumort     -2.3672920      e
## Selladores  -3.0955422      f
## Valquemado  -3.7404334      g
```

```
print(duncan_result_CV1)
```

```
## $statistics
##   MSerror  Df        Mean           CV
##         1 178 3.00344e-14 3.329516e+15
## 
## $parameters
##     test name.t ntr alpha
##   Duncan    Pop   7  0.05
## 
## $duncan
## NULL
## 
## $means
##                    CV1       std  r         Min        Max        Q25
## Alt Pallars -0.7690479 1.1788299 16 -2.81303321  1.3395138 -1.4813310
## Boumort     -2.3672920 0.6997422 18 -3.63568346 -1.2055851 -2.7218981
## Broceliande  0.9984528 0.9884370 28 -1.10578957  3.7520901  0.3724711
## El_Durazno   8.6008931 1.1733898 21  6.33932221 10.2110500  7.8455375
## Hemne        2.1988000 1.0780208 35 -0.07065486  4.6957598  1.6770840
## Selladores  -3.0955422 0.9289286 31 -5.40390220 -0.8796456 -3.5977743
## Valquemado  -3.7404334 0.9183188 36 -5.81358141 -1.7388989 -4.5507317
##                    Q50        Q75
## Alt Pallars -0.8389058  0.1371121
## Boumort     -2.3482677 -1.8117317
## Broceliande  1.1249739  1.4963012
## El_Durazno   9.1106868  9.4465399
## Hemne        2.2592546  2.8877115
## Selladores  -3.2210405 -2.5350593
## Valquemado  -3.6829339 -3.1138746
## 
## $comparison
## NULL
## 
## $groups
##                    CV1 groups
## El_Durazno   8.6008931      a
## Hemne        2.1988000      b
## Broceliande  0.9984528      c
## Alt Pallars -0.7690479      d
## Boumort     -2.3672920      e
## Selladores  -3.0955422      f
## Valquemado  -3.7404334      g
## 
## attr(,"class")
## [1] "group"
```

```
duncan_result_CV2 <- duncan.test(anova_result_CV2, "Pop", console = TRUE)
```

```
##
## Study: anova_result_CV2 ~ "Pop"
##
## Duncan's new multiple range test
## for CV2
##
## Mean Square Error:  1
##
## Pop,  means
##
##                    CV2       std  r        Min        Max
## Alt Pallars -0.8222467 0.9656373 16 -2.5003658  0.7942648
## Boumort     -0.1002861 0.7200215 18 -1.5032109  1.3958258
## Broceliande -2.0913549 0.7804819 28 -3.4999401 -0.9185630
## El_Durazno   4.5381497 1.3766773 21  1.2835833  6.9210830
## Hemne       -4.2670832 0.9094461 35 -6.3941130 -2.6005147
## Selladores   1.4975827 1.2216779 31 -1.1603137  4.3458817
## Valquemado   2.2539095 0.8936584 36  0.2613884  4.0883510
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                    CV2 groups
## El_Durazno   4.5381497      a
## Valquemado   2.2539095      b
## Selladores   1.4975827      c
## Boumort     -0.1002861      d
## Alt Pallars -0.8222467      e
## Broceliande -2.0913549      f
## Hemne       -4.2670832      g
```

```
print(duncan_result_CV2)
```

```
## $statistics
##   MSerror  Df         Mean           CV
##         1 178 1.336887e-13 7.480064e+14
## 
## $parameters
##      test name.t ntr alpha
##    Duncan    Pop   7  0.05
## 
## $duncan
## NULL
## 
## $means
##                    CV2       std  r        Min        Max        Q25        Q50
## Alt Pallars -0.8222467 0.9656373 16 -2.5003658  0.7942648 -1.4151851 -0.9186440
## Boumort     -0.1002861 0.7200215 18 -1.5032109  1.3958258 -0.5950863 -0.1776342
## Broceliande -2.0913549 0.7804819 28 -3.4999401 -0.9185630 -2.6500588 -1.9910470
## El_Durazno   4.5381497 1.3766773 21  1.2835833  6.9210830  4.1573522  4.4958670
## Hemne       -4.2670832 0.9094461 35 -6.3941130 -2.6005147 -4.7887231 -4.3377167
## Selladores   1.4975827 1.2216779 31 -1.1603137  4.3458817  0.6343038  1.2201036
## Valquemado   2.2539095 0.8936584 36  0.2613884  4.0883510  1.6891297  2.3684371
##                    Q75
## Alt Pallars -0.2112793
## Boumort      0.2843470
## Broceliande -1.5473842
## El_Durazno   5.2743486
## Hemne       -3.7755323
## Selladores   2.4598196
## Valquemado   2.8198000
## 
## $comparison
## NULL
## 
## $groups
##                    CV2 groups
## El_Durazno   4.5381497      a
## Valquemado   2.2539095      b
## Selladores   1.4975827      c
## Boumort     -0.1002861      d
## Alt Pallars -0.8222467      e
## Broceliande -2.0913549      f
## Hemne       -4.2670832      g
## 
## attr(,"class")
## [1] "group"
```

```
duncan_result_CV3 <- duncan.test(anova_result_CV3, "Pop", console = TRUE)
```

```
##
## Study: anova_result_CV3 ~ "Pop"
##
## Duncan's new multiple range test
## for CV3
##
## Mean Square Error:  1
##
## Pop,  means
##
##                     CV3       std  r        Min        Max
## Alt Pallars -2.36754444 1.2594101 16 -5.3653644 -0.6599474
## Boumort      0.13403825 0.8970748 18 -1.3927639  1.8626646
## Broceliande -3.38114188 0.8546667 28 -4.9533772 -1.7650986
## El_Durazno   0.27202147 0.7727896 21 -0.6709609  2.5116456
## Hemne        2.33535444 1.0077842 35 -0.5793254  4.1986182
## Selladores   0.09644984 0.9944564 31 -1.9613380  2.9530940
## Valquemado   1.10278316 1.1296219 36 -1.1944011  3.1676960
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                     CV3 groups
## Hemne        2.33535444      a
## Valquemado   1.10278316      b
## El_Durazno   0.27202147      c
## Boumort      0.13403825      c
## Selladores   0.09644984      c
## Alt Pallars -2.36754444      d
## Broceliande -3.38114188      e
```

```
print(duncan_result_CV3)
```

```
## $statistics
##   MSerror  Df          Mean            CV
##         1 178 -2.052582e-13 -4.871913e+14
## 
## $parameters
##     test name.t ntr alpha
##   Duncan    Pop   7  0.05
## 
## $duncan
## NULL
## 
## $means
##                     CV3       std  r        Min        Max        Q25
## Alt Pallars -2.36754444 1.2594101 16 -5.3653644 -0.6599474 -3.0782431
## Boumort      0.13403825 0.8970748 18 -1.3927639  1.8626646 -0.2868667
## Broceliande -3.38114188 0.8546667 28 -4.9533772 -1.7650986 -4.0488322
## El_Durazno   0.27202147 0.7727896 21 -0.6709609  2.5116456 -0.2419834
## Hemne        2.33535444 1.0077842 35 -0.5793254  4.1986182  1.7116747
## Selladores   0.09644984 0.9944564 31 -1.9613380  2.9530940 -0.4227925
## Valquemado   1.10278316 1.1296219 36 -1.1944011  3.1676960  0.3601891
##                     Q50        Q75
## Alt Pallars -2.07523806 -1.4781287
## Boumort     -0.04740975  0.8101820
## Broceliande -3.41586885 -2.7781450
## El_Durazno   0.11484240  0.6268051
## Hemne        2.42570198  2.9807526
## Selladores   0.11634947  0.5943242
## Valquemado   1.19478887  1.8604076
## 
## $comparison
## NULL
## 
## $groups
##                     CV3 groups
## Hemne        2.33535444      a
## Valquemado   1.10278316      b
## El_Durazno   0.27202147      c
## Boumort      0.13403825      c
## Selladores   0.09644984      c
## Alt Pallars -2.36754444      d
## Broceliande -3.38114188      e
## 
## attr(,"class")
## [1] "group"
```

```
duncan_result_CV4 <- duncan.test(anova_result_CV4, "Pop", console = TRUE)
```

```
##
## Study: anova_result_CV4 ~ "Pop"
##
## Duncan's new multiple range test
## for CV4
##
## Mean Square Error:  1
##
## Pop,  means
##
##                    CV4       std  r        Min       Max
## Alt Pallars  1.2650484 1.1039640 16 -0.5220270 3.3421346
## Boumort      3.7117075 0.9470950 18  1.9162460 5.3690170
## Broceliande -1.3030785 0.9206213 28 -3.0780290 1.2897453
## El_Durazno   0.2547646 0.9166718 21 -0.9134406 2.5080558
## Hemne       -0.2569208 1.0240165 35 -2.1109244 1.6611738
## Selladores   0.4201943 1.1078789 31 -1.5975383 2.5210947
## Valquemado  -1.6652545 0.9607455 36 -3.4864073 0.4106045
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                    CV4 groups
## Boumort      3.7117075      a
## Alt Pallars  1.2650484      b
## Selladores   0.4201943      c
## El_Durazno   0.2547646     cd
## Hemne       -0.2569208      d
## Broceliande -1.3030785      e
## Valquemado  -1.6652545      e
```

```
print(duncan_result_CV4)
```

```
## $statistics
##   MSerror  Df          Mean            CV
##         1 178 -1.716102e-13 -5.827159e+14
## 
## $parameters
##     test name.t ntr alpha
##   Duncan    Pop   7  0.05
## 
## $duncan
## NULL
## 
## $means
##                    CV4       std  r        Min       Max        Q25        Q50
## Alt Pallars  1.2650484 1.1039640 16 -0.5220270 3.3421346  0.4669654  1.3254465
## Boumort      3.7117075 0.9470950 18  1.9162460 5.3690170  3.1116721  3.9599343
## Broceliande -1.3030785 0.9206213 28 -3.0780290 1.2897453 -1.9150255 -1.4906142
## El_Durazno   0.2547646 0.9166718 21 -0.9134406 2.5080558 -0.3707363  0.1535783
## Hemne       -0.2569208 1.0240165 35 -2.1109244 1.6611738 -0.9385015 -0.2657026
## Selladores   0.4201943 1.1078789 31 -1.5975383 2.5210947 -0.4455952  0.4667263
## Valquemado  -1.6652545 0.9607455 36 -3.4864073 0.4106045 -2.3521704 -1.7563270
##                    Q75
## Alt Pallars  2.0863038
## Boumort      4.2961577
## Broceliande -0.7042021
## El_Durazno   0.3598365
## Hemne        0.4022503
## Selladores   1.3556263
## Valquemado  -1.0970113
## 
## $comparison
## NULL
## 
## $groups
##                    CV4 groups
## Boumort      3.7117075      a
## Alt Pallars  1.2650484      b
## Selladores   0.4201943      c
## El_Durazno   0.2547646     cd
## Hemne       -0.2569208      d
## Broceliande -1.3030785      e
## Valquemado  -1.6652545      e
## 
## attr(,"class")
## [1] "group"
```

```
duncan_result_CV5 <- duncan.test(anova_result_CV5, "Pop", console = TRUE)
```

```
##
## Study: anova_result_CV5 ~ "Pop"
##
## Duncan's new multiple range test
## for CV5
##
## Mean Square Error:  1
##
## Pop,  means
##
##                     CV5       std  r        Min       Max
## Alt Pallars -3.98980208 1.3815442 16 -5.9766621 -1.616312
## Boumort      1.72780065 0.9335520 18 -0.2093765  3.006900
## Broceliande  1.38487021 0.8581192 28  0.1403365  4.148546
## El_Durazno   0.01602347 1.0434946 21 -2.2142668  1.798318
## Hemne       -0.22074470 1.1695278 35 -2.6678603  2.129137
## Selladores   0.24789997 0.8918603 31 -1.4154734  2.055979
## Valquemado  -0.17597977 0.8022674 36 -1.5363935  1.650612
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                     CV5 groups
## Boumort      1.72780065      a
## Broceliande  1.38487021      a
## Selladores   0.24789997      b
## El_Durazno   0.01602347      b
## Valquemado  -0.17597977      b
## Hemne       -0.22074470      b
## Alt Pallars -3.98980208      c
```

```
print(duncan_result_CV5)
```

```
## $statistics
##   MSerror  Df          Mean            CV
##         1 178 -1.291402e-13 -7.743525e+14
## 
## $parameters
##     test name.t ntr alpha
##   Duncan    Pop   7  0.05
## 
## $duncan
## NULL
## 
## $means
##                     CV5       std  r        Min       Max        Q25
## Alt Pallars -3.98980208 1.3815442 16 -5.9766621 -1.616312 -4.8372833
## Boumort      1.72780065 0.9335520 18 -0.2093765  3.006900  1.2473678
## Broceliande  1.38487021 0.8581192 28  0.1403365  4.148546  0.7861627
## El_Durazno   0.01602347 1.0434946 21 -2.2142668  1.798318 -0.3521515
## Hemne       -0.22074470 1.1695278 35 -2.6678603  2.129137 -0.8920082
## Selladores   0.24789997 0.8918603 31 -1.4154734  2.055979 -0.3303241
## Valquemado  -0.17597977 0.8022674 36 -1.5363935  1.650612 -0.6708345
##                     Q50        Q75
## Alt Pallars -4.30783470 -3.1572536
## Boumort      2.03076744  2.3275344
## Broceliande  1.22981653  1.7161326
## El_Durazno  -0.04423576  0.7838663
## Hemne       -0.01063997  0.4559750
## Selladores   0.33317940  0.8365790
## Valquemado  -0.17546843  0.3817133
## 
## $comparison
## NULL
## 
## $groups
##                     CV5 groups
## Boumort      1.72780065      a
## Broceliande  1.38487021      a
## Selladores   0.24789997      b
## El_Durazno   0.01602347      b
## Valquemado  -0.17597977      b
## Hemne       -0.22074470      b
## Alt Pallars -3.98980208      c
## 
## attr(,"class")
## [1] "group"
```

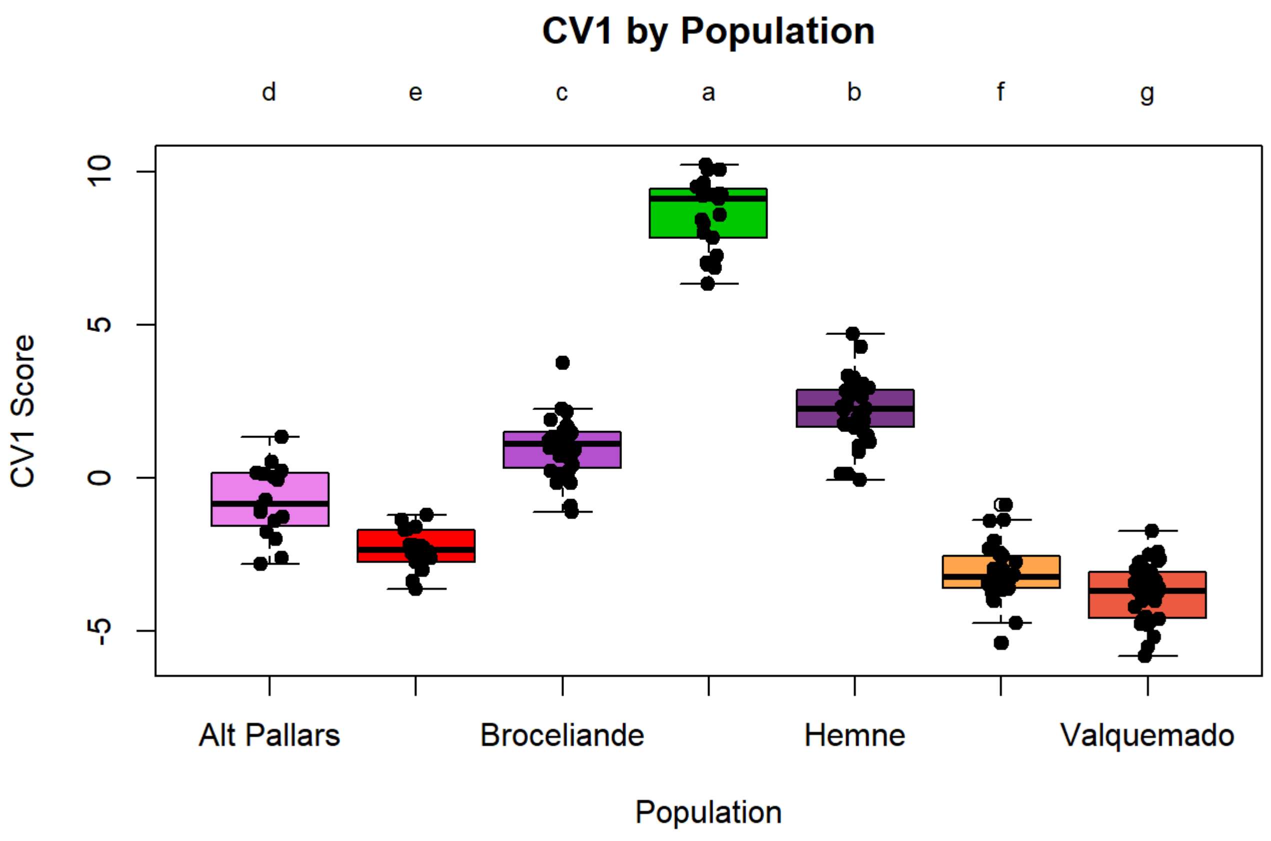
```
duncan_result_CV6 <- duncan.test(anova_result_CV6, "Pop", console = TRUE)
```

```
##
## Study: anova_result_CV6 ~ "Pop"
##
## Duncan's new multiple range test
## for CV6
##
## Mean Square Error:  1
##
## Pop,  means
##
##                     CV6       std  r       Min       Max
## Alt Pallars  0.34301036 1.0285398 16 -1.746777 2.7891176
## Boumort      1.21250219 1.1172733 18 -1.341601 3.1403918
## Broceliande  0.11786829 0.9629634 28 -1.885172 2.2699807
## El_Durazno   0.03502109 0.8897592 21 -2.023243 1.6804943
## Hemne       -0.15015147 0.8173128 35 -1.560184 1.6611945
## Selladores  -1.98983296 1.0543023 31 -3.794997 0.3773976
## Valquemado   0.98864343 1.1209868 36 -1.820500 3.9067114
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                     CV6 groups
## Boumort      1.21250219      a
## Valquemado   0.98864343      a
## Alt Pallars  0.34301036      b
## Broceliande  0.11786829      b
## El_Durazno   0.03502109      b
## Hemne       -0.15015147      b
## Selladores  -1.98983296      c
```

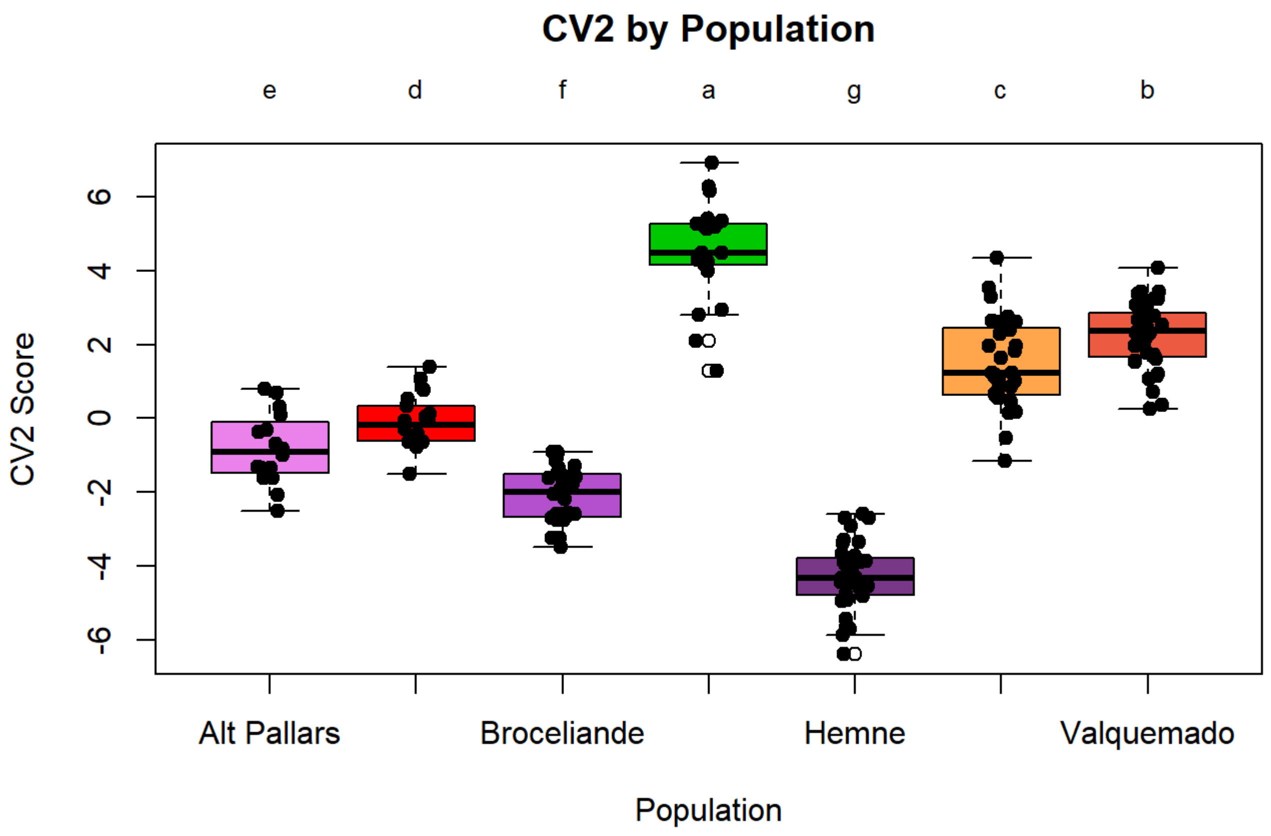
```
print(duncan_result_CV6)
```

```
## $statistics
##   MSerror  Df         Mean           CV
##         1 178 2.203547e-14 4.538138e+15
##
## $parameters
##     test name.t ntr alpha
##   Duncan    Pop   7  0.05
##
## $duncan
## NULL
##
## $means
##                      CV6       std  r       Min       Max        Q25         Q50
## Alt Pallars  0.34301036 1.0285398 16 -1.746777 2.7891176 -0.2712251  0.41023000
## Boumort      1.21250219 1.1172733 18 -1.341601 3.1403918  0.6490244  1.06064280
## Broceliande  0.11786829 0.9629634 28 -1.885172 2.2699807 -0.5237642  0.16730201
## El_Durazno   0.03502109 0.8897592 21 -2.023243 1.6804943 -0.6465122  0.05887976
## Hemne       -0.15015147 0.8173128 35 -1.560184 1.6611945 -0.8251429 -0.25082479
## Selladores  -1.98983296 1.0543023 31 -3.794997 0.3773976 -2.8064459 -2.14849523
## Valquemado   0.98864343 1.1209868 36 -1.820500 3.9067114  0.2721230  1.01083016
##                    Q75
## Alt Pallars  0.8425769
## Boumort      1.8367179
## Broceliande  0.7369765
## El_Durazno   0.6374702
## Hemne        0.3948509
## Selladores  -1.2752997
## Valquemado   1.5167418
##
## $comparison
## NULL
##
## $groups
##                      CV6 groups
## Boumort      1.21250219      a
## Valquemado   0.98864343      a
## Alt Pallars  0.34301036      b
## Broceliande  0.11786829      b
## El_Durazno   0.03502109      b
## Hemne       -0.15015147      b
## Selladores  -1.98983296      c
##
## attr(,"class")
## [1] "group"
```

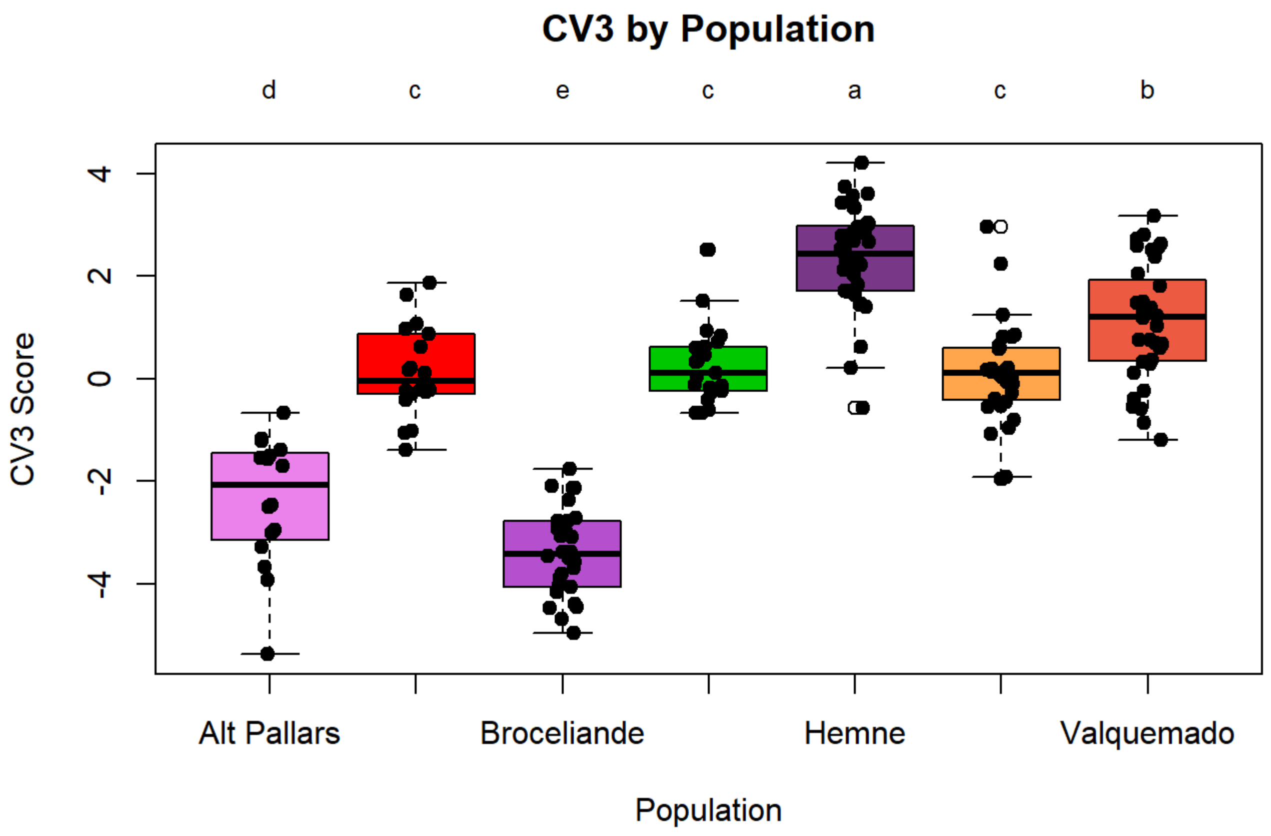
```
Colors_ALL_Cervus_pop <- c("Alt Pallars" = "violet", "Boumort" ="red",  "Broceliande" = "mediumorchid3","El_Durazno" = "#00CC00", "Hemne" = "mediumorchid4","Selladores" ="tan1",  "Valquemado" = "tomato2") # identify cervids by population

duncan_labels_CV1 <- duncan_result_CV1$groups
duncan_labels_CV1 <- duncan_labels_CV1[order(rownames(duncan_labels_CV1)), ]
CV_scores$labels <- factor(duncan_labels_CV1$groups[match(CV_scores$Pop, rownames(duncan_labels_CV1))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(CV1 ~ Pop, data = CV_scores, main = "CV1 by Population", xlab = "Population", ylab = "CV1 Score", col = Colors_ALL_Cervus_pop)
stripchart(CV1 ~ Pop, data = CV_scores, vertical = TRUE, method = "jitter", add = TRUE, pch = 19, col = "black")
mtext(duncan_labels_CV1$groups, at = 1:length(duncan_labels_CV1$groups), side = 3, line = 1, cex = 0.8)
```



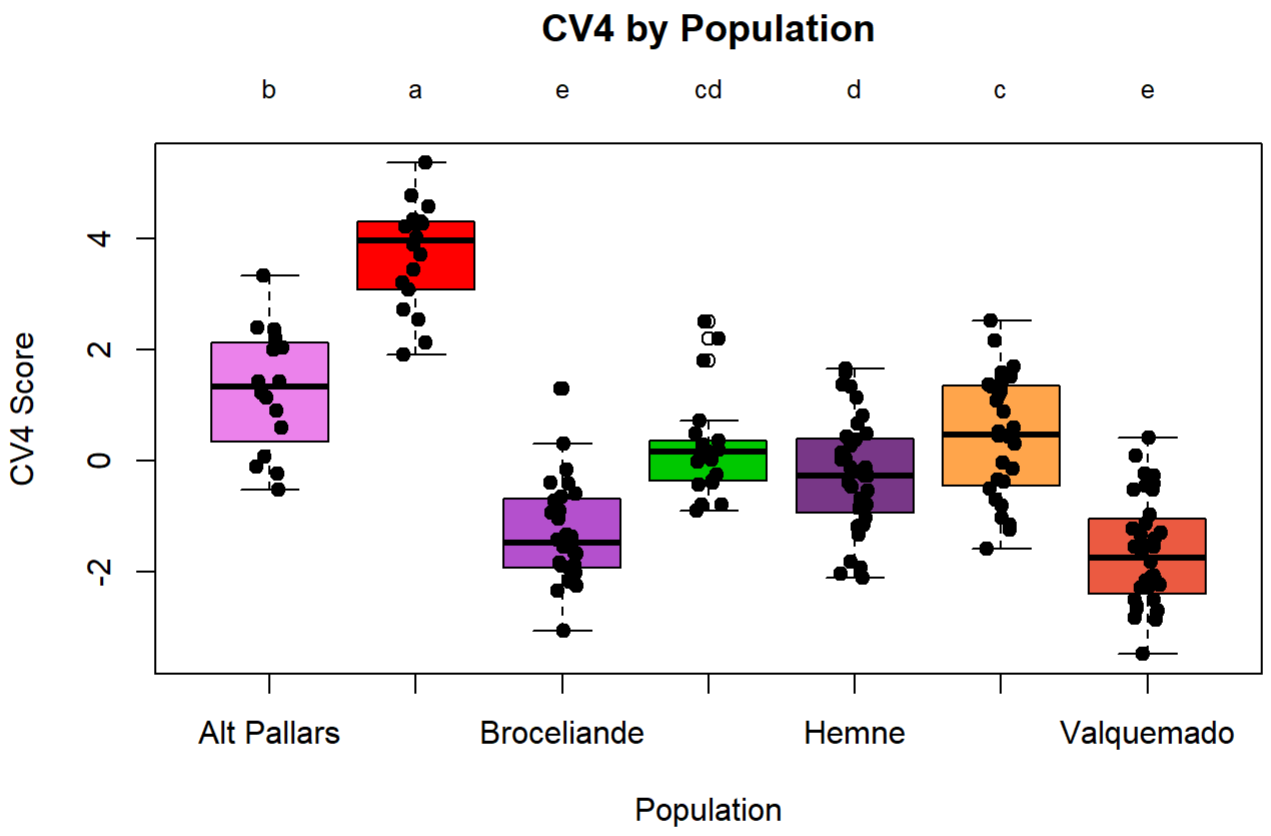
```
duncan_labels_CV2 <- duncan_result_CV2$groups
duncan_labels_CV2 <- duncan_labels_CV2[order(rownames(duncan_labels_CV2)), ]
CV_scores$labels <- factor(duncan_labels_CV2$groups[match(CV_scores$Pop, rownames(duncan_labels_CV2))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(CV2 ~ Pop, data = CV_scores, main = "CV2 by Population", xlab = "Population", ylab = "CV2 Score", col = Colors_ALL_Cervus_pop)
stripchart(CV2 ~ Pop, data = CV_scores, vertical = TRUE, method = "jitter", add = TRUE, pch = 19, col = "black")
mtext(duncan_labels_CV2$groups, at = 1:length(duncan_labels_CV1$groups), side = 3, line = 1, cex = 0.8)
```



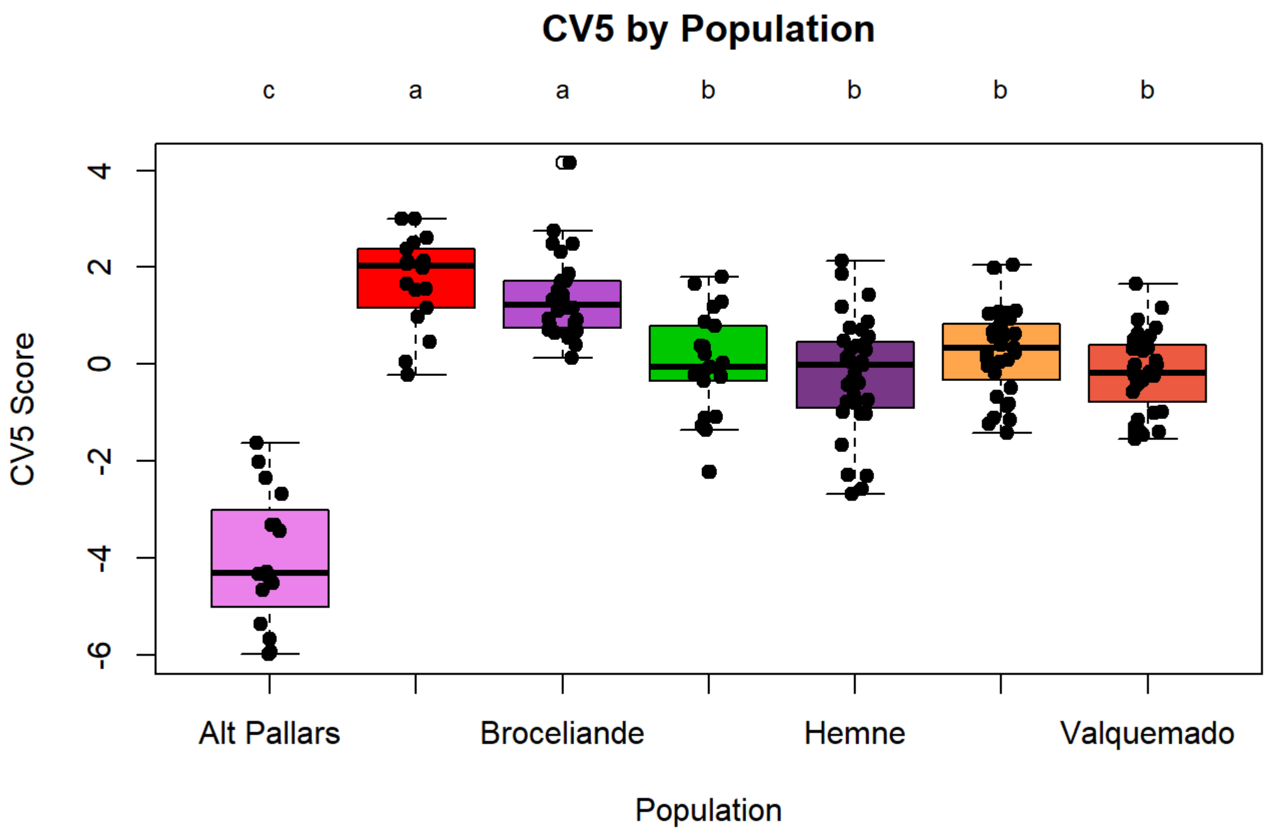
```
duncan_labels_CV3 <- duncan_result_CV3$groups
duncan_labels_CV3 <- duncan_labels_CV3[order(rownames(duncan_labels_CV3)), ]
CV_scores$labels <- factor(duncan_labels_CV3$groups[match(CV_scores$Pop, rownames(duncan_labe
ls_CV3))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(CV3 ~ Pop, data = CV_scores, main = "CV3 by Population", xlab = "Population", ylab =
"CV3 Score", col = Colors_ALL_Cervus_pop)
stripchart(CV3 ~ Pop, data = CV_scores, vertical = TRUE, method = "jitter", add = TRUE, pch =
19, col = "black")
mtext(duncan_labels_CV3$groups, at = 1:length(duncan_labels_CV1$groups), side = 3, line = 1,
cex = 0.8)
```



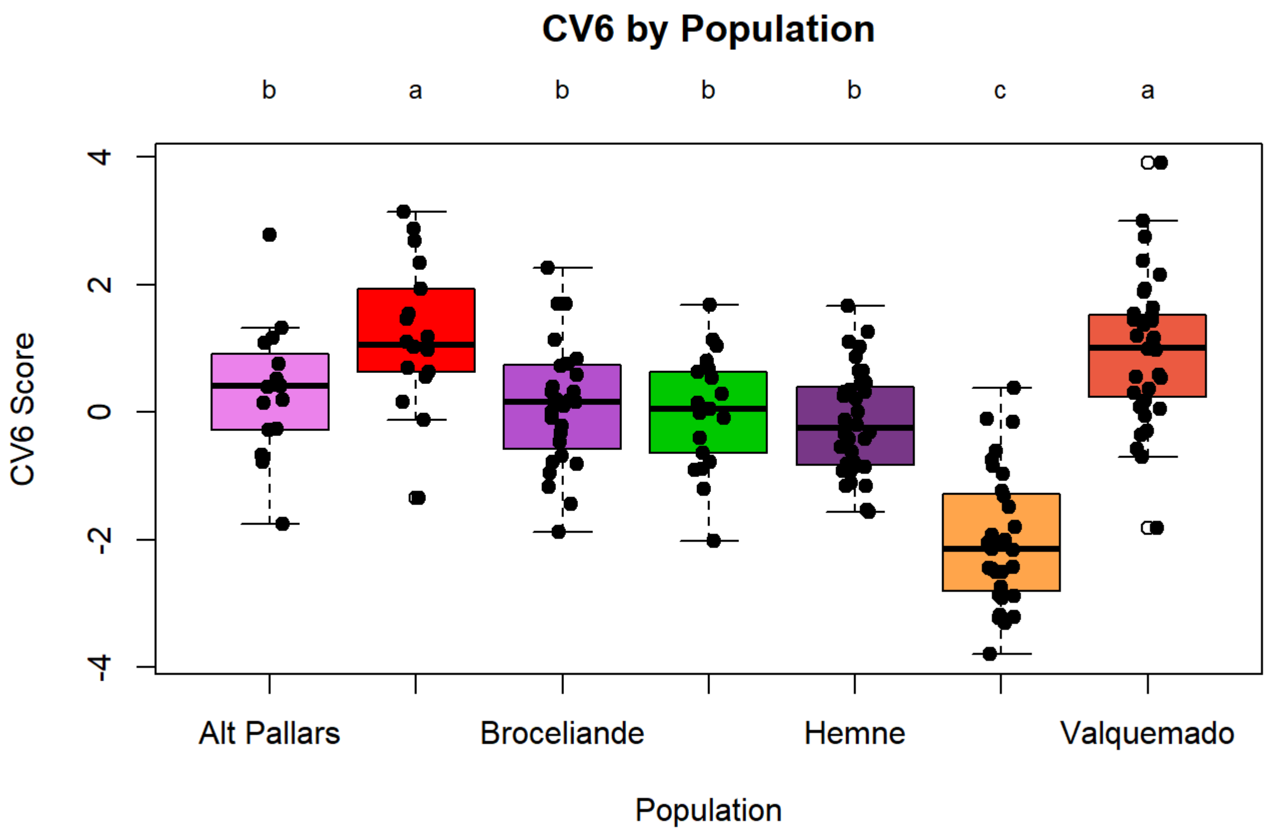
```
duncan_labels_CV4 <- duncan_result_CV4$groups
duncan_labels_CV4 <- duncan_labels_CV4[order(rownames(duncan_labels_CV4)), ]
CV_scores$labels <- factor(duncan_labels_CV4$groups[match(CV_scores$Pop, rownames(duncan_labe
ls_CV4))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(CV4 ~ Pop, data = CV_scores, main = "CV4 by Population", xlab = "Population", ylab =
"CV4 Score", col = Colors_ALL_Cervus_pop)
stripchart(CV4 ~ Pop, data = CV_scores, vertical = TRUE, method = "jitter", add = TRUE, pch =
19, col = "black")
mtext(duncan_labels_CV4$groups, at = 1:length(duncan_labels_CV4$groups), side = 3, line = 1,
cex = 0.8)
```



```
duncan_labels_CV5 <- duncan_result_CV5$groups
duncan_labels_CV5 <- duncan_labels_CV5[order(rownames(duncan_labels_CV5)), ]
CV_scores$labels <- factor(duncan_labels_CV5$groups[match(CV_scores$Pop, rownames(duncan_labe
ls_CV5))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(CV5 ~ Pop, data = CV_scores, main = "CV5 by Population", xlab = "Population", ylab =
"CV5 Score", col = Colors_ALL_Cervus_pop)
stripchart(CV5 ~ Pop, data = CV_scores, vertical = TRUE, method = "jitter", add = TRUE, pch =
19, col = "black")
mtext(duncan_labels_CV5$groups, at = 1:length(duncan_labels_CV5$groups), side = 3, line = 1,
cex = 0.8)
```



```
duncan_labels_CV6 <- duncan_result_CV6$groups
duncan_labels_CV6 <- duncan_labels_CV6[order(rownames(duncan_labels_CV6)), ]
CV_scores$labels <- factor(duncan_labels_CV6$groups[match(CV_scores$Pop, rownames(duncan_labels_CV6))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(CV6 ~ Pop, data = CV_scores, main = "CV6 by Population", xlab = "Population", ylab = "CV6 Score", col = Colors_ALL_Cervus_pop)
stripchart(CV6 ~ Pop, data = CV_scores, vertical = TRUE, method = "jitter", add = TRUE, pch = 19, col = "black")
mtext(duncan_labels_CV6$groups, at = 1:length(duncan_labels_CV6$groups), side = 3, line = 1, cex = 0.8)
```



```
# test the correlation between morphological changes on CV1 and latitude :
filtered_data <- Descriptive_ALL_Cervus[Descriptive_ALL_Cervus$Pop != "El_Durazno", ]
CV1 <- CV_scores[Descriptive_ALL_Cervus$Pop != "El_Durazno", 1]
Pop <- filtered_data$Pop
Lat <- as.numeric(as.character(filtered_data$Lat))
summary(CV1)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##  -5.814  -3.314  -1.672  -1.101   1.287   4.696
```

```
summary(Lat)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##   38.23   38.35   42.23   46.13   48.03   63.25
```

```
summary(Pop)
```

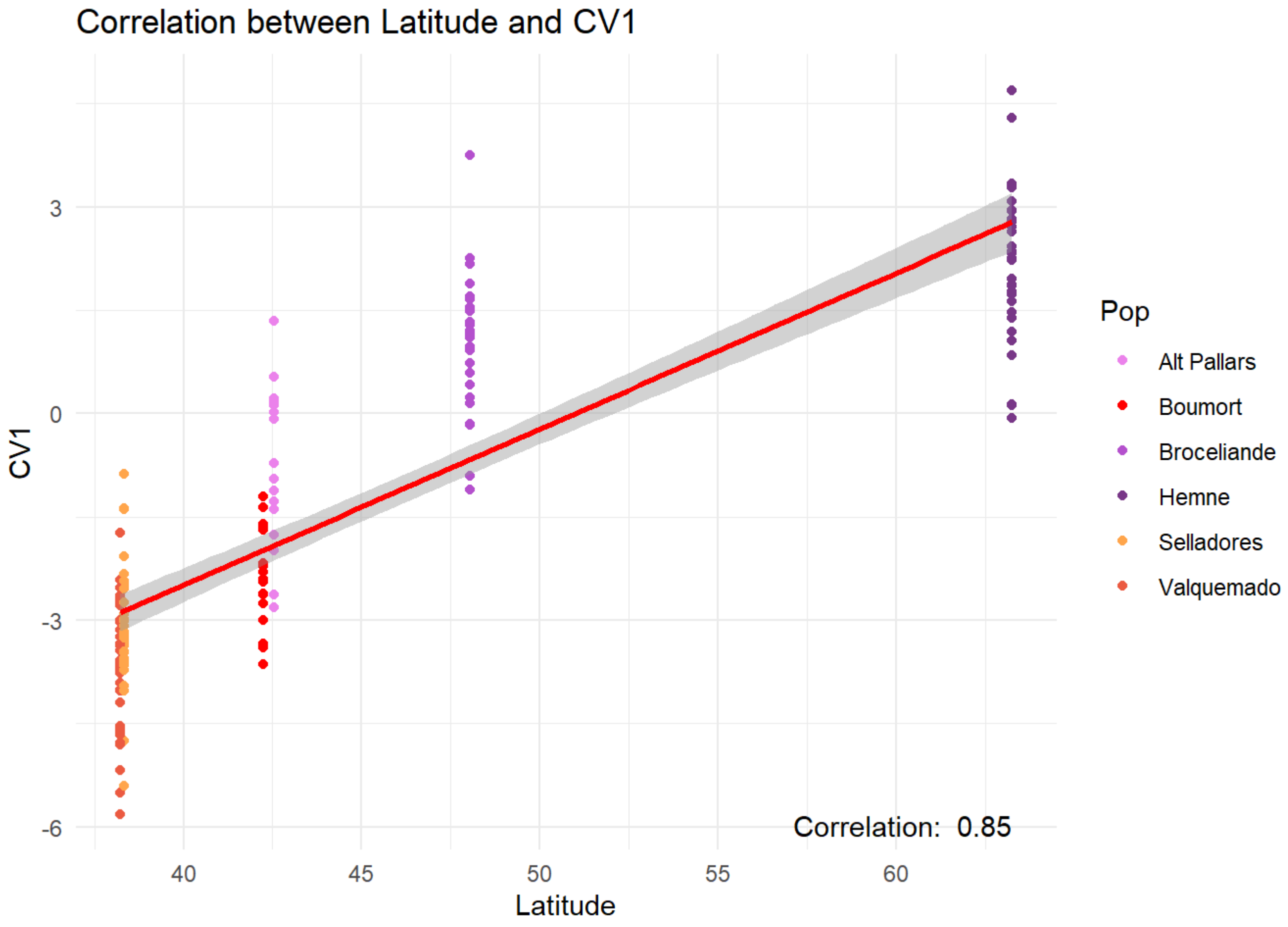
```
## Alt Pallars     Boumort Broceliande  El_Durazno       Hemne  Selladores 
##          16          18          28           0          35          31 
##  Valquemado 
##          36
```

```
correlation <- cor(Lat, CV1, use = "complete.obs")
print(paste("Correlation between Latitude and CV1: ", correlation))
```

```
## [1] "Correlation between Latitude and CV1:  0.85147947654101"
```

```
# Results :
# The correlation of 0.85 suggests a strong linear relationship between latitude and CV1 : th
e morphological variation captured by CV1 increases with latitude.
Colors_ALL_Cervus_pop <- c("Alt Pallars" = "violet",
                           "Boumort" = "red",
                           "Broceliande" = "mediumorchid3",
                           "Hemne" = "mediumorchid4",
                           "Selladores" = "tan1",
                           "Valquemado" = "tomato2")
data <- data.frame(Lat = Lat, CV1 = CV1, Pop = as.factor(Pop))
ggplot(data, aes(x = Lat, y = CV1, color = Pop)) +
  geom_point() +
  geom_smooth(method = "lm", col = "red") +
  scale_color_manual(values = Colors_ALL_Cervus_pop) +
  labs(title = "Correlation between Latitude and CV1",
       x = "Latitude",
       y = "CV1") +
  theme_minimal() +
  annotate("text", x = max(data$Lat), y = min(data$CV1),
           label = paste("Correlation: ", round(correlation, 2)),
           hjust = 1, vjust = 1)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

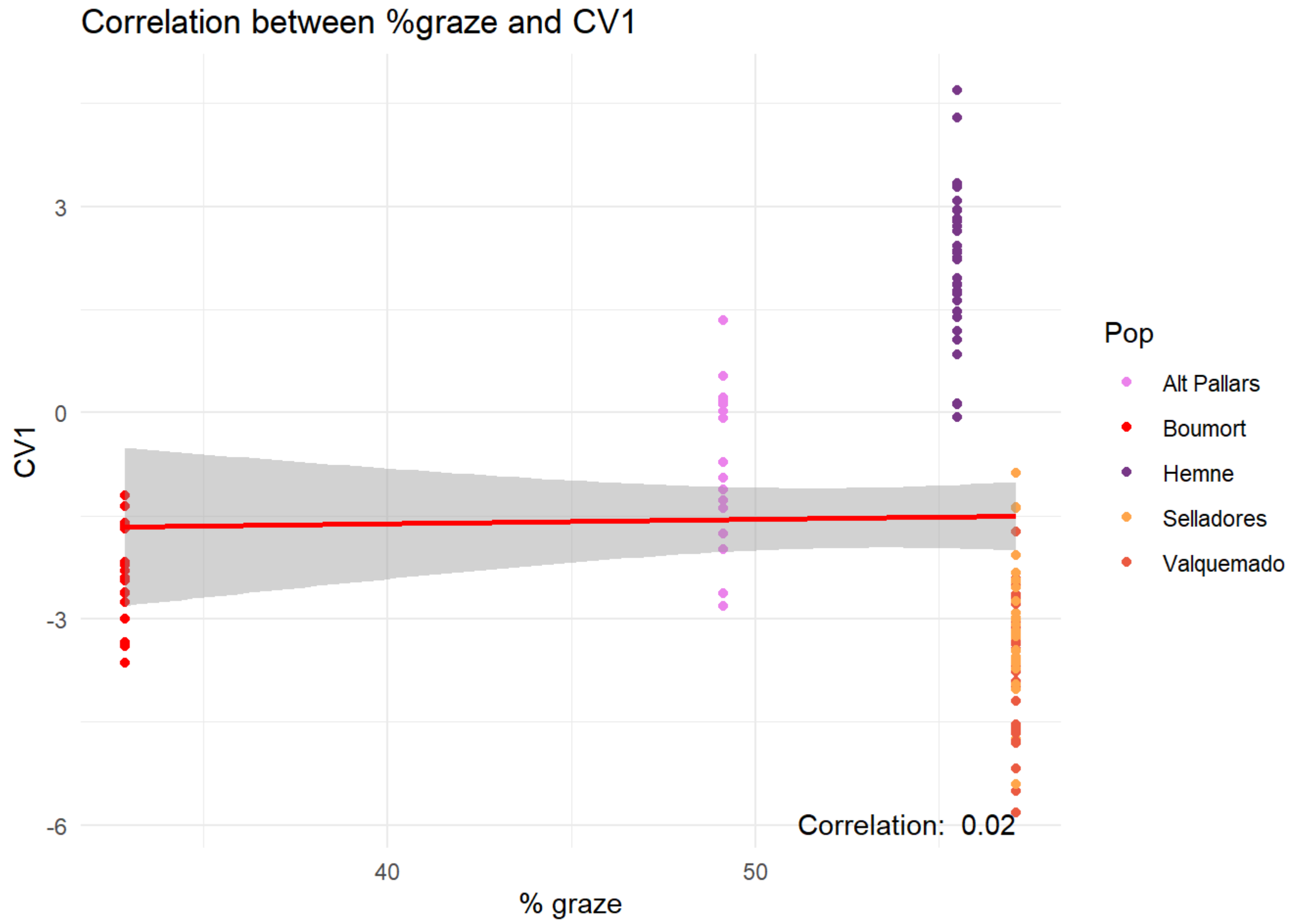


```
# test the correlation between morphological changes on CV1 and %graze :
filtered_data <- Descriptive_ALL_Cervus[!(Descriptive_ALL_Cervus$Pop %in% c("El_Durazno", "Br
oceliande")), ]
CV1 <- CV_scores[!(Descriptive_ALL_Cervus$Pop %in% c("El_Durazno", "Broceliande")), 1]
Pop <- filtered_data$Pop
Graze <- as.numeric(as.character(filtered_data$Herb_Monocots))
correlation <- cor(Graze, CV1, use = "complete.obs")
print(paste("Correlation between % of graze and CV1: ", correlation))
```

```
## [1] "Correlation between % of graze and CV1:  0.0204882978531444"
```

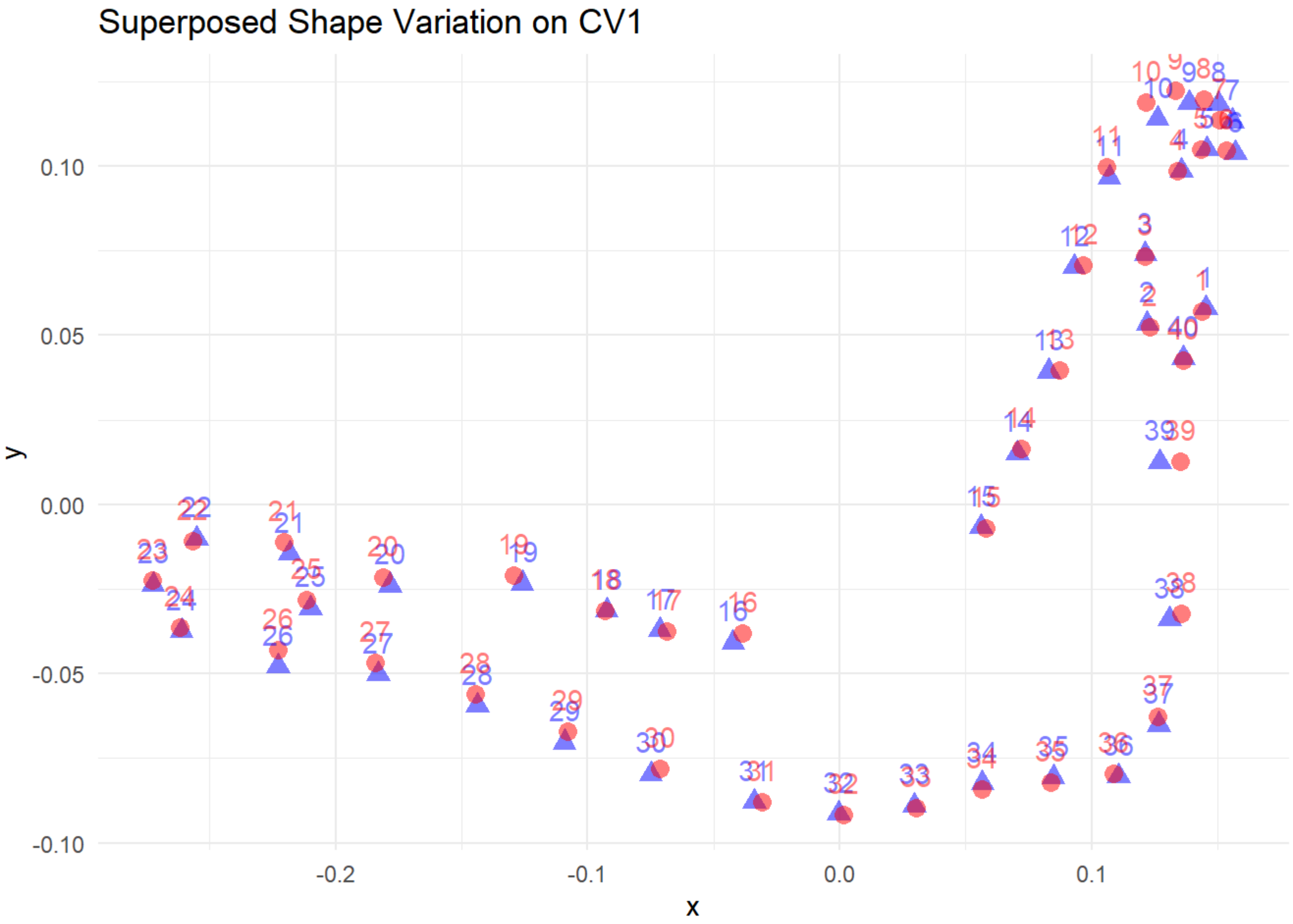
```
# correlation of 0.02048 : no relation between the 2 variables

Colors_ALL_Cervus_pop <- c("Alt Pallars" = "violet",
                           "Boumort" = "red",
                           "Hemne" = "mediumorchid4",
                           "Selladores" = "tan1",
                           "Valquemado" = "tomato2")
data <- data.frame(Graze = Graze, CV1 = CV1, Pop = as.factor(Pop))
ggplot(data, aes(x = Graze, y = CV1, color = Pop)) +
  geom_point() +
  geom_smooth(method = "lm", col = "red") +
  scale_color_manual(values = Colors_ALL_Cervus_pop) +
  labs(title = "Correlation between %graze and CV1",
       x = "% graze",
       y = "CV1") +
  theme_minimal() +
  annotate("text", x = max(data$Graze), y = min(data$CV1),
           label = paste("Correlation: ", round(correlation, 2)),
           hjust = 1, vjust = 1)
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

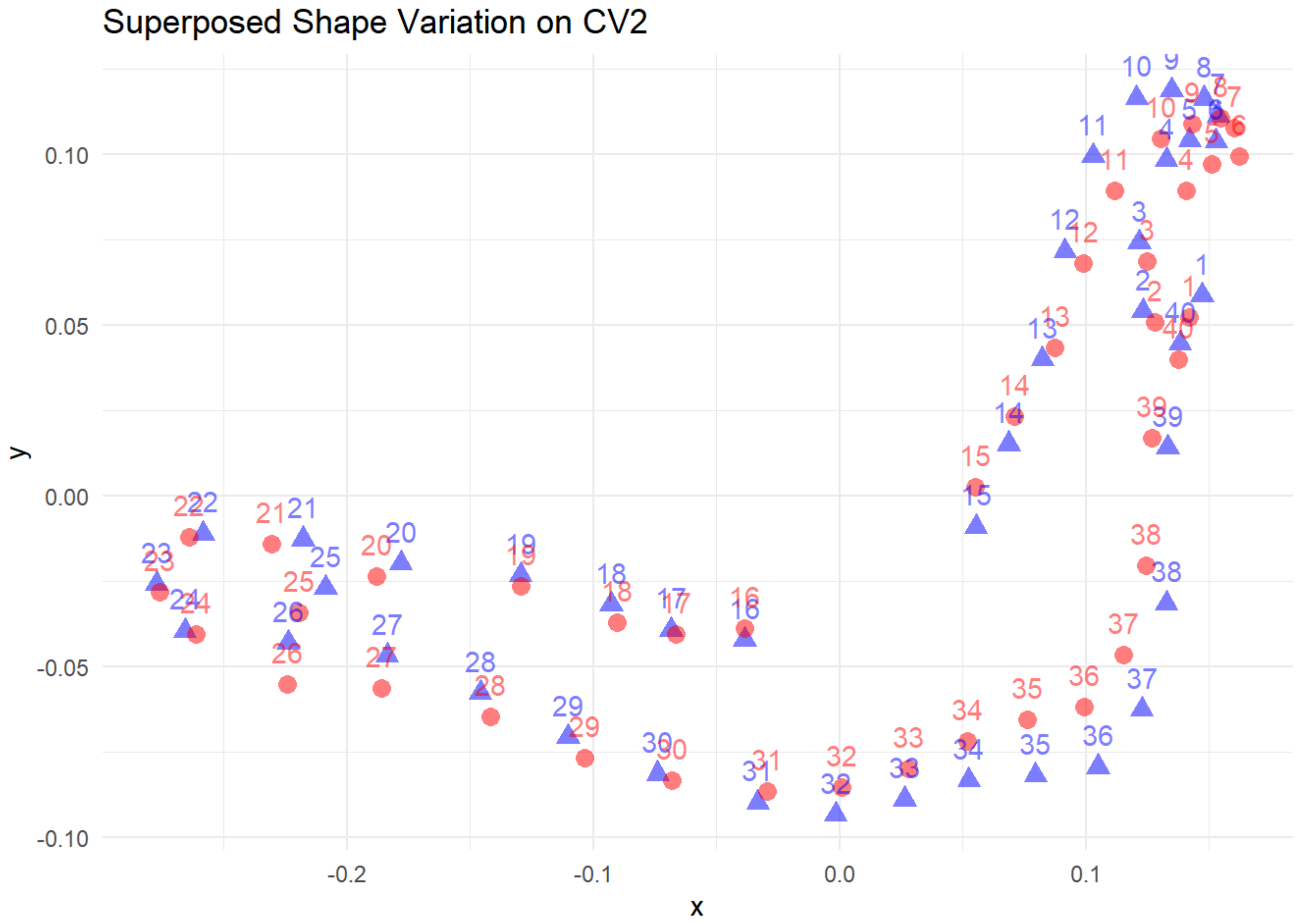


Visualize shape variation

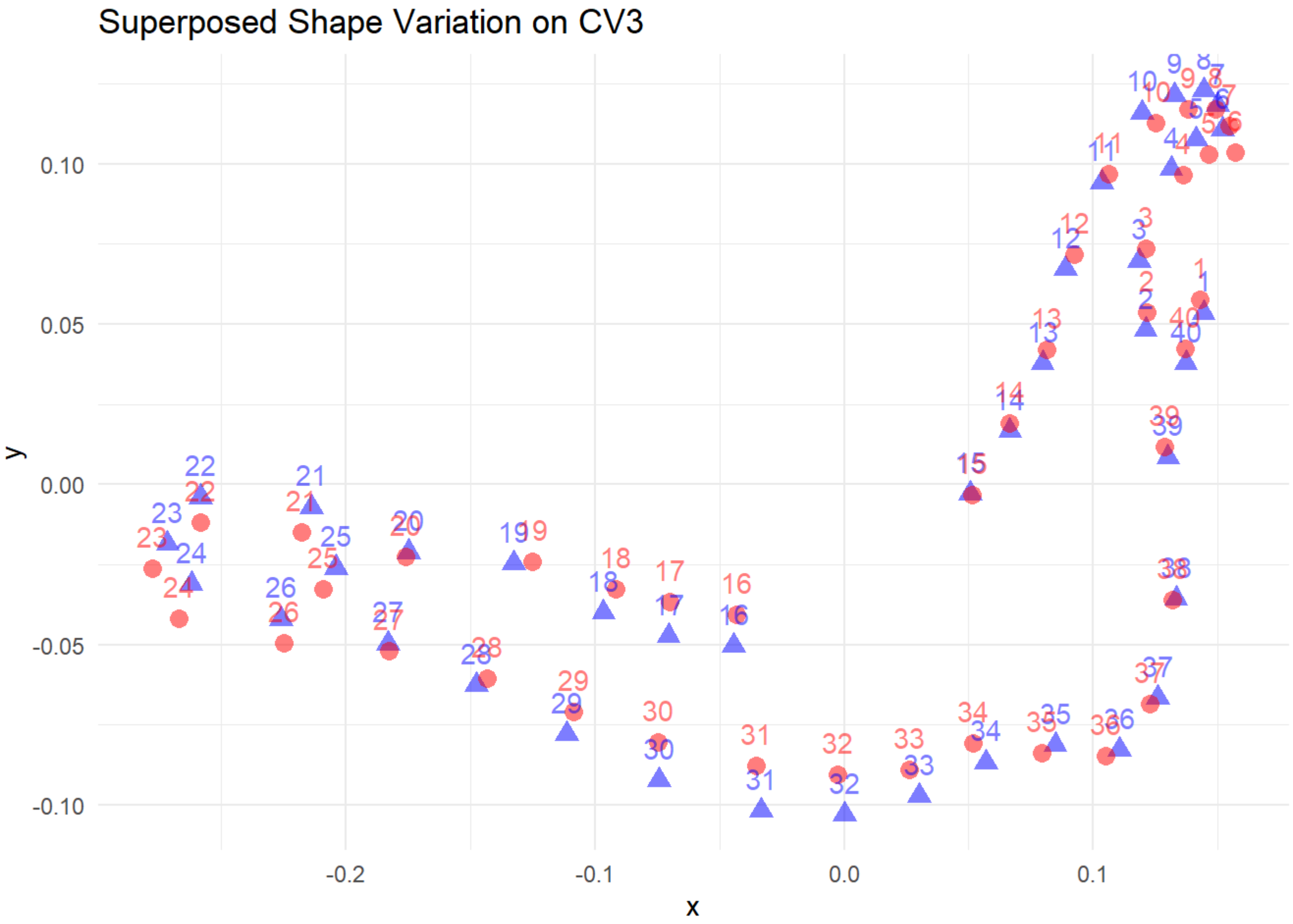
```
#Visualize shape variation on CV1
extreme_min_CV1 <- which.min(CV1)
extreme_max_CV1 <- which.max(CV1)

coords_min_CV1 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_min_CV1])
coords_max_CV1 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_max_CV1])
coords_min_CV1$landmark <- 1:nrow(coords_min_CV1)
coords_max_CV1$landmark <- 1:nrow(coords_max_CV1)

colnames(coords_min_CV1) <- c("x", "y", "landmark")
colnames(coords_max_CV1) <- c("x", "y", "landmark")
coords_min_CV1$group <- "Min CV1"
coords_max_CV1$group <- "Max CV1"

df_combined <- rbind(coords_min_CV1, coords_max_CV1)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on CV1") +
  scale_color_manual(values = c("Min CV1" = "blue", "Max CV1" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



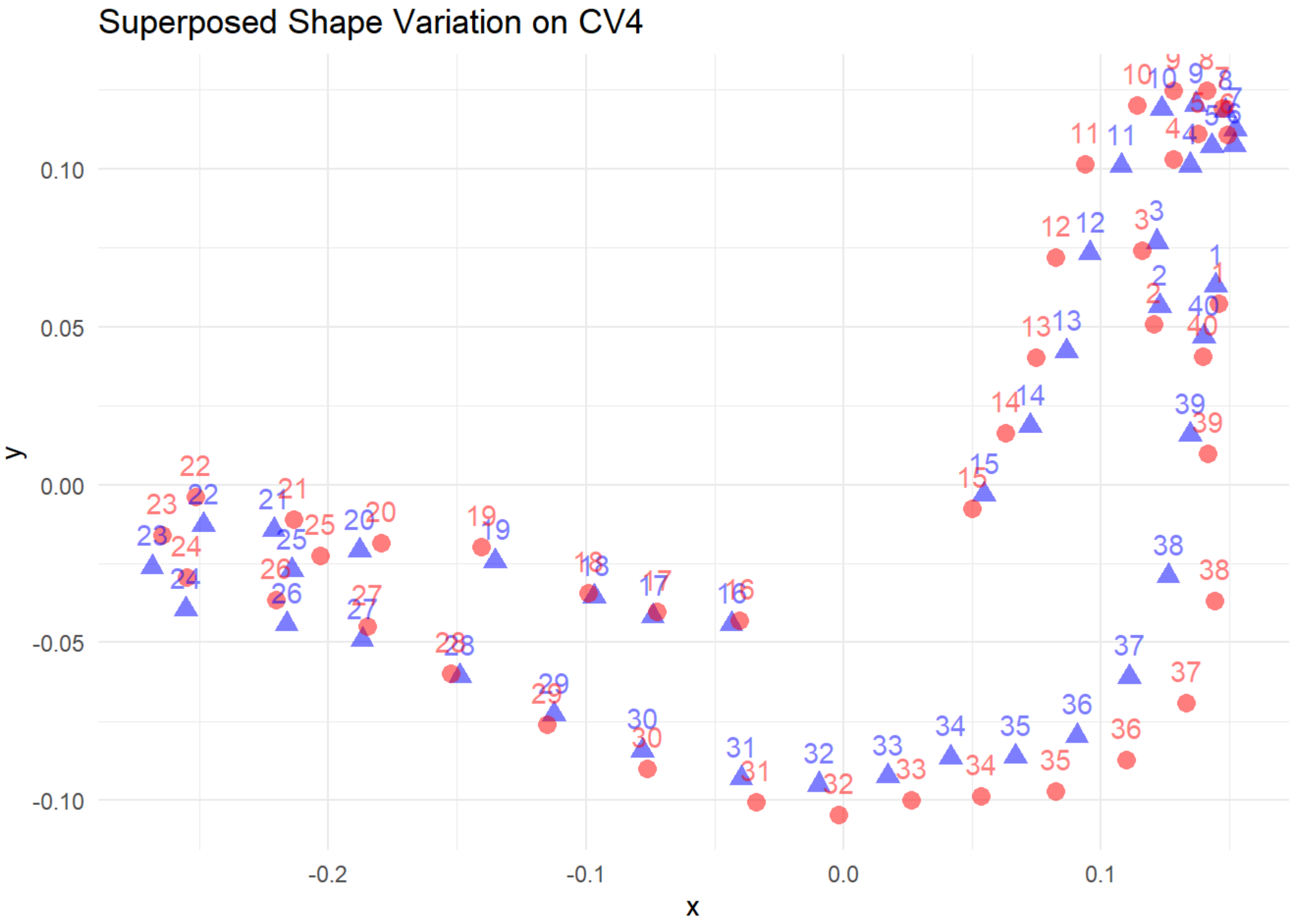
```
#Visualize shape variation on CV2
extreme_min_CV2 <- which.min(CV2)
extreme_max_CV2 <- which.max(CV2)

coords_min_CV2 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_min_CV2])
coords_max_CV2 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_max_CV2])
coords_min_CV2$landmark <- 1:nrow(coords_min_CV2)
coords_max_CV2$landmark <- 1:nrow(coords_max_CV2)

colnames(coords_min_CV2) <- c("x", "y", "landmark")
colnames(coords_max_CV2) <- c("x", "y", "landmark")
coords_min_CV2$group <- "Min CV2"
coords_max_CV2$group <- "Max CV2"

df_combined <- rbind(coords_min_CV2, coords_max_CV2)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on CV2") +
  scale_color_manual(values = c("Min CV2" = "blue", "Max CV2" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



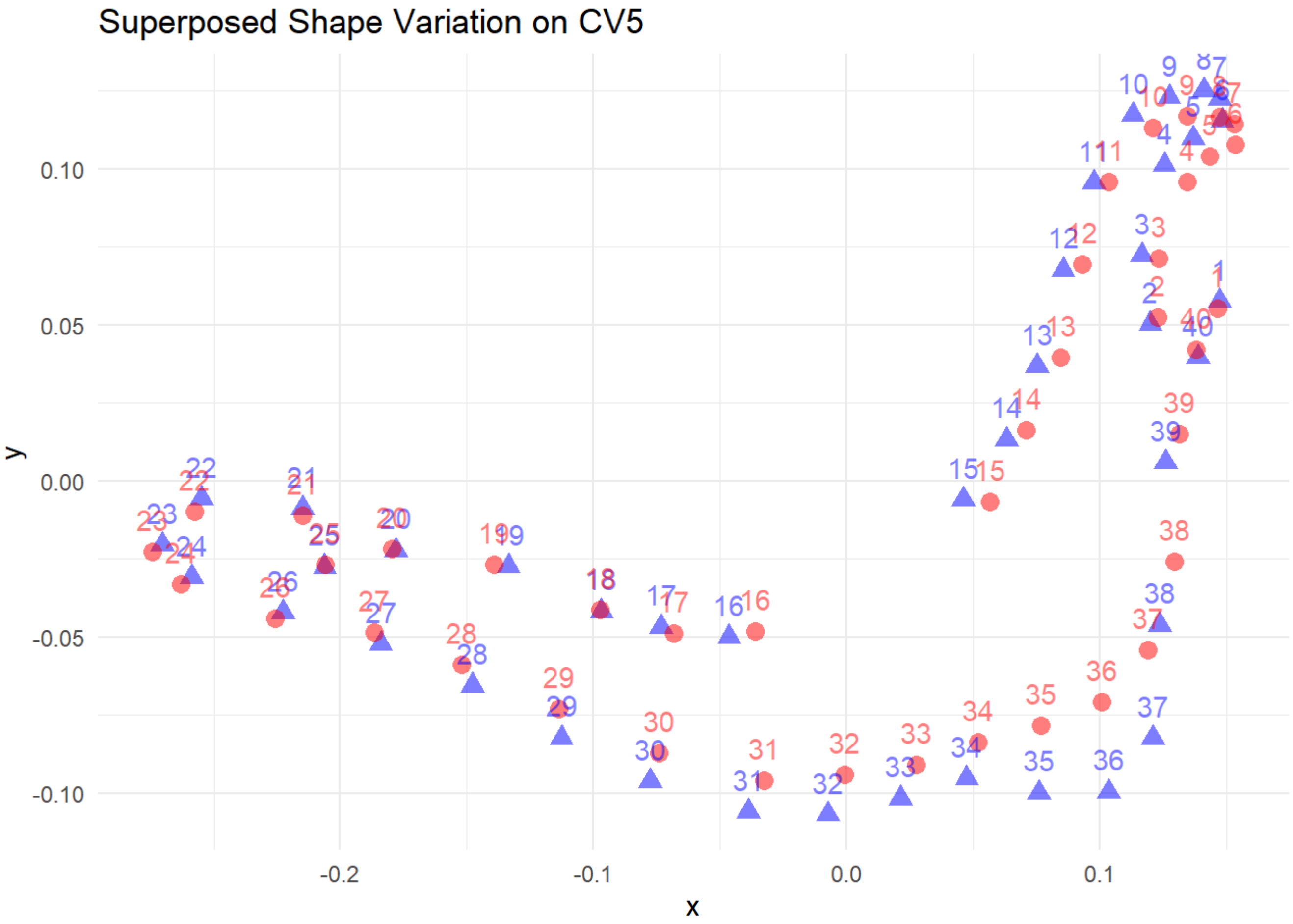
```
#Visualize shape variation on CV3
extreme_min_CV3 <- which.min(CV3)
extreme_max_CV3 <- which.max(CV3)

coords_min_CV3 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_min_CV3])
coords_max_CV3 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_max_CV3])
coords_min_CV3$landmark <- 1:nrow(coords_min_CV3)
coords_max_CV3$landmark <- 1:nrow(coords_max_CV3)

colnames(coords_min_CV3) <- c("x", "y", "landmark")
colnames(coords_max_CV3) <- c("x", "y", "landmark")
coords_min_CV3$group <- "Min CV3"
coords_max_CV3$group <- "Max CV3"

df_combined <- rbind(coords_min_CV3, coords_max_CV3)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on CV3") +
  scale_color_manual(values = c("Min CV3" = "blue", "Max CV3" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



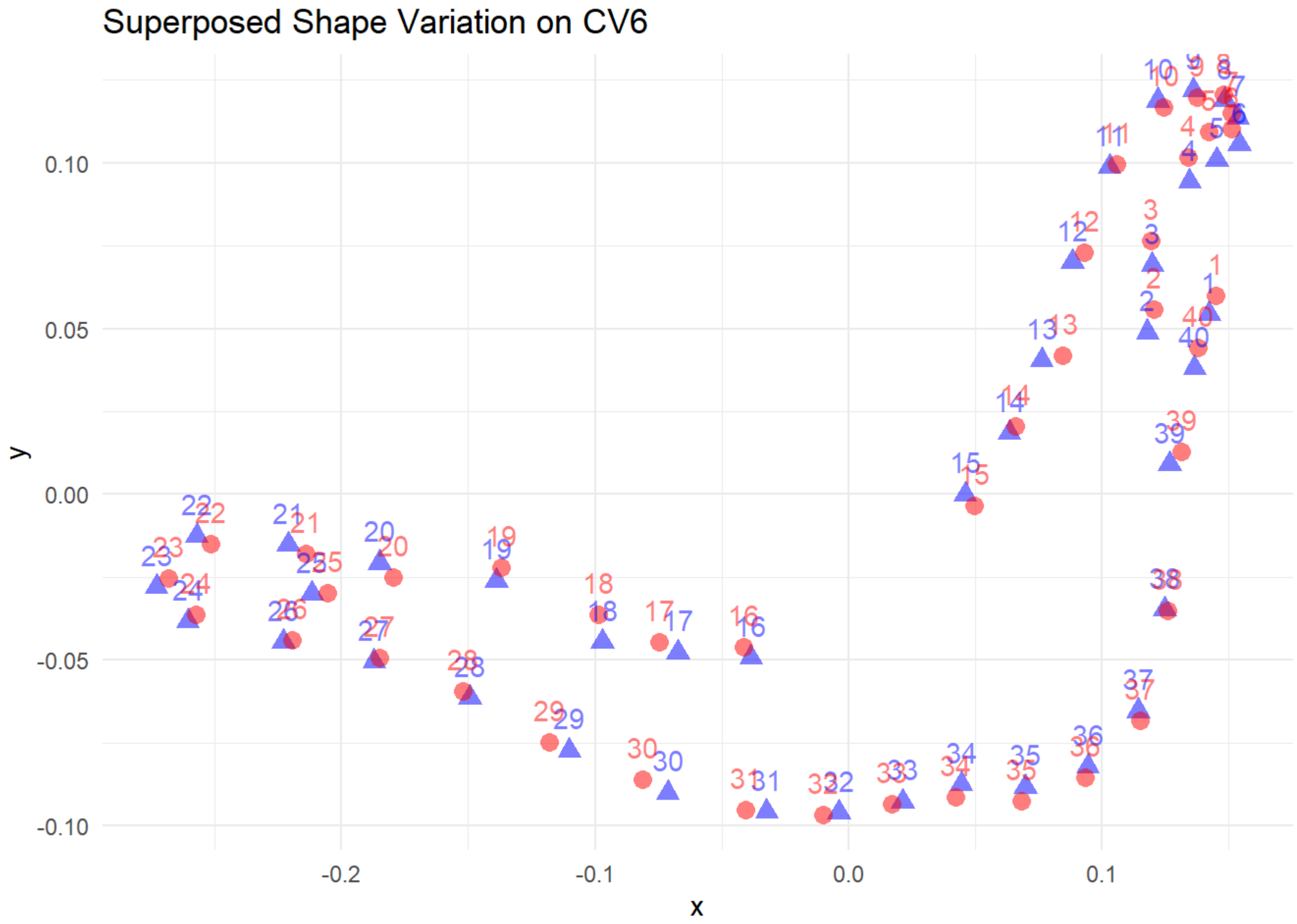
```
# Vizualize shape variation on CV4
extreme_min_CV4 <- which.min(CV4)
extreme_max_CV4 <- which.max(CV4)

coords_min_CV4 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_min_CV4])
coords_max_CV4 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_max_CV4])
coords_min_CV4$landmark <- 1:nrow(coords_min_CV4)
coords_max_CV4$landmark <- 1:nrow(coords_max_CV4)

colnames(coords_min_CV4) <- c("x", "y", "landmark")
colnames(coords_max_CV4) <- c("x", "y", "landmark")
coords_min_CV4$group <- "Min CV4"
coords_max_CV4$group <- "Max CV4"

df_combined <- rbind(coords_min_CV4, coords_max_CV4)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on CV4") +
  scale_color_manual(values = c("Min CV4" = "blue", "Max CV4" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



```
# Vizualize shape variation on CV5
extreme_min_CV5 <- which.min(CV5)
extreme_max_CV5 <- which.max(CV5)

coords_min_CV5 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_min_CV5])
coords_max_CV5 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_max_CV5])
coords_min_CV5$landmark <- 1:nrow(coords_min_CV5)
coords_max_CV5$landmark <- 1:nrow(coords_max_CV5)

colnames(coords_min_CV5) <- c("x", "y", "landmark")
colnames(coords_max_CV5) <- c("x", "y", "landmark")
coords_min_CV5$group <- "Min CV5"
coords_max_CV5$group <- "Max CV5"

df_combined <- rbind(coords_min_CV5, coords_max_CV5)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on CV5") +
  scale_color_manual(values = c("Min CV5" = "blue", "Max CV5" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



```
# Visualize shape variation on CV6
extreme_min_CV6 <- which.min(CV6)
extreme_max_CV6 <- which.max(CV6)

coords_min_CV6 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_min_CV6])
coords_max_CV6 <- as.data.frame(Slided_MorphoGeom_ALL_Cervus$coords[,,extreme_max_CV6])
coords_min_CV6$landmark <- 1:nrow(coords_min_CV6)
coords_max_CV6$landmark <- 1:nrow(coords_max_CV6)

colnames(coords_min_CV6) <- c("x", "y", "landmark")
colnames(coords_max_CV6) <- c("x", "y", "landmark")
coords_min_CV6$group <- "Min CV6"
coords_max_CV6$group <- "Max CV6"

df_combined <- rbind(coords_min_CV6, coords_max_CV6)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on CV6") +
  scale_color_manual(values = c("Min CV6" = "blue", "Max CV6" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



2.3.4 Role of mandible size and the influence of the population in these variations:

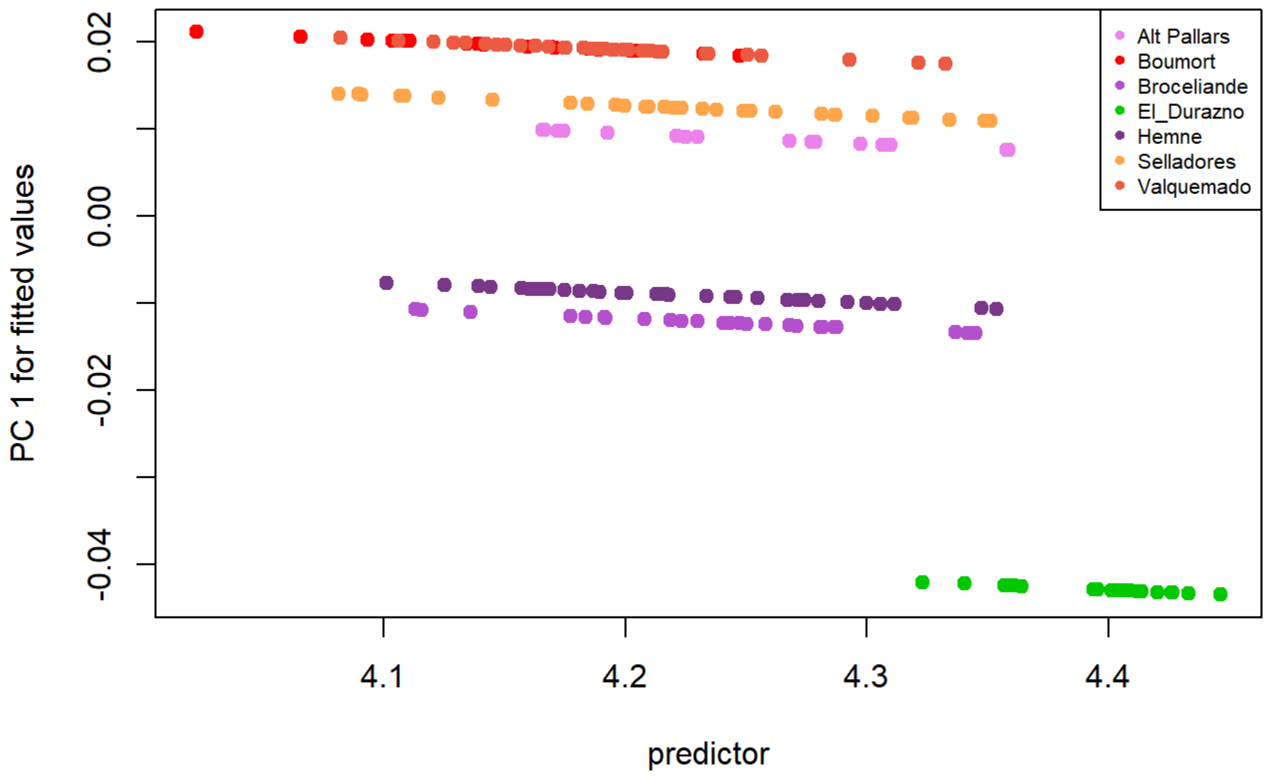
```
# Procrust regression provides an overview, while PLS analysis allows us to focus on the spec
ific influence of size.

# Procrust regression
# evaluate how shapes ( landmark coordinates) vary as a function of explanatory variables (si
ze and population).
summary(Descriptive_ALL_Cervus)
```

```
##   TPS POSITION       Ref                Length        Species
##  Min.   :  1.0   Length:185         Min.   :22.25   Length:185
##  1st Qu.: 47.0   Class :character   1st Qu.:25.96   Class :character
##  Median :203.0   Mode  :character   Median :27.03   Mode  :character
##  Mean   :171.4                      Mean   :27.63
##  3rd Qu.:259.0                      3rd Qu.:28.98
##  Max.   :315.0                      Max.   :35.88
##
##      Sex                    Pop             Lat              Long
##  Length:185         Alt Pallars:16   -34.545929:21   -65.298216:21
##  Class :character   Boumort    :18   38.228798 :36   -4.162476 :36
##  Mode  :character   Broceliande:28   38.349735 :31   -3.842862 :31
##                     El_Durazno :21   42.23133  :18   -2.13     :28
##                     Hemne      :35   42.545246 :16   1.123522  :18
##                     Selladores :31   48.03     :28   1.278943  :16
##                     Valquemado :36   63.25     :35   9.02      :35
##            Vegetation_type Climat   Genet  Herb_Monocots   Centroid_Size
##  12                 :35     Bsk:67   A:21   Min.   :32.86   Min.   :55.84
##  241                :28     Bwh:21   B:35   1st Qu.:49.14   1st Qu.:64.83
##  731                :31     Cfb:28   C:44   Median :55.50   Median :67.96
##  732                :36     Dfb:34   D:85   Mean   :51.55   Mean   :69.22
##  81                 :34     Dfc:35          3rd Qu.:57.10   3rd Qu.:72.73
##  Temperate mountain:21                      Max.   :57.10   Max.   :85.31
##                                             NA's   :28
##  labels
##  a :35
##  ab:36
##  bc:52
##  c :34
##  d :28
##
##
```

```
Csize <- Descriptive_ALL_Cervus$Centroid_Size
Pop <- Descriptive_ALL_Cervus$Pop
coords <- Slided_MorphoGeom_ALL_Cervus

gdf <- geomorph.data.frame(coords, Pop = Pop, Csize = Csize)
fit.size <- procD.lm(coords ~ log(Csize) + Pop, data = gdf, print.progress = FALSE)
summary(fit.size)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type I
## Effect sizes (Z) based on F distributions
##
##              Df       SS       MS     Rsq      F       Z Pr(>F)
## log(Csize)    1 0.037655 0.037655 0.13963 43.674  5.1801  0.001 ***
## Pop           6 0.079411 0.013235 0.29447 15.351 10.1882  0.001 ***
## Residuals   177 0.152607 0.000862 0.56590
## Total       184 0.269673
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: procD.lm(f1 = coords ~ log(Csize) + Pop, data = gdf, print.progress = FALSE)
```

```
# Plot Allometry
# Allometry is the study of differential growth relationships between different parts of an o
rganism.
Colors_ALL_Cervus_pop <- c("Alt Pallars" = "violet", "Boumort" ="red",  "Broceliande" = "medi
umorchid3","El_Durazno" = "#00CC00", "Hemne" = "mediumorchid4","Selladores" ="tan1",  "Valque
mado" = "tomato2") # identify cervids by population
plotAllometry(fit.size, size = gdf$Csize, logsz = TRUE, method = "PredLine", col = Colors_ALL
_Cervus_pop[ALL_Cervus_pop], pch = 19)
legend("topright", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch =
19, cex= 0.65)
```



```
###Results ###############
# p-value = 0.001 : landmark coordinates (shape) change according to the centroid size.
# p-value = 0.001 : landmark coordinates (shape) change according to the population.
# R²: 14% of the variance is explained by log(centroid size) and 29% by the population.
##########################

# evaluate how shapes vary as a function of explanatory variables (size and habitat) on the a
xes with inter-habitat differences.
PC1 <- PC_scores_PCA_ALL_Cervus[, 1]
PC2 <- PC_scores_PCA_ALL_Cervus[, 2]
PC3 <- PC_scores_PCA_ALL_Cervus[, 3]
PC4 <- PC_scores_PCA_ALL_Cervus[, 4]
PC5 <- PC_scores_PCA_ALL_Cervus[, 5]

fit.size.PC1 <- procD.lm(PC1 ~ log(Csize) + Pop)
fit.size.PC2 <- procD.lm(PC2 ~ log(Csize) + Pop)
fit.size.PC3 <- procD.lm(PC3 ~ log(Csize) + Pop)
fit.size.PC4 <- procD.lm(PC4 ~ log(Csize) + Pop)
fit.size.PC5 <- procD.lm(PC5 ~ log(Csize) + Pop)

summary(fit.size.PC1)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type I
## Effect sizes (Z) based on F distributions
##
##              Df       SS        MS     Rsq       F      Z Pr(>F)
## log(Csize)   1 0.031464 0.0314642 0.31247 187.054  6.092  0.001 ***
## Pop          6 0.039457 0.0065762 0.39185  39.095 10.025  0.001 ***
## Residuals  177 0.029773 0.0001682 0.29568
## Total      184 0.100694
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: procD.lm(f1 = PC1 ~ log(Csize) + Pop)
```

```
summary(fit.size.PC2)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type I
## Effect sizes (Z) based on F distributions
##
##              Df       SS        MS     Rsq      F      Z Pr(>F)
## log(Csize)   1 0.003695 0.0036950 0.05284 15.403 2.9396  0.001 ***
## Pop          6 0.023770 0.0039617 0.33993 16.515 7.4453  0.001 ***
## Residuals  177 0.042460 0.0002399 0.60722
## Total      184 0.069925
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: procD.lm(f1 = PC2 ~ log(Csize) + Pop)
```

```
summary(fit.size.PC3)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type I
## Effect sizes (Z) based on F distributions
##
##              Df        SS         MS     Rsq      F       Z Pr(>F)
## log(Csize)   1 0.0000598 5.9844e-05 0.00273 0.5212 0.15764  0.448
## Pop          6 0.0015248 2.5413e-04 0.06960 2.2132 1.71627  0.045 *
## Residuals  177 0.0203239 1.1482e-04 0.92767
## Total      184 0.0219085
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: procD.lm(f1 = PC3 ~ log(Csize) + Pop)
```

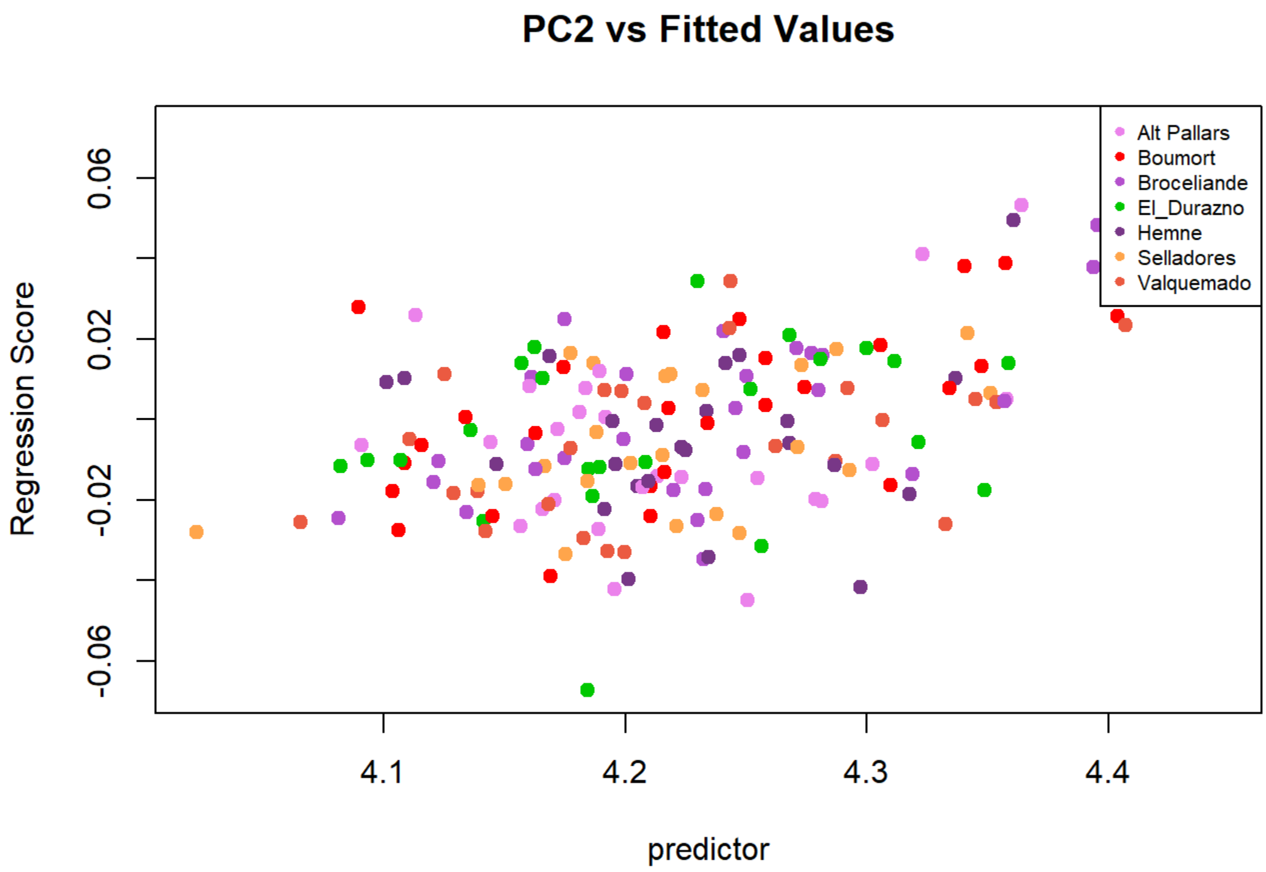
```
summary(fit.size.PC4)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type I
## Effect sizes (Z) based on F distributions
##
##              Df        SS         MS     Rsq       F      Z Pr(>F)
## log(Csize)   1 0.0004810 0.00048098 0.02897  9.1848 2.4425  0.003 **
## Pop          6 0.0068546 0.00114243 0.41282 21.8160 7.9325  0.001 ***
## Residuals  177 0.0092689 0.00005237 0.55822
## Total      184 0.0166045
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: procD.lm(f1 = PC4 ~ log(Csize) + Pop)
```

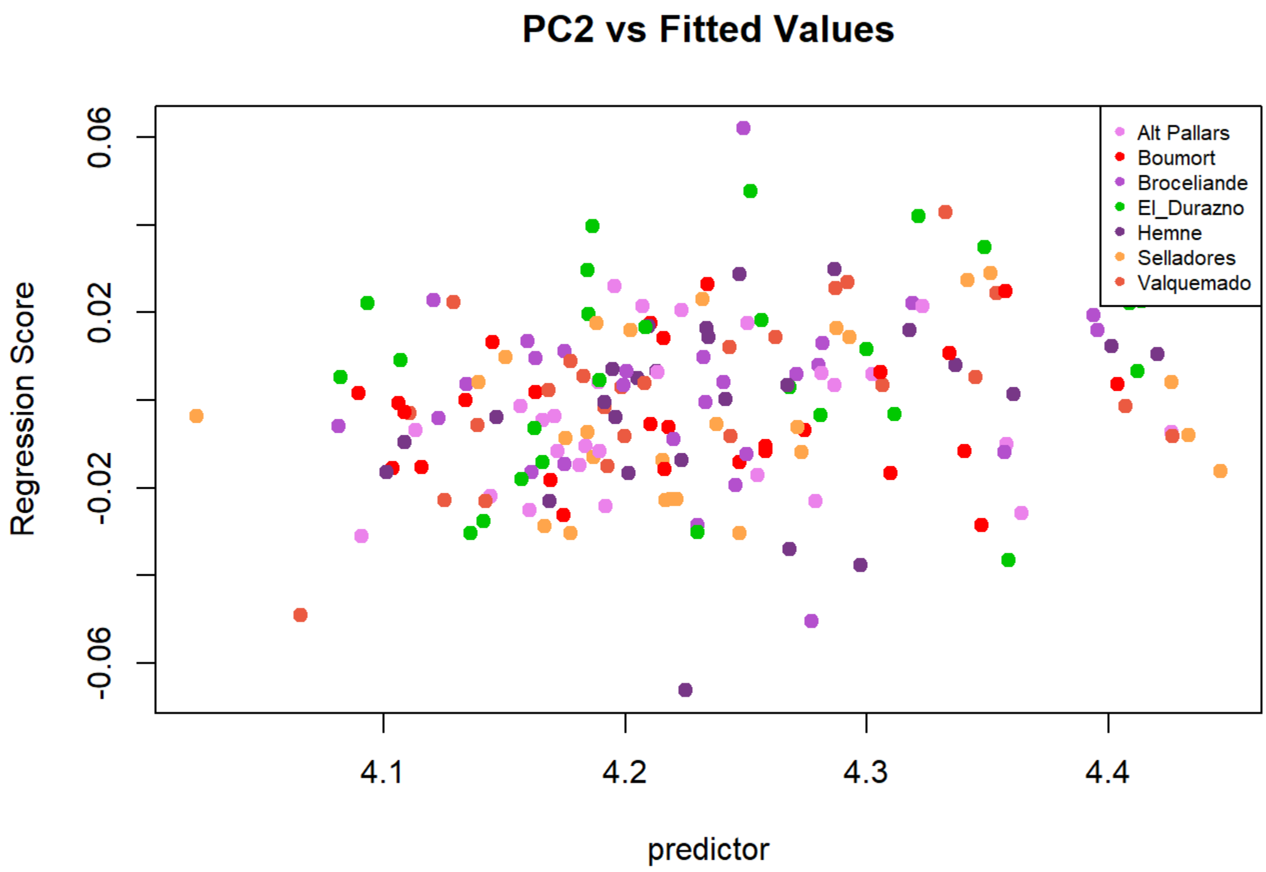
```
summary(fit.size.PC5)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type I
## Effect sizes (Z) based on F distributions
##
##              Df        SS         MS     Rsq       F      Z Pr(>F)
## log(Csize)   1 0.0003255 0.00032554 0.02732  6.9244 2.0620  0.012 *
## Pop          6 0.0032671 0.00054451 0.27422 11.5819 5.7118  0.001 ***
## Residuals  177 0.0083215 0.00004701 0.69846
## Total      184 0.0119141
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: procD.lm(f1 = PC5 ~ log(Csize) + Pop)
```

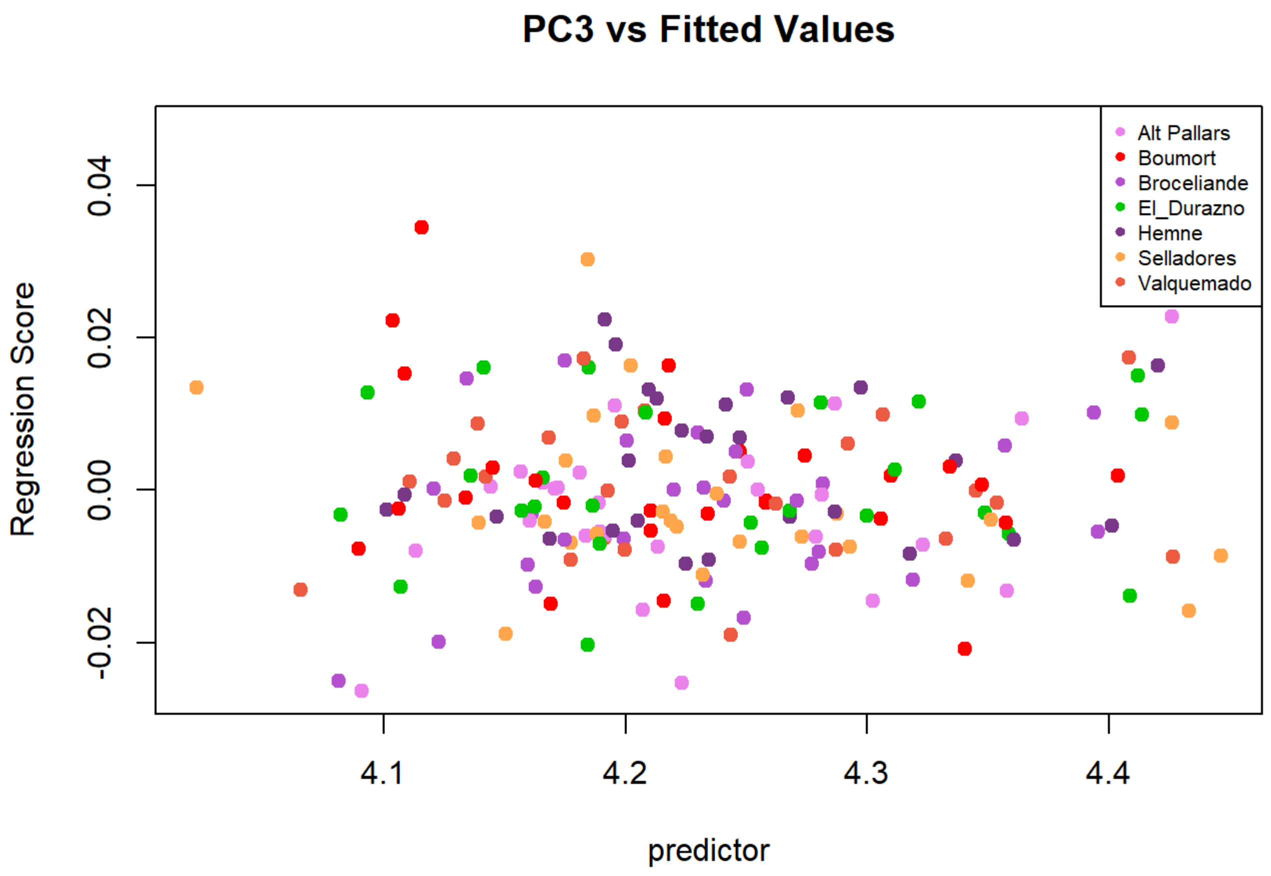
```
# Graphic "PC1 vs Csize"
plot(fit.size.PC1, type = "regression", predictor = log(gdf$Csize), reg.type = "RegScore", pc
h = 19, col = Colors_ALL_Cervus_pop, main = "PC2 vs Fitted Values")
legend("topright", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch =
19, cex= 0.65)
```



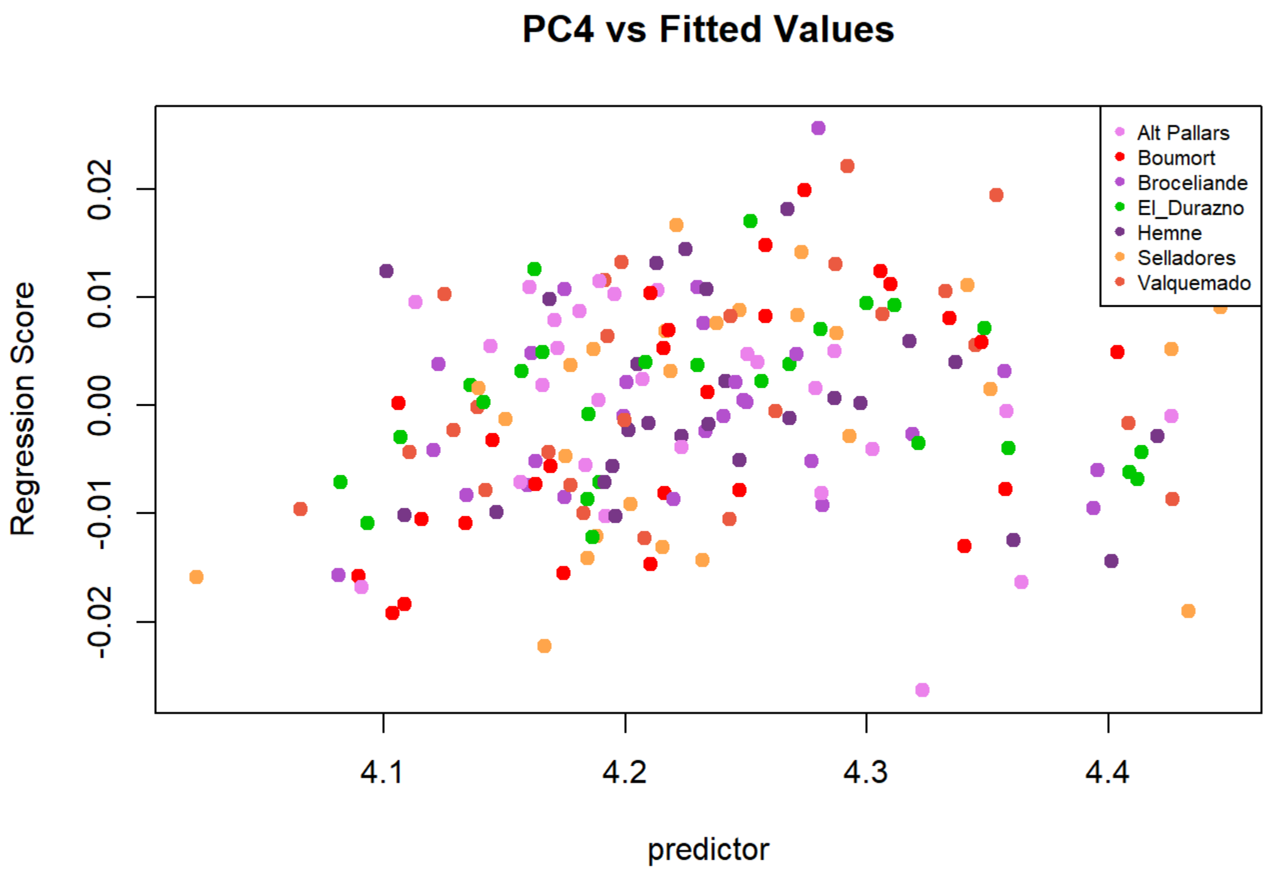
```
# Graphic "PC2 vs Csize"
plot(fit.size.PC2, type = "regression", predictor = log(gdf$Csize), reg.type = "RegScore", pc
h = 19, col = Colors_ALL_Cervus_pop, main = "PC2 vs Fitted Values")
legend("topright", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch =
19, cex= 0.65)
```



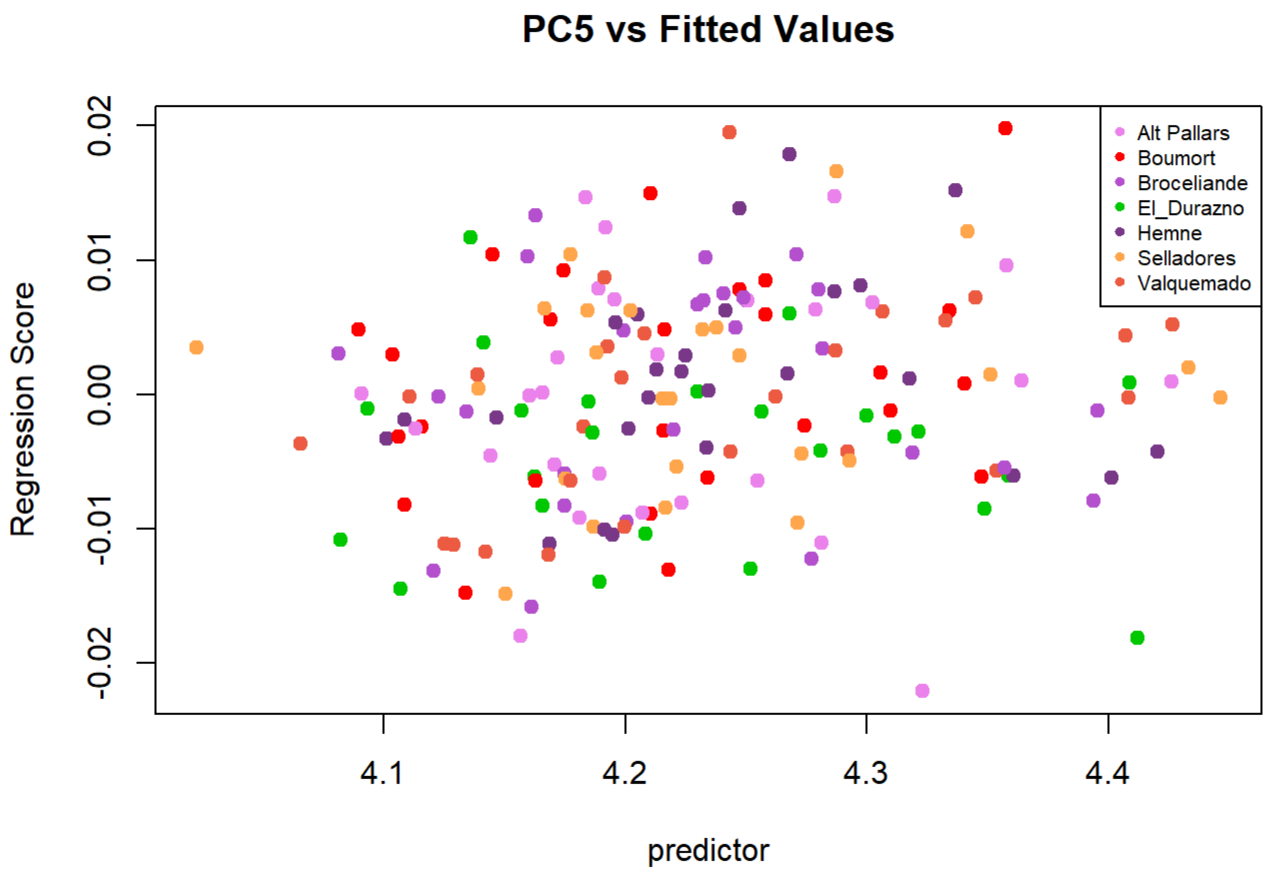
```
# Graphic "PC3 vs Fitted Values"
plot(fit.size.PC3, type = "regression", predictor = log(gdf$Csize), reg.type = "RegScore", pc
h = 19, col = Colors_ALL_Cervus_pop, main = "PC3 vs Fitted Values")
legend("topright", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch =
19, cex= 0.65)
```



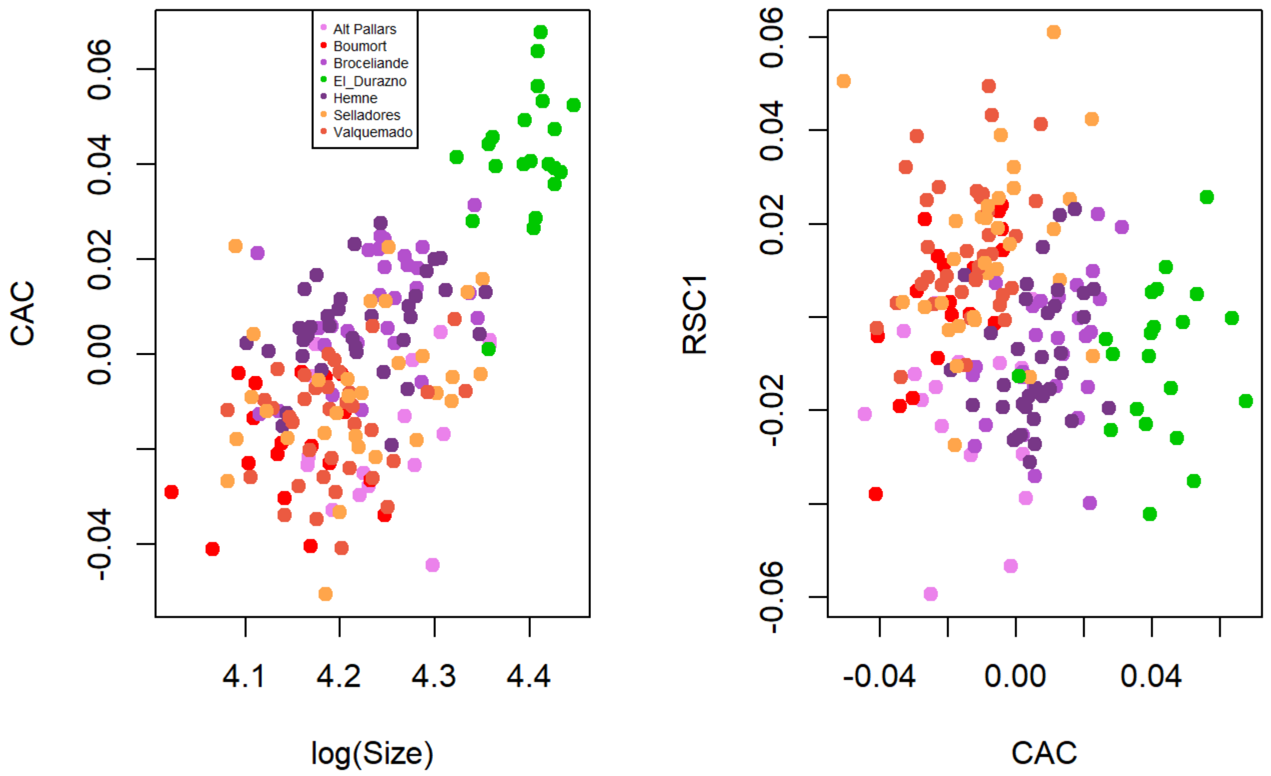
```
# Graphic "PC4 vs Fitted Values"
plot(fit.size.PC4, type = "regression", predictor = log(gdf$Csize), reg.type = "RegScore", pc
h = 19, col = Colors_ALL_Cervus_pop, main = "PC4 vs Fitted Values")
legend("topright", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch =
19, cex= 0.65)
```



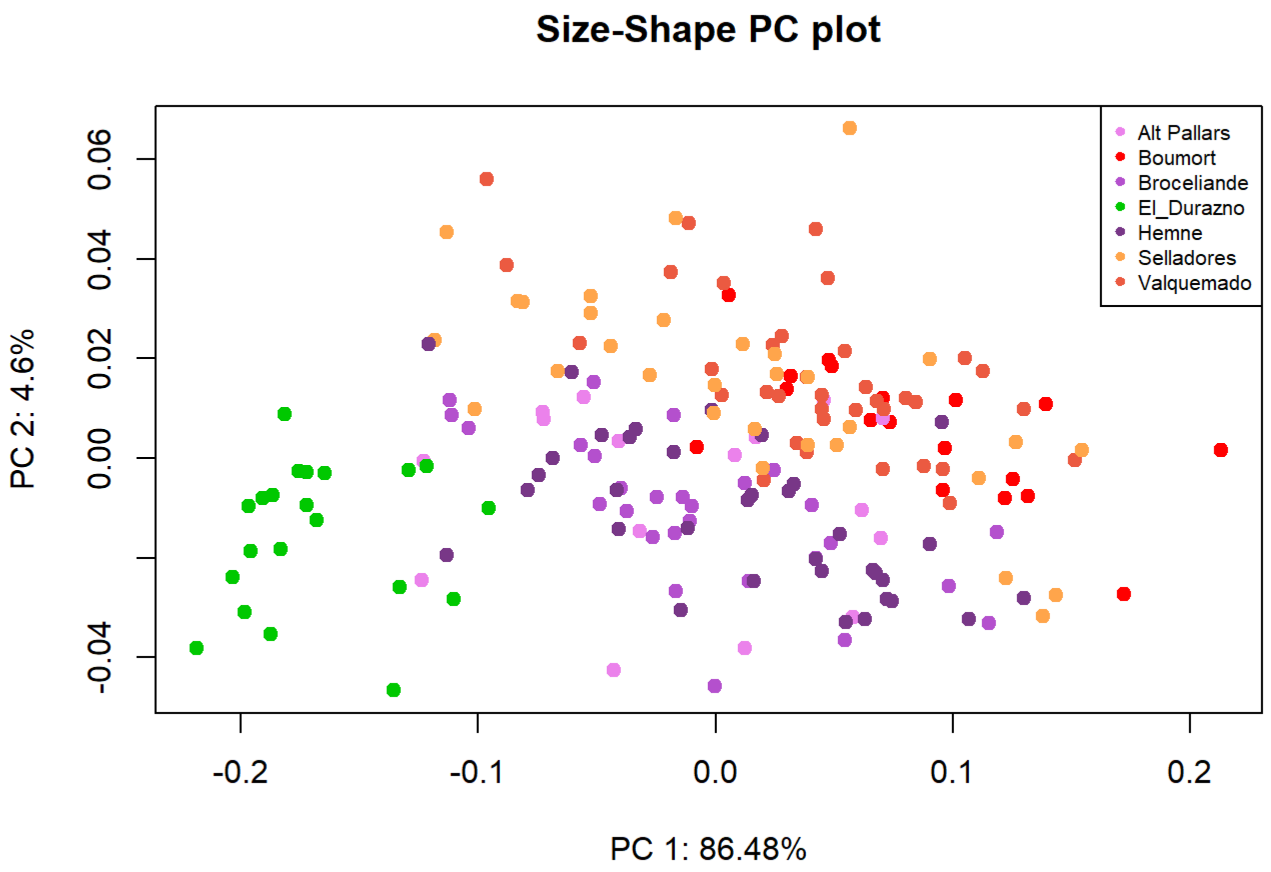
```
# Graphic "PC5 vs Fitted Values"
plot(fit.size.PC5, type = "regression", predictor = log(gdf$Csize), reg.type = "RegScore", pc
h = 19, col = Colors_ALL_Cervus_pop, main = "PC5 vs Fitted Values")
legend("topright", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch =
19, cex= 0.65)
```



```
###Results ###############
# PC1 : size effect (p-value 0.001; R²: 31.25%); pop effect (p-value 0.001; R²: 39.19%)
# PC2 : size effect (p-value 0.001; R²: 5.28%); pop effect (p-value 0.001; R²: 34.0%)
# PC3 : size effect (p-value 0.448; R²: 0.27%); pop effect (p-value 0.045; R²: 6.96%)
# PC4 : size effect (p-value 0.003; R²: 2.9%); pop effect (p-value 0.001; R²: 41.28%)
# PC5 : size effect (p-value 0.012; R²: 2.7%); pop effect (p-value 0.001; R²: 27.42%)
# landmark coordinates (shape) change according to the centroid size and pop (only pop for PC 3). The variance explained by populations is always greater.
##########################

plotAllometry(fit.size, size = gdf$Csize, logsz = TRUE, method = "CAC", col = Colors_ALL_Cervus_pop[ALL_Cervus_pop], pch = 19)
legend("topleft", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch = 19, cex= 0.45) #  visualise how the shape of cervid mandibles changes according to their size.
```



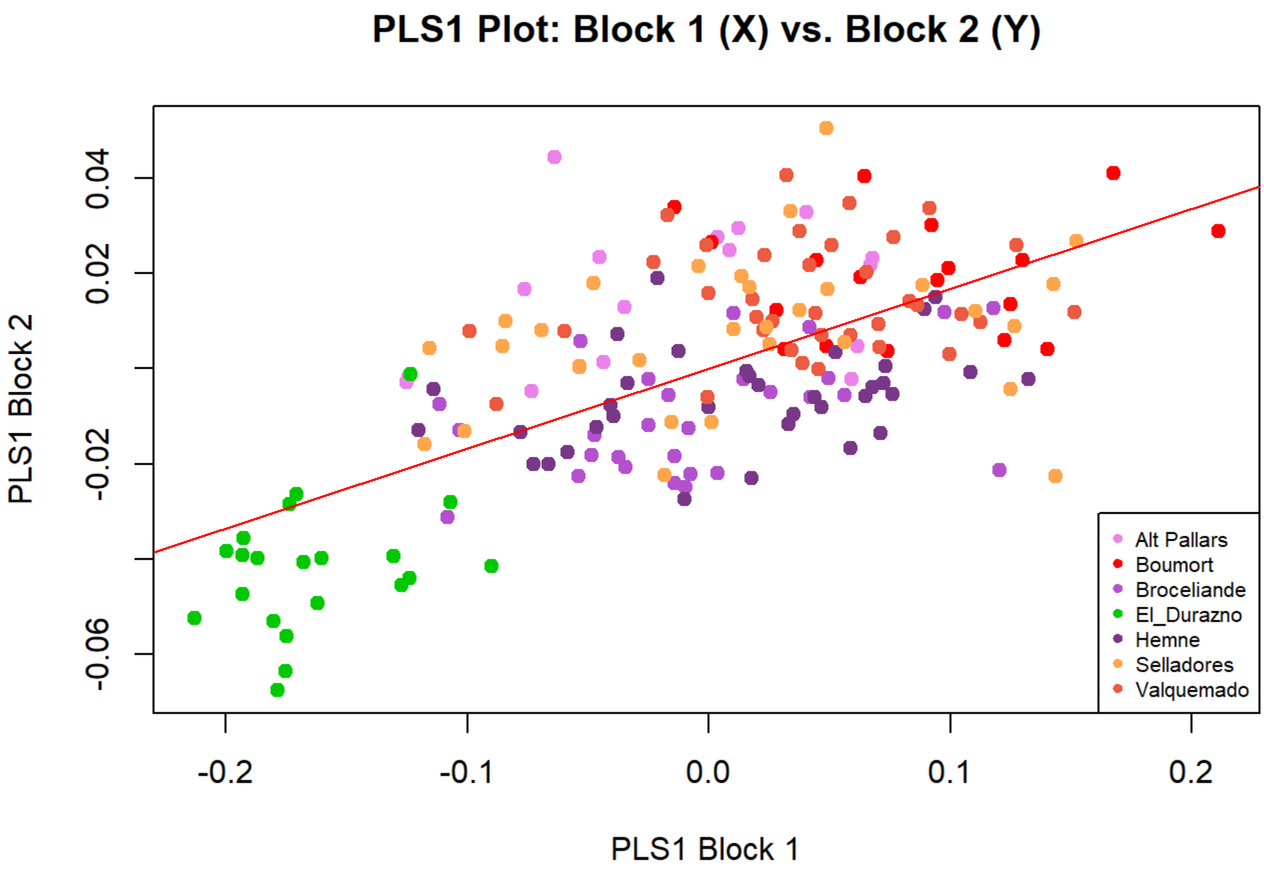
```
plotAllometry(fit.size, size = gdf$Csize, logsz = TRUE, method = "size.shape", col = Colors_A
LL_Cervus_pop[ALL_Cervus_pop], pch = 19)
legend("topright", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch =
19, cex= 0.65)
```



```
# Partial Least Squares : explore the relationship between the logarithmic centroid size and
the coordinates of the landmarks. PLS analysis seeks to maximise the covariance between centr
oid size and landmark coordinates. r-PLS² gives an estimate of the proportion of variance in
landmark coordinates that is explained by centroid size alone.
PLS <- two.b.pls(log(gdf$Csize), gdf$coords, print.progress = FALSE)
PLS # (r-PLS varies between -1 and 1)
```

```
##
## Call:
## two.b.pls(A1 = log(gdf$Csize), A2 = gdf$coords, print.progress = FALSE)
##
##
##
## r-PLS: 0.641
##
## Effect Size (Z): 6.2082
##
## P-value: 0.001
##
## Based on 1000 random permutations
```

```
plot(PLS, col = Colors_ALL_Cervus_pop[ALL_Cervus_pop], pch = 19)
legend("bottomright", legend = names(Colors_ALL_Cervus_pop), col = Colors_ALL_Cervus_pop, pch
= 19, cex= 0.65)
```



```
###Results ###############
#There is a moderate-strong (r-PLS: 0.641) and statistically significant (P-value: 0.001) cor
relation between centroid size and mandible shape. The variance explained by size is R²≈(r-PL
S)²=0.428, indicating that 43% of the variation in shape is due to size, while 57% is explain
ed by other factors.
# Effect Size (Z): 6.2082 : Indicates a significant difference between the observed correlati
on and the null distribution, suggesting a significative correlation between shape and size
##########################
```

3 DATASET 3 : ALL_Rusa

i. Can we identify shape and size differences at the intra-population scale, between contrasted environments ?

3.1 Part 1 : data preparation :

```
Descriptive_ALL_Rusa <- read_excel("Descriptive_ALL_Rusa.xlsx") # importing environmental inf
ormation
View(Descriptive_ALL_Rusa)
summary(Descriptive_ALL_Rusa)
```

```
##   TPS POSITION        Ref               Length        Species         
##  Min.   : 60.00   Length:130         Min.   :18.41   Length:130        
##  1st Qu.: 92.25   Class :character   1st Qu.:20.07   Class :character  
##  Median :133.50   Mode  :character   Median :20.89   Mode  :character  
##  Mean   :138.93                      Mean   :20.83                     
##  3rd Qu.:165.75                      3rd Qu.:21.58                     
##  Max.   :272.00                      Max.   :23.18                     
##      Sex                Pop                 Lat             Long       
##  Length:130         Length:130         Min.   :165.2   Min.   :-21.65  
##  Class :character   Class :character   1st Qu.:165.2   1st Qu.:-21.61  
##  Mode  :character   Mode  :character   Median :165.4   Median :-21.57  
##                                        Mean   :165.4   Mean   :-21.54  
##                                        3rd Qu.:165.6   3rd Qu.:-21.46  
##                                        Max.   :165.8   Max.   :-21.46  
##  Vegetation_type       Climat            Genet         Herb_Monocots  
##  Length:130         Length:130         Mode:logical   Mode:logical   
##  Class :character   Class :character   NA's:130       NA's:130       
##  Mode  :character   Mode  :character                                 
##                                                                      
##                                                                      
## 
```

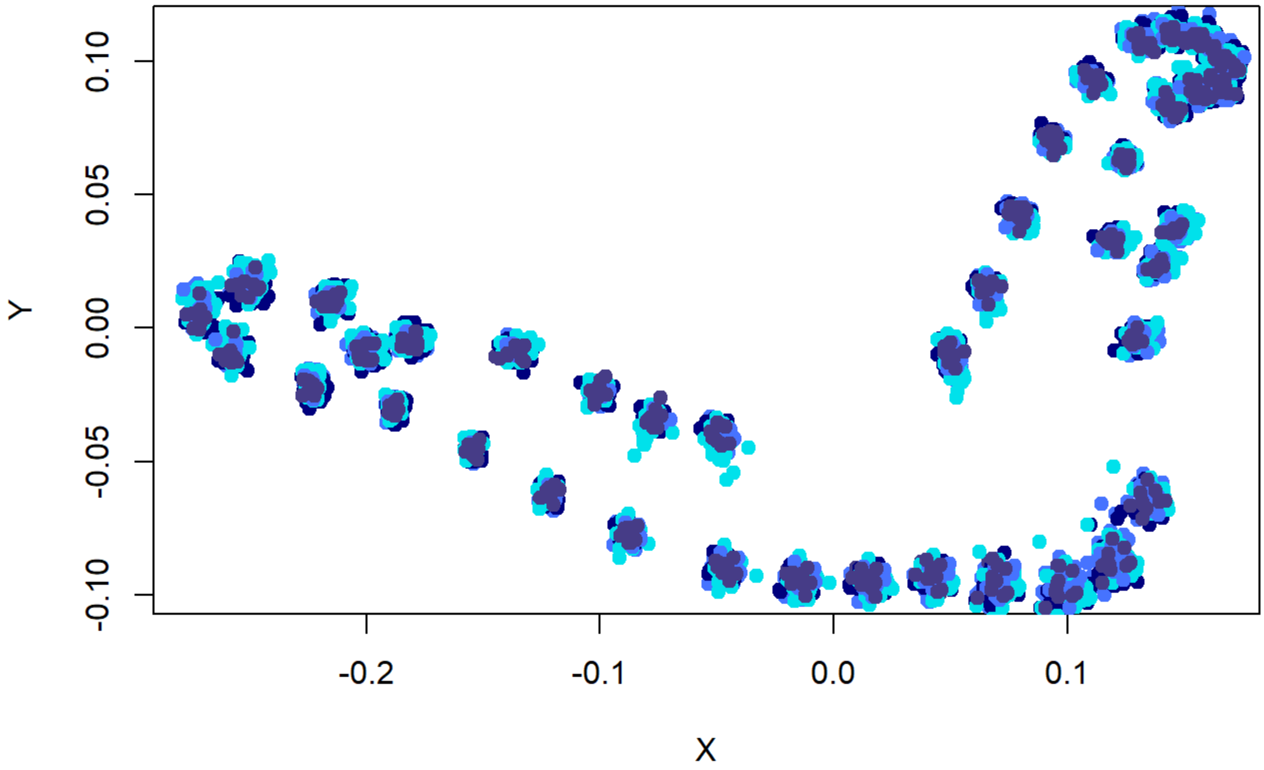
```
ALL_Rusa_pop <- Descriptive_ALL_Rusa$Pop
ALL_Rusa_sex<- Descriptive_ALL_Rusa$Sex

## morphometry-geometry data :
# We import in R the tps file produced with tps and Matlab :

MorphoGeom_ALL_Rusa <- readland.tps("MorphoGeom_ALL_Rusa.TPS", specID = "ID")
```

```
## 
## No curves detected; all points appear to be fixed landmarks.
```

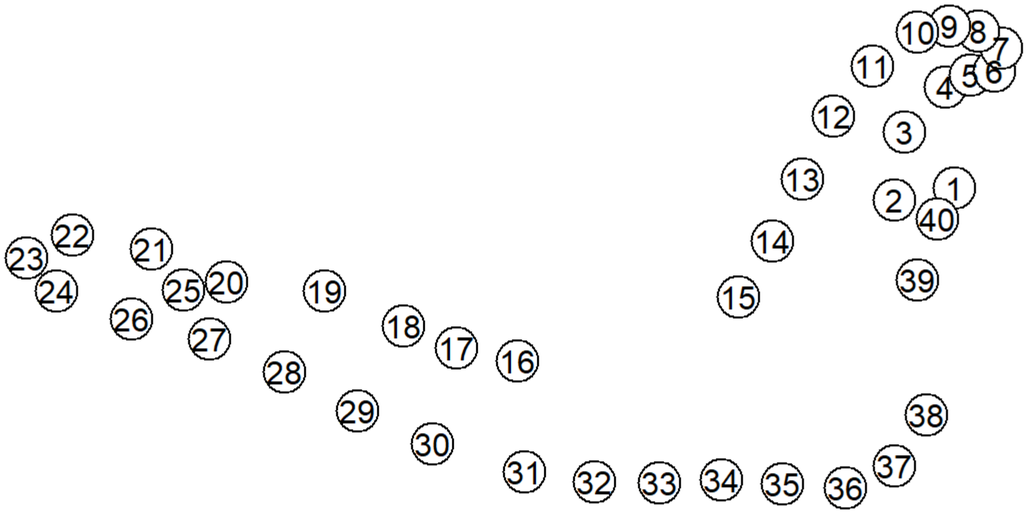
```
# In "MorphoGeom_ALL_Rusa", no curves are detected; all points appear to be fixed landmarks.
# To connect the points, we generate a matrix with gmShiny ("Matrix")
Matrix <- as.matrix(read.csv("Matrix.csv"))

# Semi-landmarks are identified, slided and a procrust analysis is done:
Slided_MorphoGeom_ALL_Rusa <- gpagen(MorphoGeom_ALL_Rusa, PrinAxes = FALSE, print.progress = 
FALSE, curves = Matrix)
options(max.print=1000000000)
```

3.2 Part 2: data visualization:

```
Colors_ALL_Rusa_pop <- c("Gouaro_Deva"= "turquoise2", "Le-Cap"= "royalblue1", "Misere"= "dark
slateblue", "PGF"= "navyblue") # identify Rusa deer by habitat
point_colors_pop <- Colors_ALL_Rusa_pop[ALL_Rusa_pop] # Color vector by habitats

# shape variation :
plot(Slided_MorphoGeom_ALL_Rusa$coords[, , 1], col = point_colors_pop, pch = 19)
for (i in 2:dim(Slided_MorphoGeom_ALL_Rusa$coords)[3]) {
  points(Slided_MorphoGeom_ALL_Rusa$coords[, , i], col = point_colors_pop[i], pch = 19)
}
```



```
mean_shape <- mshape(Slided_MorphoGeom_ALL_Rusa$coords)  # Consensus shape
plot(mean_shape)
```



3.3 Part 3 : Analysis

3.3.1 Centroid size :

```
centroid_sizes <- Slided_MorphoGeom_ALL_Rusa$Csize
Descriptive_ALL_Rusa$Centroid_Size <- centroid_sizes
summary(Descriptive_ALL_Rusa)
```

```
##   TPS POSITION        Ref                 Length        Species         
##  Min.   : 60.00   Length:130         Min.   :18.41   Length:130        
##  1st Qu.: 92.25   Class :character   1st Qu.:20.07   Class :character  
##  Median :133.50   Mode  :character   Median :20.89   Mode  :character  
##  Mean   :138.93                      Mean   :20.83                     
##  3rd Qu.:165.75                      3rd Qu.:21.58                     
##  Max.   :272.00                      Max.   :23.18                     
##      Sex                Pop                 Lat             Long       
##  Length:130         Length:130         Min.   :165.2   Min.   :-21.65  
##  Class :character   Class :character   1st Qu.:165.2   1st Qu.:-21.61  
##  Mode  :character   Mode  :character   Median :165.4   Median :-21.57  
##                                        Mean   :165.4   Mean   :-21.54  
##                                        3rd Qu.:165.6   3rd Qu.:-21.46  
##                                        Max.   :165.8   Max.   :-21.46  
##  Vegetation_type       Climat           Genet         Herb_Monocots 
##  Length:130         Length:130         Mode:logical   Mode:logical  
##  Class :character   Class :character   NA's:130       NA's:130      
##  Mode  :character   Mode  :character                                
##                                                                     
##                                                                     
##                                                                     
##  Centroid_Size  
##  Min.   :44.56  
##  1st Qu.:48.52  
##  Median :50.46  
##  Mean   :50.37  
##  3rd Qu.:51.89  
##  Max.   :57.46
```

```
view(Descriptive_ALL_Rusa)
Gouaro_Deva_centroid_sizes <- Descriptive_ALL_Rusa$Centroid_Size[Descriptive_ALL_Rusa$Pop == "Gouaro_Deva"]
LeCap_centroid_sizes <- Descriptive_ALL_Rusa$Centroid_Size[Descriptive_ALL_Rusa$Pop == "Le-Cap"]
Misere_centroid_sizes <- Descriptive_ALL_Rusa$Centroid_Size[Descriptive_ALL_Rusa$Pop == "Misere"]
PGF_centroid_sizes <- Descriptive_ALL_Rusa$Centroid_Size[Descriptive_ALL_Rusa$Pop == "PGF"]

anova_result <- aov(Centroid_Size ~ Pop, data = Descriptive_ALL_Rusa)
summary(anova_result)
```

```
##              Df Sum Sq Mean Sq F value   Pr(>F)    
## Pop           3  137.8   45.95    7.66 9.61e-05 ***
## Residuals   126  755.8    6.00                     
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

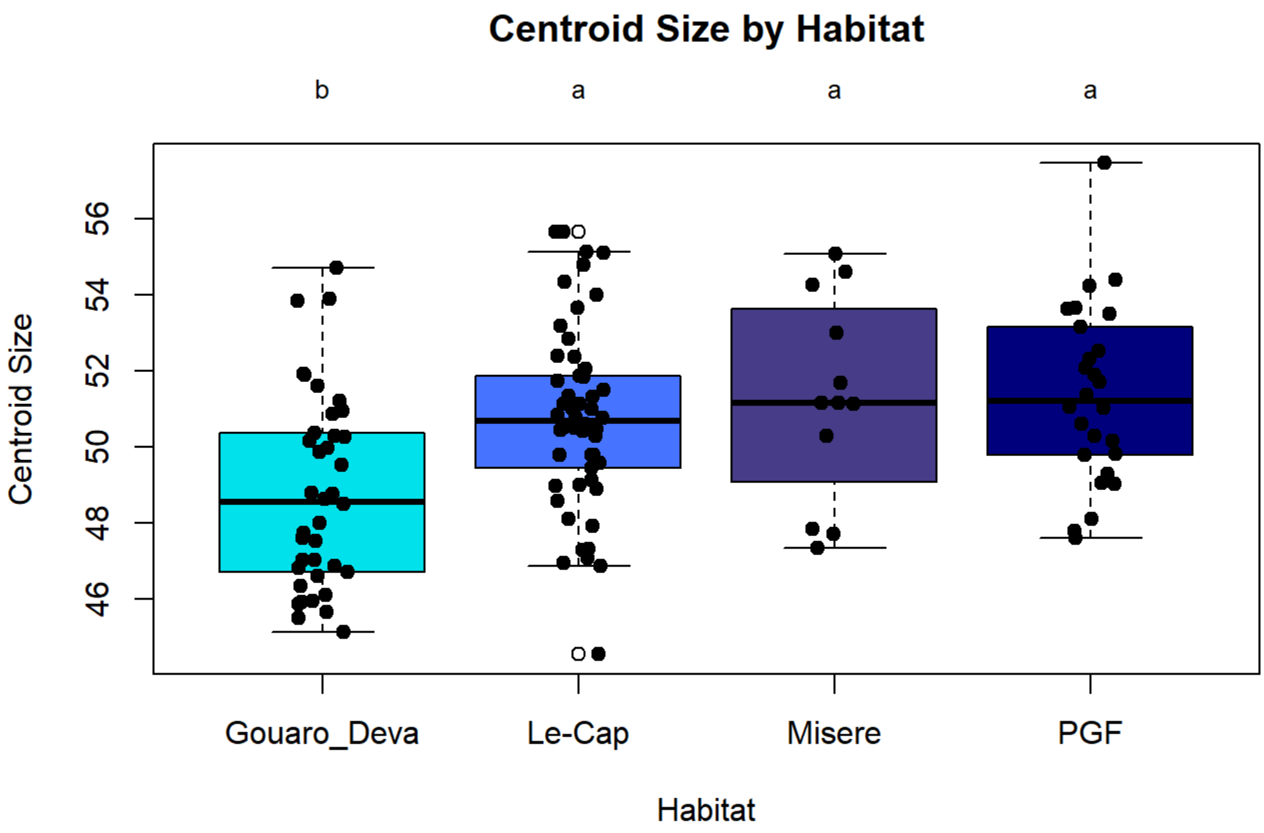
```
###Results ###############
# p-value = 9.61e-05 : Based on the anova, Rusa deer from different habitats differ statistic
ally in size. See detail of the Duncan test for inter-population differences in size
##########################

# Duncan post-hoc test:
duncan_result <- duncan.test(anova_result, "Pop", console = TRUE)
```

```
##
## Study: anova_result ~ "Pop"
##
## Duncan's new multiple range test
## for Centroid_Size
##
## Mean Square Error:  5.998182
##
## Pop,  means
##
##             Centroid_Size      std  r      Min      Max
## Gouaro_Deva      48.80802 2.546040 38 45.14950 54.70470
## Le-Cap           50.77977 2.383276 54 44.56368 55.67220
## Misere           51.28140 2.666933 12 47.36255 55.08639
## PGF              51.37179 2.337923 26 47.61163 57.46461
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##             Centroid_Size groups
## PGF              51.37179      a
## Misere           51.28140      a
## Le-Cap           50.77977      a
## Gouaro_Deva      48.80802      b
```

```
print(duncan_result)
```

```
## $statistics
##    MSerror  Df     Mean       CV
##   5.998182 126 50.36812 4.862438
##
## $parameters
##     test name.t ntr alpha
##   Duncan    Pop   4  0.05
##
## $duncan
## NULL
##
## $means
##             Centroid_Size      std  r      Min      Max      Q25      Q50
## Gouaro_Deva      48.80802 2.546040 38 45.14950 54.70470 46.73693 48.56485
## Le-Cap           50.77977 2.383276 54 44.56368 55.67220 49.47951 50.68526
## Misere           51.28140 2.666933 12 47.36255 55.08639 49.68780 51.16805
## PGF              51.37179 2.337923 26 47.61163 57.46461 49.79575 51.22293
##                  Q75
## Gouaro_Deva 50.35379
## Le-Cap      51.87844
## Misere      53.30869
## PGF         52.99900
##
## $comparison
## NULL
##
## $groups
##             Centroid_Size groups
## PGF              51.37179      a
## Misere           51.28140      a
## Le-Cap           50.77977      a
## Gouaro_Deva      48.80802      b
##
## attr(,"class")
## [1] "group"
```

```
duncan_labels <- duncan_result$groups
duncan_labels <- duncan_labels[order(rownames(duncan_labels)), ]
Descriptive_ALL_Rusa$labels <- factor(duncan_labels$groups[match(Descriptive_ALL_Rusa$Pop, rownames(duncan_labels))])

par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(Centroid_Size ~ Pop, data = Descriptive_ALL_Rusa, main = "Centroid Size by Habitat", xlab = "Habitat", ylab = "Centroid Size", col = c("turquoise2","royalblue1","darkslateblue","navyblue"))
stripchart(Centroid_Size ~ Pop, data = Descriptive_ALL_Rusa, vertical = TRUE, method = "jitter", add = TRUE, pch = 19, col = "black")
mtext(duncan_labels$groups, at = 1:length(duncan_labels$groups), side = 3, line = 1, cex = 0.8)
```



3.3.2 Principal Component Analysis (PCA):

```
PCA_ALL_Rusa <- gm.prcomp(Slided_MorphoGeom_ALL_Rusa$coords)
summary(PCA_ALL_Rusa)
```

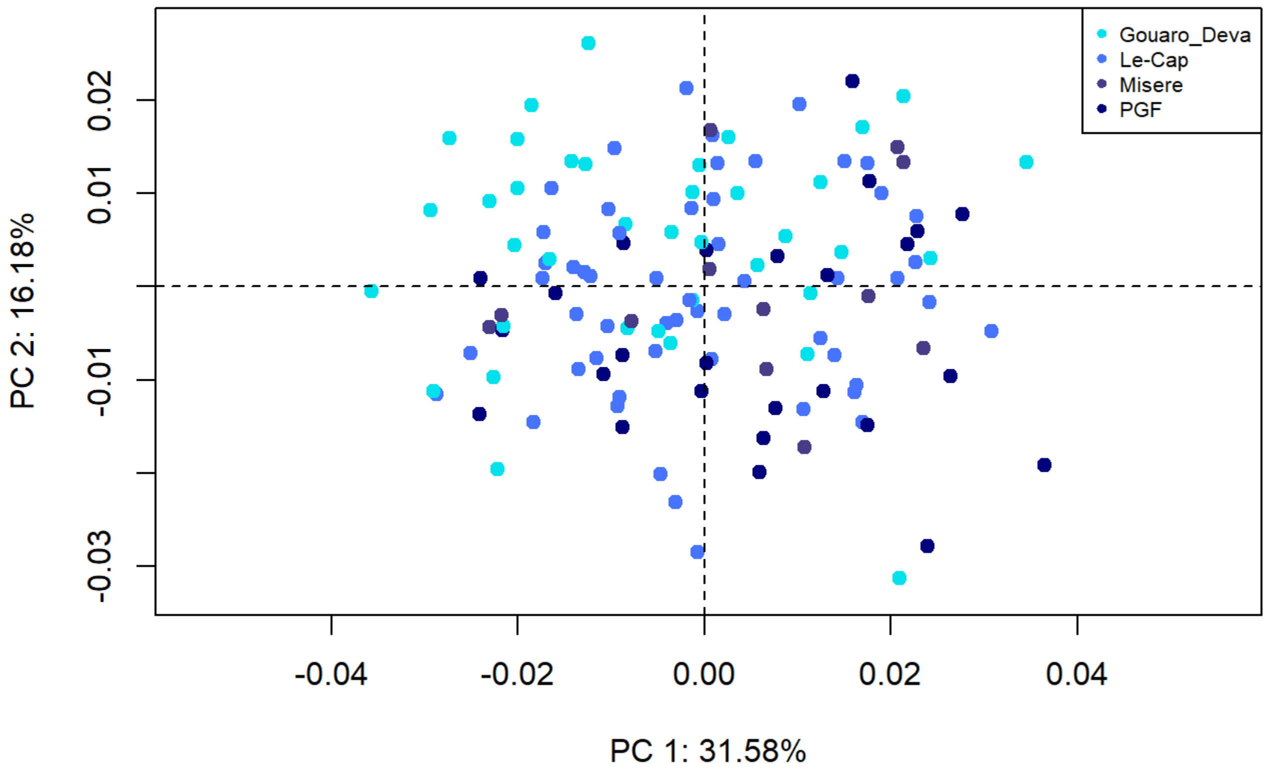
```
##
## Ordination type: Principal Component Analysis
## Centering by OLS mean
## Orthogonal projection of OLS residuals
## Number of observations: 130
## Number of vectors 78
##
## Importance of Components:
##                               Comp1        Comp2        Comp3        Comp4
## Eigenvalues            0.0002571217 0.0001317077 8.822072e-05 0.0000530167
## Proportion of Variance 0.3158143890 0.1617724154 1.083587e-01 0.0651187237
## Cumulative Proportion  0.3158143890 0.4775868044 5.859455e-01 0.6510642281
##                               Comp5        Comp6        Comp7        Comp8
## Eigenvalues            4.632857e-05 3.592713e-05 3.454956e-05 2.193714e-05
## Proportion of Variance 5.690391e-02 4.412815e-02 4.243613e-02 2.694469e-02
## Cumulative Proportion  7.079681e-01 7.520963e-01 7.945324e-01 8.214771e-01
##                               Comp9       Comp10       Comp11       Comp12
## Eigenvalues            1.952721e-05 1.755023e-05 1.557606e-05 1.261781e-05
## Proportion of Variance 2.398465e-02 2.155639e-02 1.913158e-02 1.549805e-02
## Cumulative Proportion  8.454618e-01 8.670181e-01 8.861497e-01 9.016478e-01
##                              Comp13       Comp14       Comp15       Comp16
## Eigenvalues            1.024885e-05 8.503219e-06 6.696332e-06 6.199234e-06
## Proportion of Variance 1.258834e-02 1.044423e-02 8.224890e-03 7.614322e-03
## Cumulative Proportion  9.142361e-01 9.246803e-01 9.329052e-01 9.405196e-01
##                              Comp17       Comp18       Comp19       Comp20
## Eigenvalues            5.098849e-06 4.446505e-06 4.296511e-06 3.976548e-06
## Proportion of Variance 6.262753e-03 5.461500e-03 5.277267e-03 4.884267e-03
## Cumulative Proportion  9.467823e-01 9.522438e-01 9.575211e-01 9.624053e-01
##                              Comp21       Comp22       Comp23       Comp24
## Eigenvalues            2.912715e-06 2.698811e-06 2.479884e-06 2.194219e-06
## Proportion of Variance 3.577595e-03 3.314864e-03 3.045963e-03 2.695090e-03
## Cumulative Proportion  9.659829e-01 9.692978e-01 9.723438e-01 9.750388e-01
##                              Comp25       Comp26       Comp27       Comp28
## Eigenvalues            2.044486e-06 2.008307e-06 1.686008e-06 1.585496e-06
## Proportion of Variance 2.511178e-03 2.466740e-03 2.070870e-03 1.947414e-03
## Cumulative Proportion  9.775500e-01 9.800168e-01 9.820876e-01 9.840351e-01
##                              Comp29       Comp30       Comp31       Comp32
## Eigenvalues            1.428093e-06 1.226231e-06 1.131207e-06 9.772767e-07
## Proportion of Variance 1.754081e-03 1.506141e-03 1.389425e-03 1.200358e-03
## Cumulative Proportion  9.857891e-01 9.872953e-01 9.886847e-01 9.898851e-01
##                              Comp33       Comp34       Comp35       Comp36
## Eigenvalues            9.138389e-07 8.532153e-07 7.830076e-07 7.107082e-07
## Proportion of Variance 1.122439e-03 1.047977e-03 9.617432e-04 8.729403e-04
## Cumulative Proportion  9.910075e-01 9.920555e-01 9.930172e-01 9.938902e-01
##                              Comp37       Comp38       Comp39       Comp40
## Eigenvalues            6.433006e-07 5.537866e-07 5.305267e-07 5.146236e-07
## Proportion of Variance 7.901456e-04 6.801984e-04 6.516291e-04 6.320958e-04
## Cumulative Proportion  9.946803e-01 9.953605e-01 9.960121e-01 9.966442e-01
##                              Comp41       Comp42       Comp43       Comp44
## Eigenvalues            4.082765e-07 3.336406e-07 3.176950e-07 2.981548e-07
## Proportion of Variance 5.014731e-04 4.098001e-04 3.902146e-04 3.662140e-04
## Cumulative Proportion  9.971457e-01 9.975555e-01 9.979457e-01 9.983119e-01
##                              Comp45       Comp46       Comp47       Comp48
## Eigenvalues            2.741090e-07 2.255784e-07 2.079630e-07 1.673278e-07
## Proportion of Variance 3.366794e-04 2.770708e-04 2.554343e-04 2.055234e-04
```

```
## Cumulative Proportion  9.986486e-01 9.989257e-01 9.991811e-01 9.993866e-01
##                              Comp49       Comp50       Comp51       Comp52
## Eigenvalues            1.456958e-07 1.101109e-07 8.767784e-08 4.998987e-08
## Proportion of Variance 1.789535e-04 1.352457e-04 1.076919e-04 6.140097e-05
## Cumulative Proportion  9.995656e-01 9.997008e-01 9.998085e-01 9.998699e-01
##                              Comp53       Comp54       Comp55       Comp56
## Eigenvalues            3.583891e-08 1.380891e-08 1.084597e-08 8.977543e-09
## Proportion of Variance 4.401978e-05 1.696104e-05 1.332176e-05 1.102683e-05
## Cumulative Proportion  9.999139e-01 9.999309e-01 9.999442e-01 9.999553e-01
##                              Comp57       Comp58       Comp59       Comp60
## Eigenvalues            6.872444e-09 5.486381e-09 4.289668e-09 3.764642e-09
## Proportion of Variance 8.441203e-06 6.738747e-06 5.268862e-06 4.623989e-06
## Cumulative Proportion  9.999637e-01 9.999704e-01 9.999757e-01 9.999803e-01
##                              Comp61       Comp62       Comp63       Comp64
## Eigenvalues            2.431077e-09 2.096434e-09 1.814018e-09 1.705003e-09
## Proportion of Variance 2.986014e-06 2.574983e-06 2.228100e-06 2.094201e-06
## Cumulative Proportion  9.999833e-01 9.999859e-01 9.999881e-01 9.999902e-01
##                              Comp65       Comp66       Comp67       Comp68
## Eigenvalues            1.337926e-09 1.189902e-09 1.088917e-09 8.766919e-10
## Proportion of Variance 1.643332e-06 1.461519e-06 1.337482e-06 1.076813e-06
## Cumulative Proportion  9.999919e-01 9.999933e-01 9.999947e-01 9.999957e-01
##                              Comp69       Comp70       Comp71       Comp72
## Eigenvalues            7.479718e-10 6.370670e-10 5.419106e-10 4.356540e-10
## Proportion of Variance 9.187100e-07 7.824891e-07 6.656115e-07 5.351000e-07
## Cumulative Proportion  9.999966e-01 9.999974e-01 9.999981e-01 9.999986e-01
##                              Comp73       Comp74       Comp75       Comp76
## Eigenvalues            3.888268e-10 2.712544e-10 1.888312e-10 1.440981e-10
## Proportion of Variance 4.775836e-07 3.331732e-07 2.319354e-07 1.769911e-07
## Cumulative Proportion  9.999991e-01 9.999994e-01 9.999997e-01 9.999999e-01
##                              Comp77       Comp78
## Eigenvalues            6.910121e-11 5.098935e-11
## Proportion of Variance 8.487481e-08 6.262859e-08
## Cumulative Proportion  9.999999e-01 1.000000e+00
```

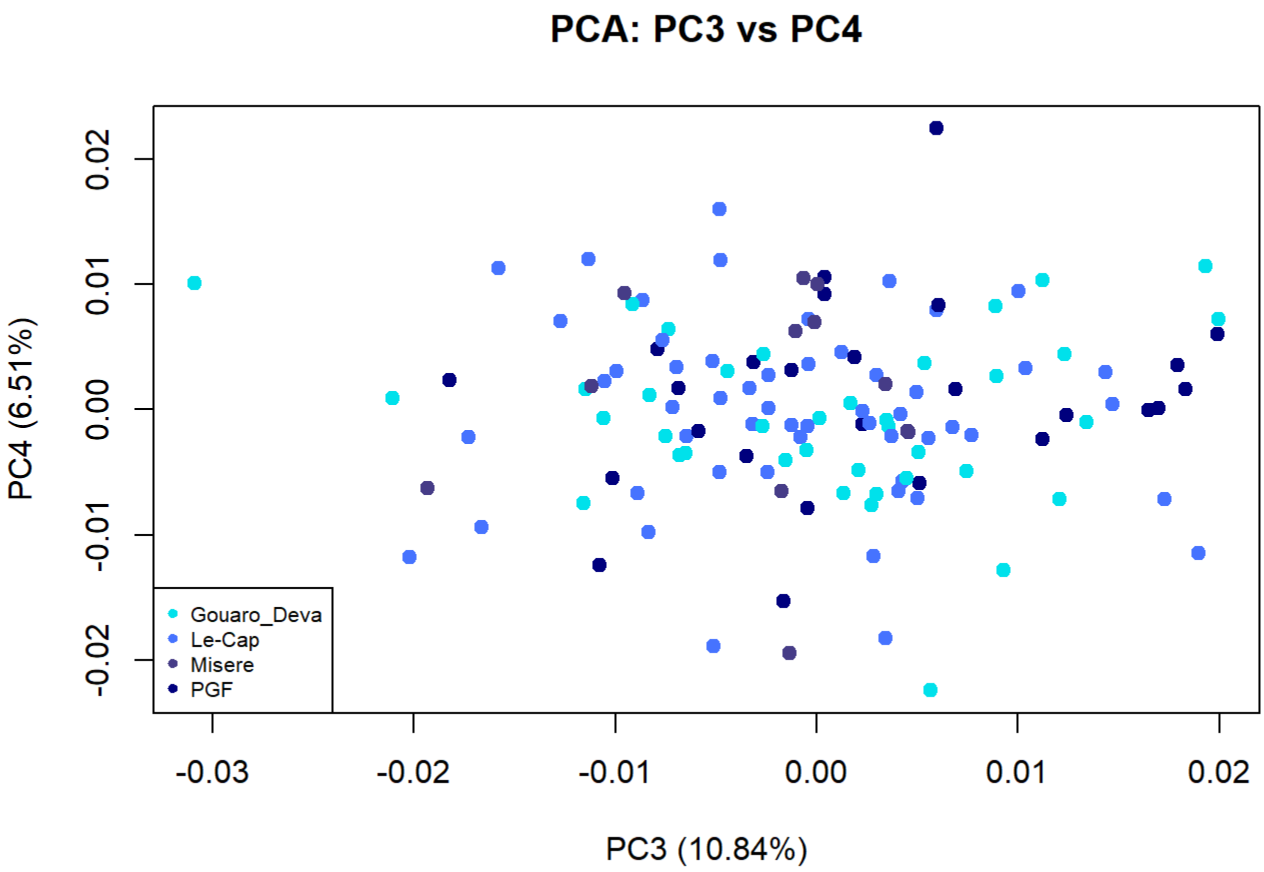
```
PC_scores_PCA_ALL_Rusa <- PCA_ALL_Rusa$x # Extract PC scores
view(PC_scores_PCA_ALL_Rusa)

eigenvalues <- PCA_ALL_Rusa$sdev^2
explained_variance <- eigenvalues / sum(eigenvalues) * 100 # eighenvalues in %
cumulative_variance <- cumsum(explained_variance)
cumulative_variance # (PC 1-8 explain >80% of the variance)
```

```
##     Comp1     Comp2     Comp3     Comp4     Comp5     Comp6     Comp7     Comp8 
##  31.58144  47.75868  58.59455  65.10642  70.79681  75.20963  79.45324  82.14771 
##     Comp9    Comp10    Comp11    Comp12    Comp13    Comp14    Comp15    Comp16 
##  84.54618  86.70181  88.61497  90.16478  91.42361  92.46803  93.29052  94.05196 
##    Comp17    Comp18    Comp19    Comp20    Comp21    Comp22    Comp23    Comp24 
##  94.67823  95.22438  95.75211  96.24053  96.59829  96.92978  97.23438  97.50388 
##    Comp25    Comp26    Comp27    Comp28    Comp29    Comp30    Comp31    Comp32 
##  97.75500  98.00168  98.20876  98.40351  98.57891  98.72953  98.86847  98.98851 
##    Comp33    Comp34    Comp35    Comp36    Comp37    Comp38    Comp39    Comp40 
##  99.10075  99.20555  99.30172  99.38902  99.46803  99.53605  99.60121  99.66442 
##    Comp41    Comp42    Comp43    Comp44    Comp45    Comp46    Comp47    Comp48 
##  99.71457  99.75555  99.79457  99.83119  99.86486  99.89257  99.91811  99.93866 
##    Comp49    Comp50    Comp51    Comp52    Comp53    Comp54    Comp55    Comp56 
##  99.95656  99.97008  99.98085  99.98699  99.99139  99.99309  99.99442  99.99553 
##    Comp57    Comp58    Comp59    Comp60    Comp61    Comp62    Comp63    Comp64 
##  99.99637  99.99704  99.99757  99.99803  99.99833  99.99859  99.99881  99.99902 
##    Comp65    Comp66    Comp67    Comp68    Comp69    Comp70    Comp71    Comp72 
##  99.99919  99.99933  99.99947  99.99957  99.99966  99.99974  99.99981  99.99986 
##    Comp73    Comp74    Comp75    Comp76    Comp77    Comp78 
##  99.99991  99.99994  99.99997  99.99999  99.99999 100.00000
```

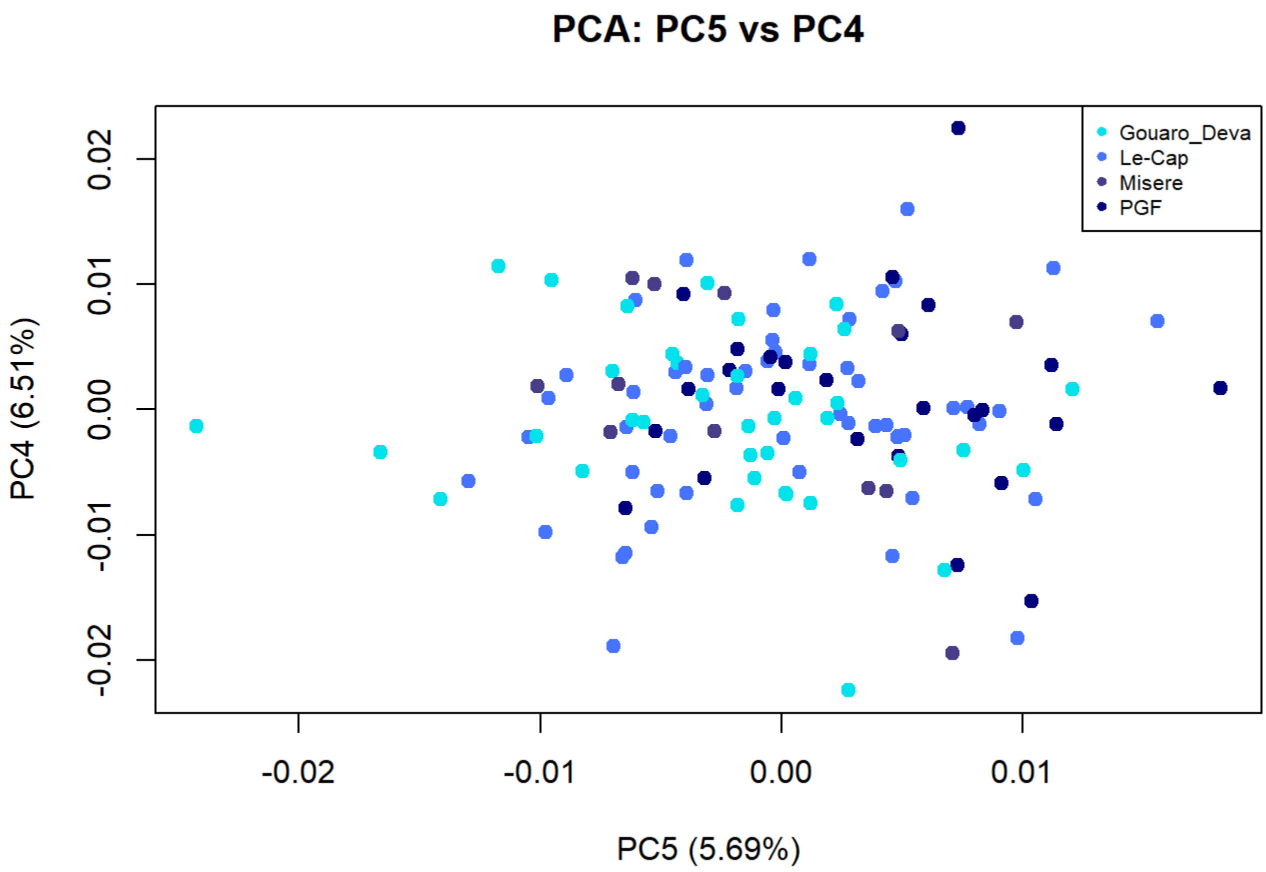
```
PC_scores_PCA_ALL_Rusa <- PCA_ALL_Rusa$x # Extract PC scores
PC1<-PC_scores_PCA_ALL_Rusa[,1]
PC2<-PC_scores_PCA_ALL_Rusa[,2]
PC3<-PC_scores_PCA_ALL_Rusa[,3]
PC4<-PC_scores_PCA_ALL_Rusa[,4]
PC5<-PC_scores_PCA_ALL_Rusa[,5]
PC6<-PC_scores_PCA_ALL_Rusa[,6]
PC7<-PC_scores_PCA_ALL_Rusa[,7]
PC8<-PC_scores_PCA_ALL_Rusa[,8]

plot(PCA_ALL_Rusa, col = Colors_ALL_Rusa_pop[ALL_Rusa_pop], pch = 19)
legend("topright", legend = names(Colors_ALL_Rusa_pop), col = Colors_ALL_Rusa_pop, pch = 19,
cex= 0.65)
```



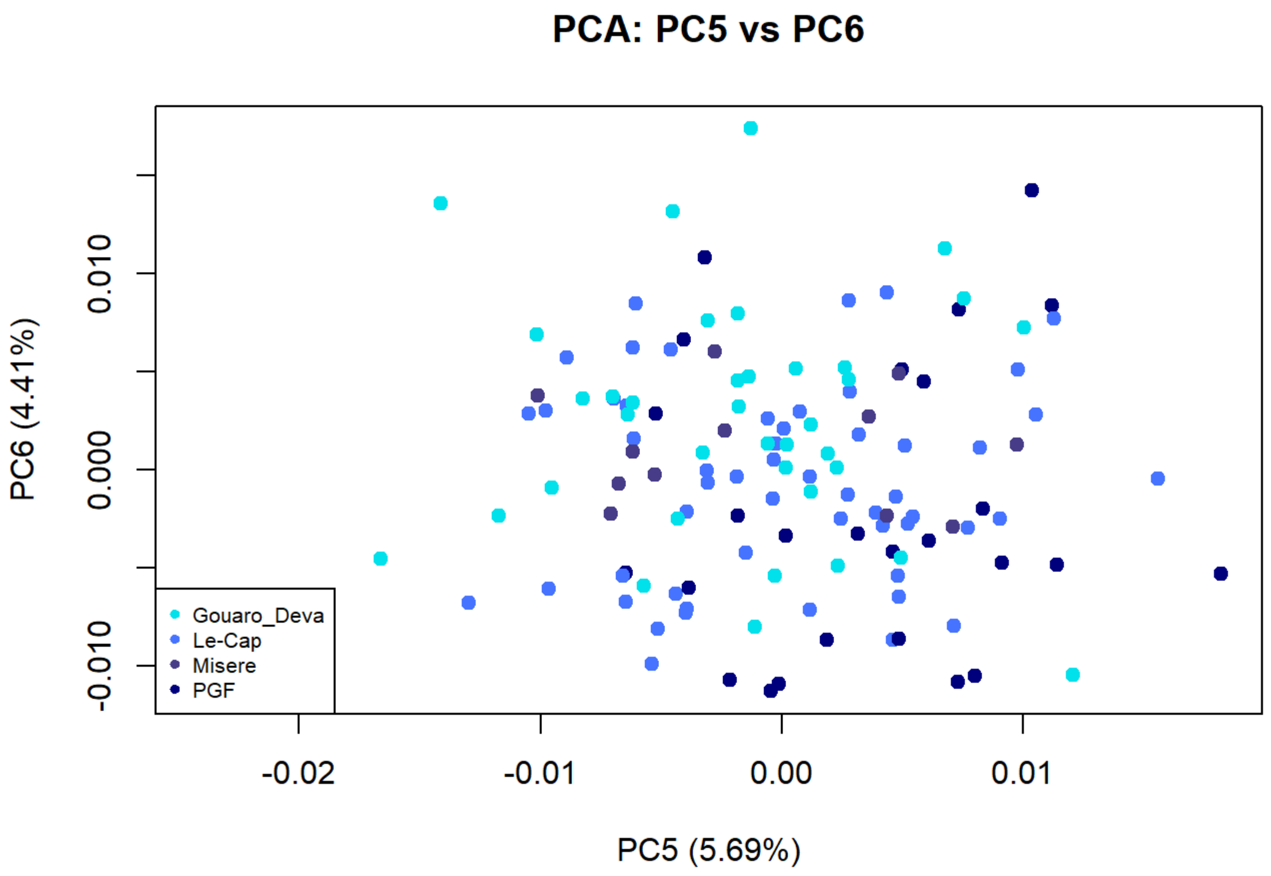
```
plot(PC3, PC4, col = Colors_ALL_Rusa_pop[ALL_Rusa_pop], pch = 19, xlab = paste0("PC3 (", roun
d(explained_variance[3], 2), "%)"), ylab = paste0("PC4 (", round(explained_variance[4], 2),
"%)"), main = "PCA: PC3 vs PC4")
legend("bottomleft", legend = names(Colors_ALL_Rusa_pop), col = Colors_ALL_Rusa_pop, pch = 1
9, cex= 0.65)
```



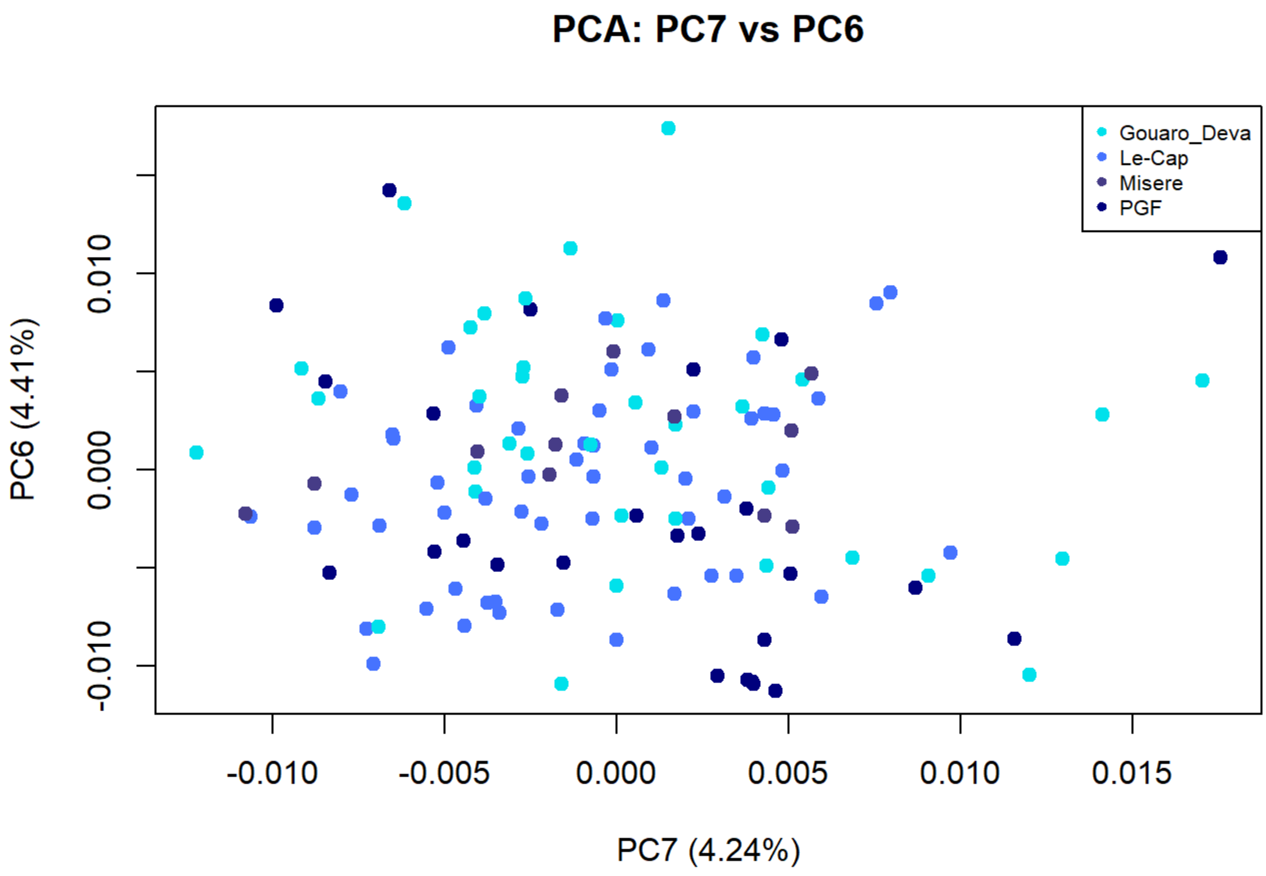
```
plot(PC5, PC4, col = Colors_ALL_Rusa_pop[ALL_Rusa_pop], pch = 19, xlab = paste0("PC5 (", roun
d(explained_variance[5], 2), "%)"), ylab = paste0("PC4 (", round(explained_variance[4], 2),
"%)"), main = "PCA: PC5 vs PC4")
legend("topright", legend = names(Colors_ALL_Rusa_pop), col = Colors_ALL_Rusa_pop, pch = 19,
cex= 0.65)
```



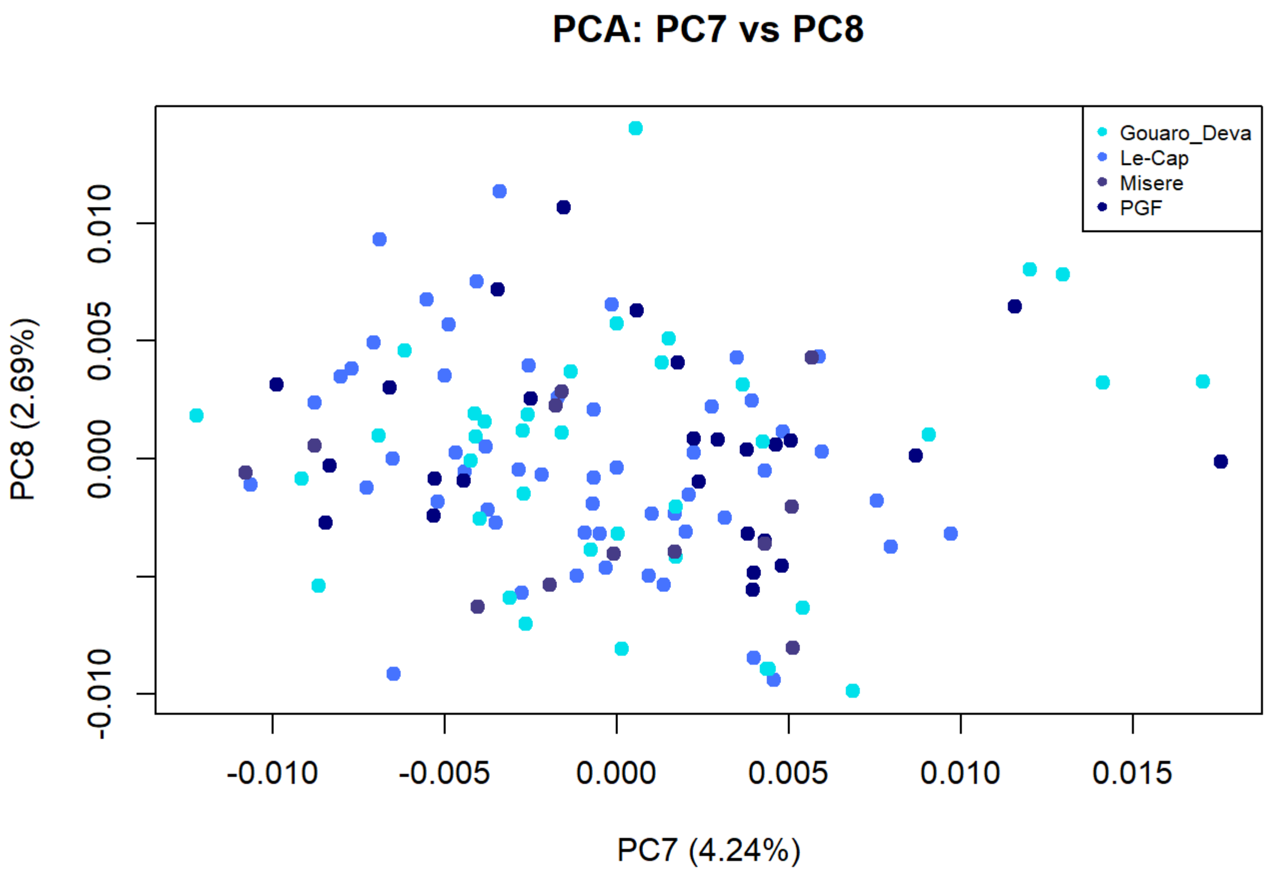
```
plot(PC5, PC6, col = Colors_ALL_Rusa_pop[ALL_Rusa_pop], pch = 19, xlab = paste0("PC5 (", roun
d(explained_variance[5], 2), "%)"), ylab = paste0("PC6 (", round(explained_variance[6], 2),
"%)"), main = "PCA: PC5 vs PC6")
legend("bottomleft", legend = names(Colors_ALL_Rusa_pop), col = Colors_ALL_Rusa_pop, pch = 1
9, cex= 0.65)
```



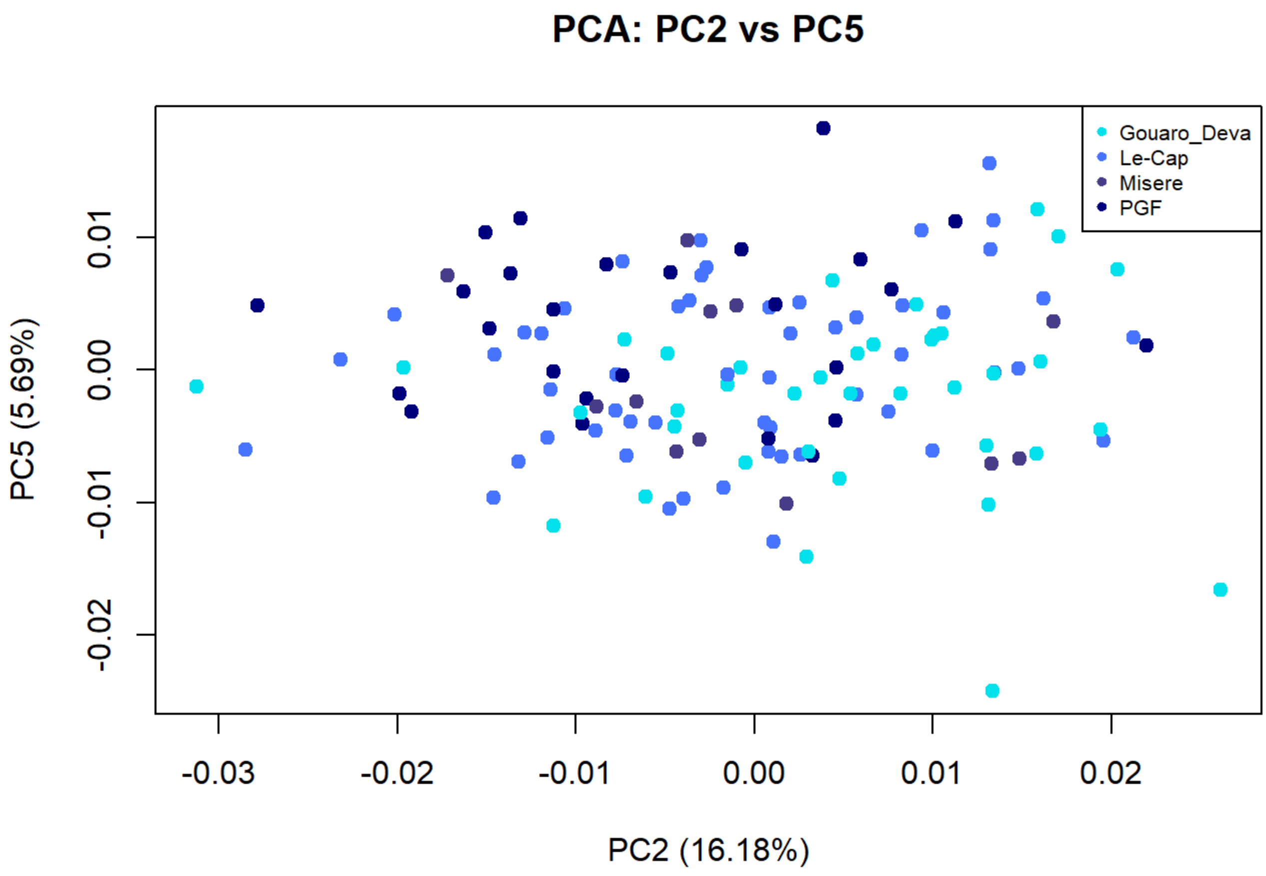
```
plot(PC7, PC6, col = Colors_ALL_Rusa_pop[ALL_Rusa_pop], pch = 19, xlab = paste0("PC7 (", round(explained_variance[7], 2), "%)"), ylab = paste0("PC6 (", round(explained_variance[6], 2), "%)"), main = "PCA: PC7 vs PC6")
legend("topright", legend = names(Colors_ALL_Rusa_pop), col = Colors_ALL_Rusa_pop, pch = 19, cex= 0.65)
```



```
plot(PC7, PC8, col = Colors_ALL_Rusa_pop[ALL_Rusa_pop], pch = 19, xlab = paste0("PC7 (", roun
d(explained_variance[7], 2), "%)"), ylab = paste0("PC8 (", round(explained_variance[8], 2),
"%)"), main = "PCA: PC7 vs PC8")
legend("topright", legend = names(Colors_ALL_Rusa_pop), col = Colors_ALL_Rusa_pop, pch = 19,
cex= 0.65)
```



```
plot(PC2, PC5, col = Colors_ALL_Rusa_pop[ALL_Rusa_pop], pch = 19, xlab = paste0("PC2 (", roun
d(explained_variance[2], 2), "%)"), ylab = paste0("PC5 (", round(explained_variance[5], 2),
"%)"), main = "PCA: PC2 vs PC5")
legend("topright", legend = names(Colors_ALL_Rusa_pop), col = Colors_ALL_Rusa_pop, pch = 19,
cex= 0.65)
```



```
### test for significative differences :
anova_PC1 <- aov(PC1 ~ ALL_Rusa_pop) # Test inter-habitat differences on PC1
summary(anova_PC1)
```

```
##               Df   Sum Sq   Mean Sq F value Pr(>F)
## ALL_Rusa_pop   3 0.001971 0.0006570   2.654 0.0515 .
## Residuals    126 0.031198 0.0002476
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_PC2 <- aov(PC2 ~ ALL_Rusa_pop) # Test inter-habitat differences on PC2
summary(anova_PC2)
```

```
##               Df   Sum Sq   Mean Sq F value  Pr(>F)
## ALL_Rusa_pop   3 0.001612 0.0005372   4.402 0.00557 **
## Residuals    126 0.015379 0.0001221
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_PC3 <- aov(PC3 ~ ALL_Rusa_pop) # Test inter-habitat differences on PC3
summary(anova_PC3)
```

```
##               Df   Sum Sq   Mean Sq F value Pr(>F)
## ALL_Rusa_pop   3 0.000361 1.202e-04   1.375  0.254
## Residuals    126 0.011020 8.746e-05
```

```
anova_PC4 <- aov(PC4 ~ ALL_Rusa_pop) # Test inter-habitat differences on PC4
summary(anova_PC4)
```

```
##               Df   Sum Sq   Mean Sq F value Pr(>F)
## ALL_Rusa_pop   3 0.000059 1.981e-05   0.368  0.776
## Residuals    126 0.006780 5.381e-05
```

```
anova_PC5 <- aov(PC5 ~ ALL_Rusa_pop) # Test inter-habitat differences on PC5
summary(anova_PC5)
```

```
##               Df   Sum Sq   Mean Sq F value  Pr(>F)
## ALL_Rusa_pop   3 0.000567 1.889e-04     4.4 0.00558 **
## Residuals    126 0.005410 4.293e-05
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_PC6 <- aov(PC6 ~ ALL_Rusa_pop) # Test inter-habitat differences on PC6
summary(anova_PC6)
```

```
##               Df   Sum Sq   Mean Sq F value Pr(>F)
## ALL_Rusa_pop   3 0.000330 1.101e-04   3.223  0.025 *
## Residuals    126 0.004304 3.416e-05
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_PC7 <- aov(PC7 ~ ALL_Rusa_pop) # Test inter-habitat differences on PC7
summary(anova_PC7)
```

```
##               Df   Sum Sq   Mean Sq F value Pr(>F)
## ALL_Rusa_pop   3 0.000123 4.108e-05   1.194  0.315
## Residuals    126 0.004334 3.439e-05
```

```
anova_PC8 <- aov(PC8 ~ ALL_Rusa_pop) # Test inter-habitat differences on PC8
summary(anova_PC8)
```

```
##               Df    Sum Sq   Mean Sq F value Pr(>F)
## ALL_Rusa_pop   3 0.0000623 2.077e-05   0.946  0.421
## Residuals    126 0.0027676 2.197e-05
```

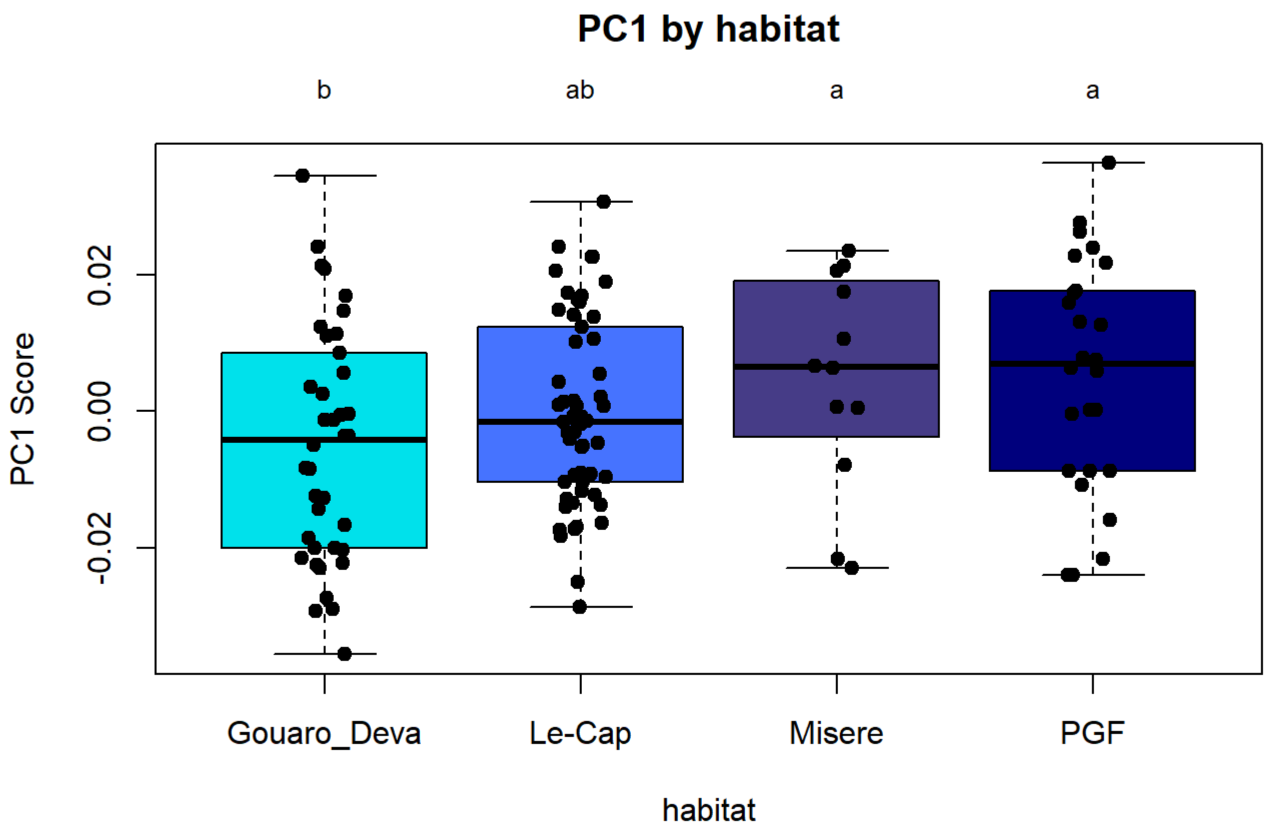
```
###Results ###############
# p-value > 0.05 : On PC1, PC3, PC4, PC7, PC8 : no difference
# p-value = 0.00557 : On PC2, significative differences between habitats
# p-value = 0.00558 : On PC5, significative differences between habitats
# p-value = 0.025 : On PC6, significative differences between habitats
##########################

duncan_result <- duncan.test(anova_PC1, "ALL_Rusa_pop", console = TRUE) # post-hoc test of Duncan
```

```
##
## Study: anova_PC1 ~ "ALL_Rusa_pop"
##
## Duncan's new multiple range test
## for PC1
##
## Mean Square Error:  0.0002476
##
## ALL_Rusa_pop,  means
##
##                       PC1        std  r         Min        Max
## Gouaro_Deva -0.0049949936 0.01727667 38 -0.03564599 0.03454614
## Le-Cap      -0.0001249547 0.01385424 54 -0.02872947 0.03077330
## Misere       0.0046148520 0.01582537 12 -0.02302263 0.02352639
## PGF          0.0054299650 0.01700121 26 -0.02408386 0.03646349
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                       PC1 groups
## PGF          0.0054299650      a
## Misere       0.0046148520      a
## Le-Cap      -0.0001249547     ab
## Gouaro_Deva -0.0049949936      b
```

```
print(duncan_result)
```

```
## $statistics
##     MSerror  Df          Mean            CV
##   0.0002476 126 -3.287609e-18 -4.786248e+17
##
## $parameters
##     test       name.t ntr alpha
##   Duncan ALL_Rusa_pop   4  0.05
##
## $duncan
## NULL
##
## $means
##                       PC1        std  r         Min        Max          Q25
## Gouaro_Deva -0.0049949936 0.01727667 38 -0.03564599 0.03454614 -0.020055367
## Le-Cap      -0.0001249547 0.01385424 54 -0.02872947 0.03077330 -0.010374191
## Misere       0.0046148520 0.01582537 12 -0.02302263 0.02352639 -0.001589433
## PGF          0.0054299650 0.01700121 26 -0.02408386 0.03646349 -0.008721465
##                     Q50         Q75
## Gouaro_Deva -0.004243315 0.007907949
## Le-Cap      -0.001511389 0.012017157
## Misere       0.006484556 0.018334558
## PGF          0.006982004 0.017629572
##
## $comparison
## NULL
##
## $groups
##                       PC1 groups
## PGF          0.0054299650      a
## Misere       0.0046148520      a
## Le-Cap      -0.0001249547     ab
## Gouaro_Deva -0.0049949936      b
##
## attr(,"class")
## [1] "group"
```

```
duncan_labels <- duncan_result$groups
duncan_labels <- duncan_labels[order(rownames(duncan_labels)), ]
Descriptive_ALL_Rusa$labels <- factor(duncan_labels$groups[match(Descriptive_ALL_Rusa$Pop, ro
wnames(duncan_labels))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(PC1 ~ ALL_Rusa_pop, main = "PC1 by habitat", xlab = "habitat", ylab = "PC1 Score", co
l = Colors_ALL_Rusa_pop)
stripchart(PC1 ~ ALL_Rusa_pop, vertical = TRUE, method = "jitter", add = TRUE, pch = 19, col
= "black")
mtext(duncan_labels$groups, at = 1:length(duncan_labels$groups), side = 3, line = 1, cex = 0.
8)
```



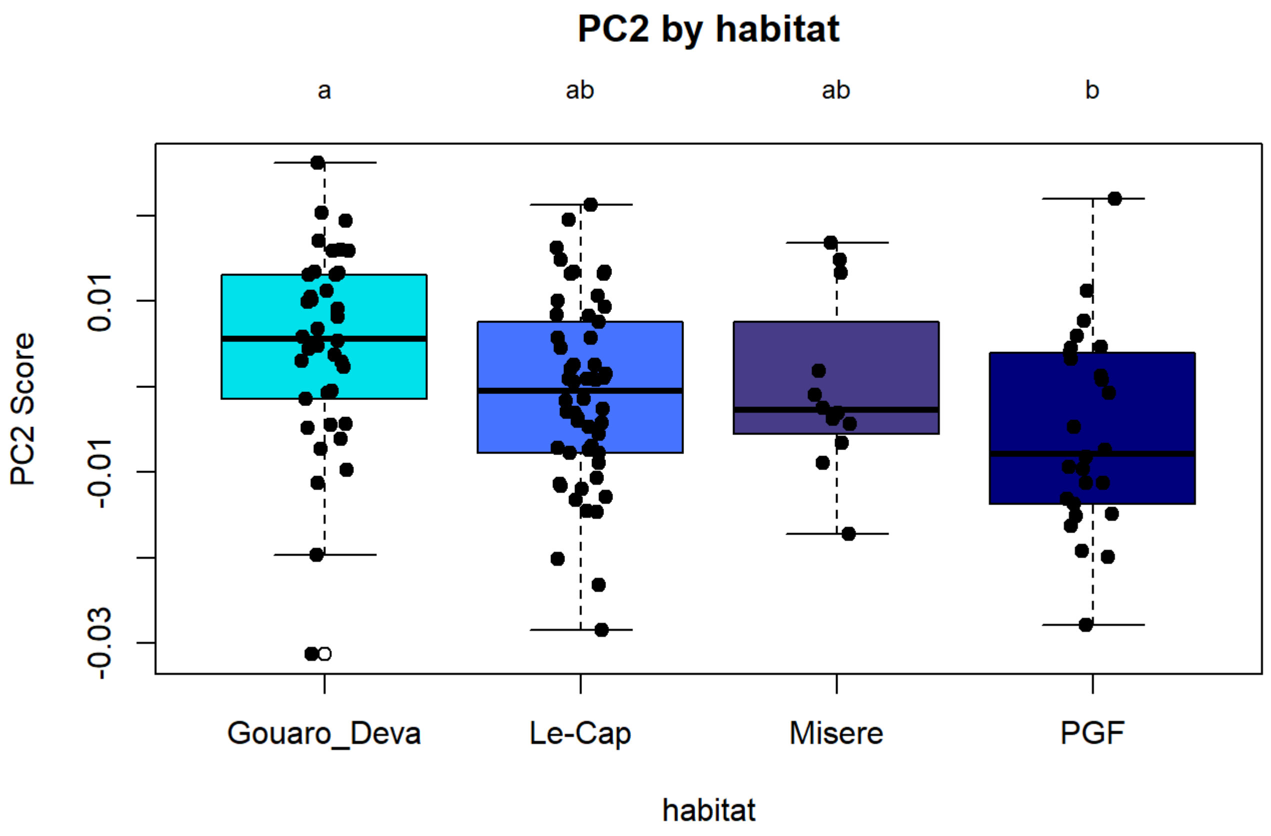
```
duncan_result <- duncan.test(anova_PC2, "ALL_Rusa_pop", console = TRUE) # post-hoc Duncan
```

```
##
## Study: anova_PC2 ~ "ALL_Rusa_pop"
##
## Duncan's new multiple range test
## for PC2
##
## Mean Square Error:  0.0001220524
##
## ALL_Rusa_pop,  means
##
##                        PC2        std  r         Min        Max
## Gouaro_Deva  4.746273e-03 0.01148464 38 -0.03123962 0.02612432
## Le-Cap      -7.950100e-04 0.01073876 54 -0.02847686 0.02125036
## Misere      -3.859262e-05 0.01022269 12 -0.01718455 0.01676347
## PGF         -5.267873e-03 0.01137871 26 -0.02779621 0.02195955
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                        PC2 groups
## Gouaro_Deva  4.746273e-03      a
## Misere      -3.859262e-05     ab
## Le-Cap      -7.950100e-04     ab
## PGF         -5.267873e-03      b
```

```
print(duncan_result)
```

```
## $statistics
##        MSerror  Df          Mean            CV
##   0.0001220524 126 -2.306845e-18 -4.789109e+17
## 
## $parameters
##     test       name.t ntr alpha
##   Duncan ALL_Rusa_pop   4  0.05
## 
## $duncan
## NULL
## 
## $means
##                       PC2        std  r         Min        Max          Q25
## Gouaro_Deva  4.746273e-03 0.01148464 38 -0.03123962 0.02612432 -0.001291945
## Le-Cap      -7.950100e-04 0.01073876 54 -0.02847686 0.02125036 -0.007608843
## Misere      -3.859262e-05 0.01022269 12 -0.01718455 0.01676347 -0.004918029
## PGF         -5.267873e-03 0.01137871 26 -0.02779621 0.02195955 -0.013513069
##                       Q50         Q75
## Gouaro_Deva  0.0056071236 0.013090621
## Le-Cap      -0.0004535329 0.007081798
## Misere      -0.0027524892 0.004688210
## PGF         -0.0078159150 0.003744585
## 
## $comparison
## NULL
## 
## $groups
##                       PC2 groups
## Gouaro_Deva  4.746273e-03      a
## Misere      -3.859262e-05     ab
## Le-Cap      -7.950100e-04     ab
## PGF         -5.267873e-03      b
## 
## attr(,"class")
## [1] "group"
```

```
duncan_labels <- duncan_result$groups
duncan_labels <- duncan_labels[order(rownames(duncan_labels)), ]
Descriptive_ALL_Rusa$labels <- factor(duncan_labels$groups[match(Descriptive_ALL_Rusa$Pop, rownames(duncan_labels))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(PC2 ~ ALL_Rusa_pop, main = "PC2 by habitat", xlab = "habitat", ylab = "PC2 Score", col = Colors_ALL_Rusa_pop)
stripchart(PC2 ~ ALL_Rusa_pop, vertical = TRUE, method = "jitter", add = TRUE, pch = 19, col = "black")
mtext(duncan_labels$groups, at = 1:length(duncan_labels$groups), side = 3, line = 1, cex = 0.8)
```



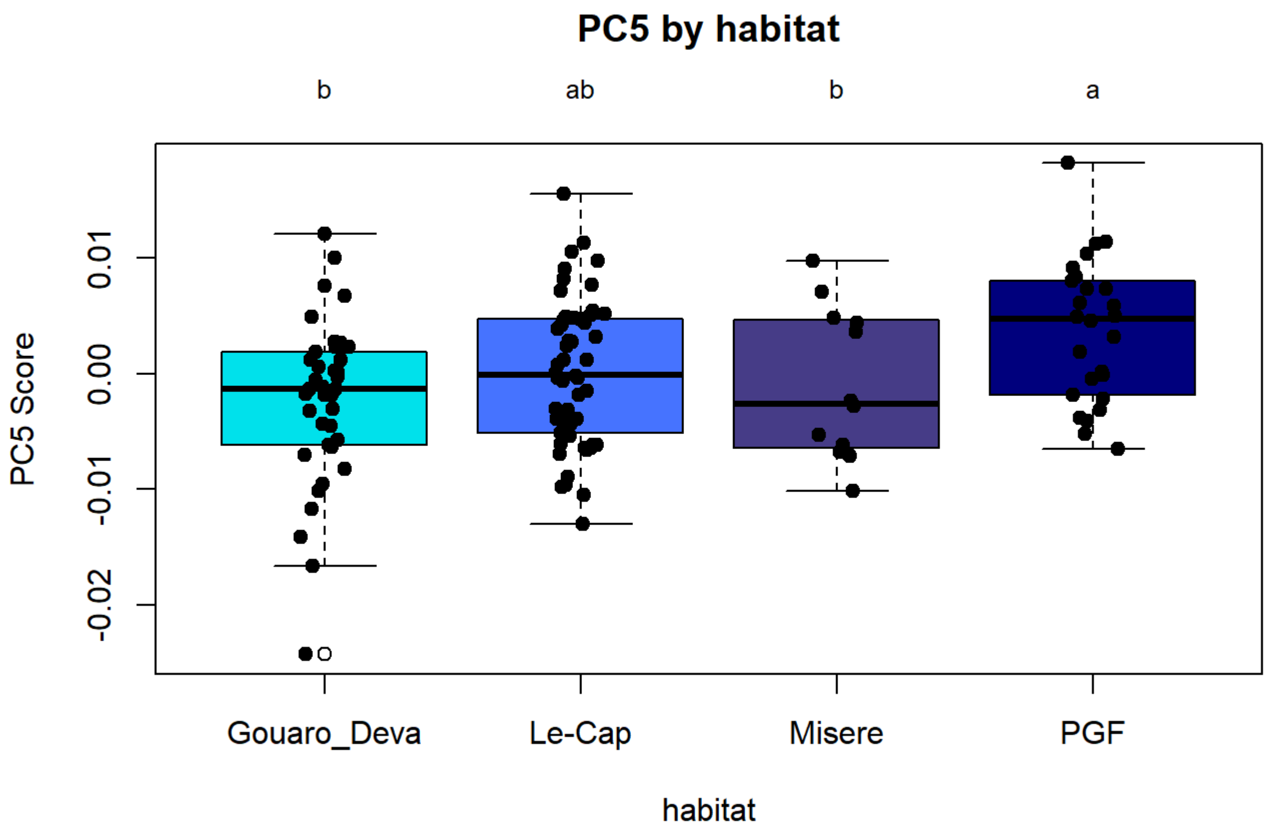
```
duncan_result <- duncan.test(anova_PC5, "ALL_Rusa_pop", console = TRUE) # post-hoc Duncan
```

```
##
## Study: anova_PC5 ~ "ALL_Rusa_pop"
##
## Duncan's new multiple range test
## for PC5
##
## Mean Square Error:  4.293406e-05
##
## ALL_Rusa_pop,  means
##
##                       PC5         std  r          Min         Max
## Gouaro_Deva -2.334017e-03 0.007161398 38 -0.024250383 0.012072045
## Le-Cap       8.017853e-05 0.006301188 54 -0.012985038 0.015579667
## Misere      -9.119398e-04 0.006525811 12 -0.010120433 0.009737746
## PGF          3.665626e-03 0.006129642 26 -0.006476401 0.018186616
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                       PC5 groups
## PGF          3.665626e-03      a
## Le-Cap       8.017853e-05     ab
## Misere      -9.119398e-04      b
## Gouaro_Deva -2.334017e-03      b
```

```
print(duncan_result)
```

```
## $statistics
##        MSerror  Df         Mean           CV
##   4.293406e-05 126 4.286032e-18 1.528782e+17
## 
## $parameters
##     test       name.t ntr alpha
##   Duncan ALL_Rusa_pop   4  0.05
## 
## $duncan
## NULL
## 
## $means
##                       PC5         std  r          Min         Max          Q25
## Gouaro_Deva -2.334017e-03 0.007161398 38 -0.024250383 0.012072045 -0.006076665
## Le-Cap       8.017853e-05 0.006301188 54 -0.012985038 0.015579667 -0.005002701
## Misere      -9.119398e-04 0.006525811 12 -0.010120433 0.009737746 -0.006312970
## PGF          3.665626e-03 0.006129642 26 -0.006476401 0.018186616 -0.001472677
##                      Q50         Q75
## Gouaro_Deva -1.329566e-03 0.001730153
## Le-Cap      -8.410952e-05 0.004701668
## Misere      -2.584214e-03 0.004480827
## PGF          4.720629e-03 0.007817573
## 
## $comparison
## NULL
## 
## $groups
##                       PC5 groups
## PGF          3.665626e-03      a
## Le-Cap       8.017853e-05     ab
## Misere      -9.119398e-04      b
## Gouaro_Deva -2.334017e-03      b
## 
## attr(,"class")
## [1] "group"
```

```
duncan_labels <- duncan_result$groups
duncan_labels <- duncan_labels[order(rownames(duncan_labels)), ]
Descriptive_ALL_Rusa$labels <- factor(duncan_labels$groups[match(Descriptive_ALL_Rusa$Pop, ro
wnames(duncan_labels))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(PC5 ~ ALL_Rusa_pop, main = "PC5 by habitat", xlab = "habitat", ylab = "PC5 Score", co
l = Colors_ALL_Rusa_pop)
stripchart(PC5 ~ ALL_Rusa_pop, vertical = TRUE, method = "jitter", add = TRUE, pch = 19, col
= "black")
mtext(duncan_labels$groups, at = 1:length(duncan_labels$groups), side = 3, line = 1, cex = 0.
8)
```



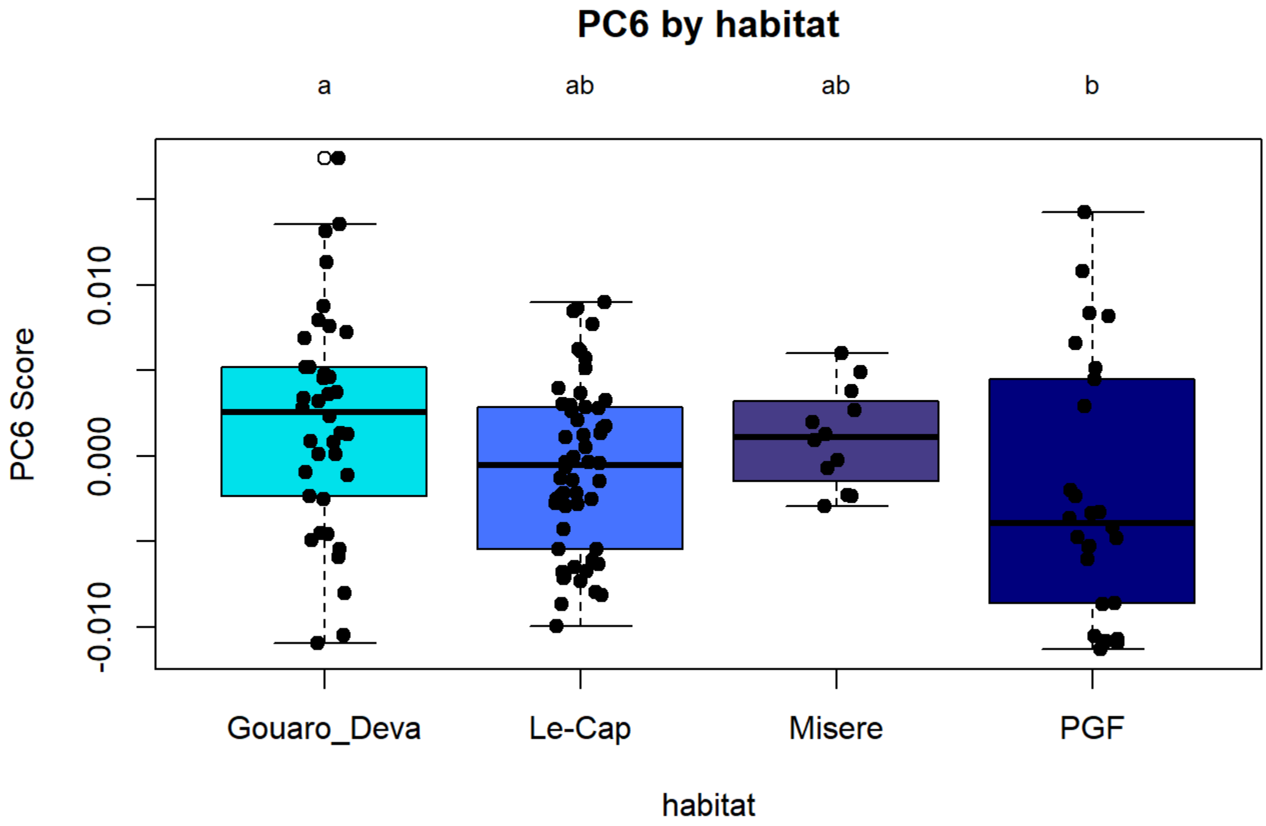
```
duncan_result <- duncan.test(anova_PC6, "ALL_Rusa_pop", console = TRUE) # post-hoc Duncan
```

```
##
## Study: anova_PC6 ~ "ALL_Rusa_pop"
##
## Duncan's new multiple range test
## for PC6
##
## Mean Square Error:  3.416125e-05
##
## ALL_Rusa_pop,  means
##
##                       PC6         std  r          Min         Max
## Gouaro_Deva  0.0021149727 0.006448243 38 -0.010918481 0.017405205
## Le-Cap      -0.0007022699 0.004946191 54 -0.009917783 0.009031949
## Misere       0.0011007110 0.002919554 12 -0.002909887 0.006025583
## PGF         -0.0021405737 0.007417459 26 -0.011293190 0.014248563
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                       PC6 groups
## Gouaro_Deva  0.0021149727      a
## Misere       0.0011007110     ab
## Le-Cap      -0.0007022699     ab
## PGF         -0.0021405737      b
```

```
print(duncan_result)
```

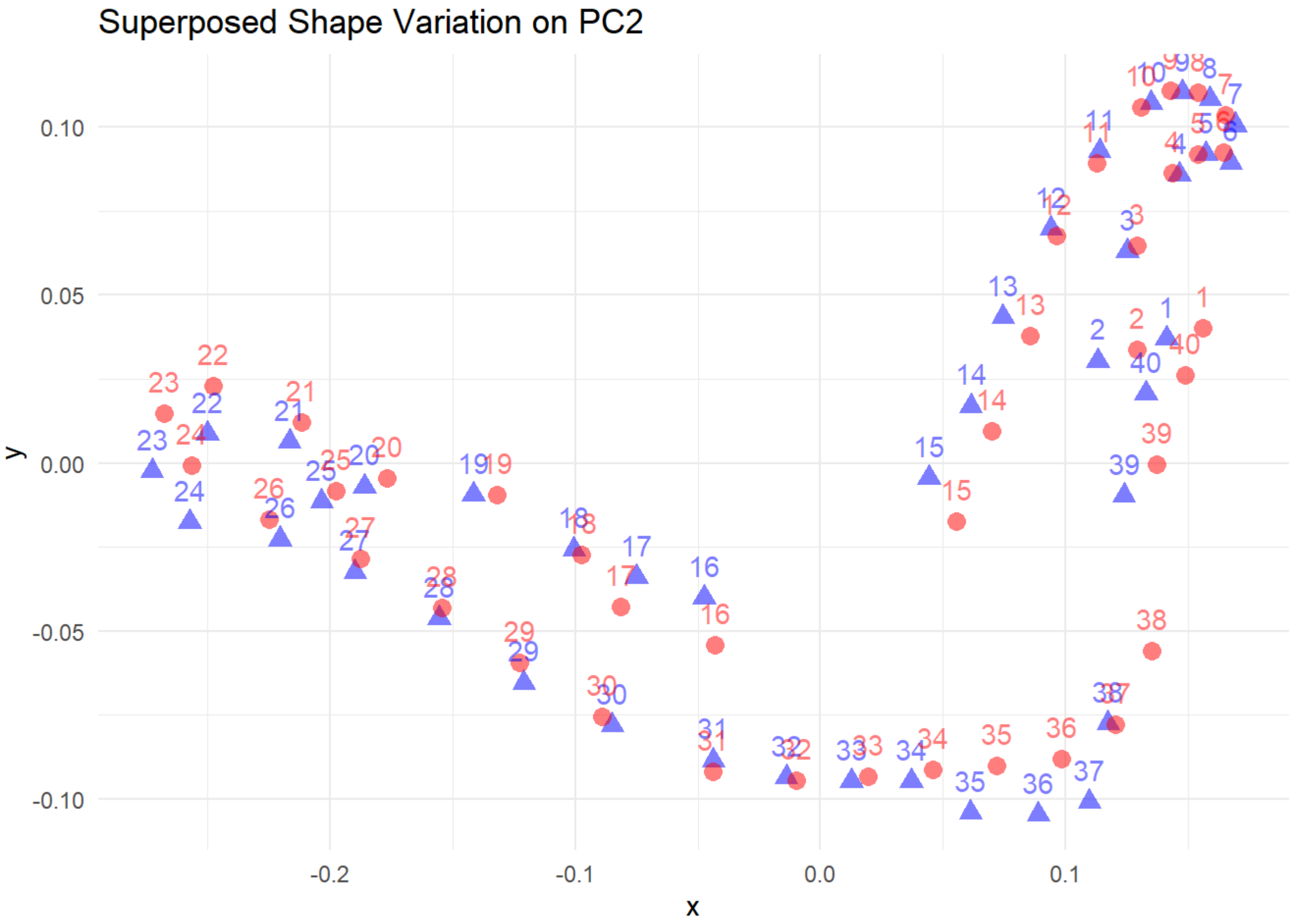
```
## $statistics
##        MSerror  Df          Mean            CV
##   3.416125e-05 126 -2.865762e-18 -2.039514e+17
## 
## $parameters
##     test       name.t ntr alpha
##   Duncan ALL_Rusa_pop   4  0.05
## 
## $duncan
## NULL
## 
## $means
##                       PC6         std  r          Min         Max          Q25
## Gouaro_Deva  0.0021149727 0.006448243 38 -0.010918481 0.017405205 -0.002035974
## Le-Cap      -0.0007022699 0.004946191 54 -0.009917783 0.009031949 -0.005123225
## Misere       0.0011007110 0.002919554 12 -0.002909887 0.006025583 -0.001086544
## PGF         -0.0021405737 0.007417459 26 -0.011293190 0.014248563 -0.007973719
##                       Q50         Q75
## Gouaro_Deva  0.0025595758 0.005213556
## Le-Cap      -0.0005477341 0.002855054
## Misere       0.0010998384 0.002965081
## PGF         -0.0038954825 0.004099955
## 
## $comparison
## NULL
## 
## $groups
##                       PC6 groups
## Gouaro_Deva  0.0021149727      a
## Misere       0.0011007110     ab
## Le-Cap      -0.0007022699     ab
## PGF         -0.0021405737      b
## 
## attr(,"class")
## [1] "group"
```

```
duncan_labels <- duncan_result$groups
duncan_labels <- duncan_labels[order(rownames(duncan_labels)), ]
Descriptive_ALL_Rusa$labels <- factor(duncan_labels$groups[match(Descriptive_ALL_Rusa$Pop, ro
wnames(duncan_labels))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(PC6 ~ ALL_Rusa_pop, main = "PC6 by habitat", xlab = "habitat", ylab = "PC6 Score", co
l = Colors_ALL_Rusa_pop)
stripchart(PC6 ~ ALL_Rusa_pop, vertical = TRUE, method = "jitter", add = TRUE, pch = 19, col
= "black")
mtext(duncan_labels$groups, at = 1:length(duncan_labels$groups), side = 3, line = 1, cex = 0.
8)
```

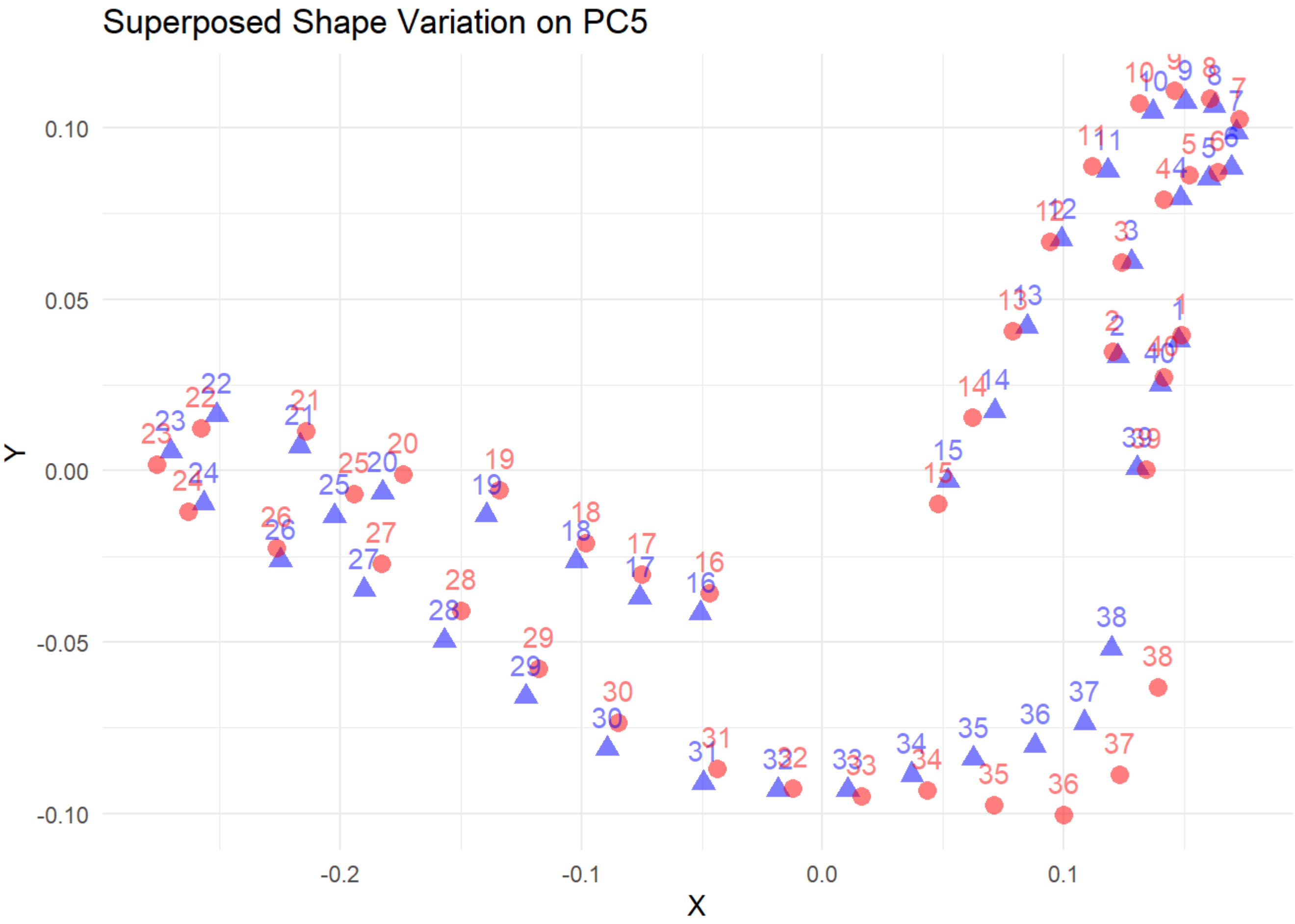


Vizualize shape variation:

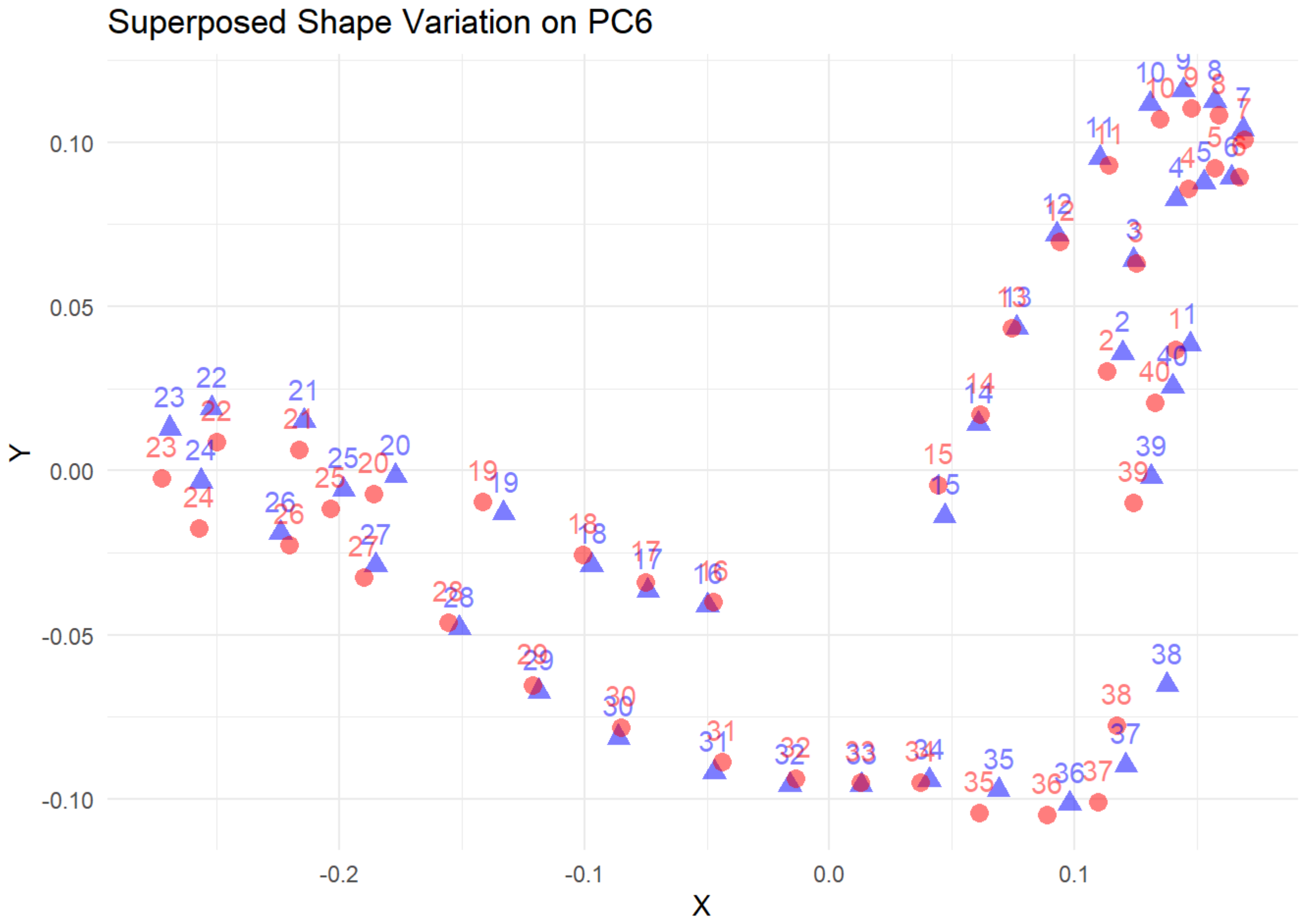
```
#Vizualize shape variation on PC2:
extreme_min_PC2 <- which.min(PC2)
extreme_max_PC2 <- which.max(PC2)

coords_min_PC2 <- as.data.frame(Slided_MorphoGeom_ALL_Rusa$coords[,,extreme_min_PC2])
coords_max_PC2 <- as.data.frame(Slided_MorphoGeom_ALL_Rusa$coords[,,extreme_max_PC2])
coords_min_PC2$landmark <- 1:nrow(coords_min_PC2)
coords_max_PC2$landmark <- 1:nrow(coords_max_PC2)

colnames(coords_min_PC2) <- c("x", "y", "landmark")
colnames(coords_max_PC2) <- c("x", "y", "landmark")
coords_min_PC2$group <- "Min PC2"
coords_max_PC2$group <- "Max PC2"

df_combined <- rbind(coords_min_PC2, coords_max_PC2)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on PC2") +
  scale_color_manual(values = c("Min PC2" = "blue", "Max PC2" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



```
# Vizualize shape variation on PC5
extreme_min_PC5 <- which.min(PC5)
extreme_max_PC5 <- which.max(PC5)

coords_min_PC5 <- as.data.frame(Slided_MorphoGeom_ALL_Rusa$coords[,,extreme_min_PC5])
coords_max_PC5 <- as.data.frame(Slided_MorphoGeom_ALL_Rusa$coords[,,extreme_max_PC5])
coords_min_PC5$landmark <- 1:nrow(coords_min_PC5)
coords_max_PC5$landmark <- 1:nrow(coords_max_PC5)

colnames(coords_min_PC5) <- c("x", "y", "landmark")
colnames(coords_max_PC5) <- c("x", "y", "landmark")
coords_min_PC5$group <- "Min PC5"
coords_max_PC5$group <- "Max PC5"

df_combined <- rbind(coords_min_PC5, coords_max_PC5)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on PC5", x = "X", y = "Y") +
  scale_color_manual(values = c("Min PC5" = "blue", "Max PC5" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



```
#Vizualize shape variation on PC6
extreme_min_PC6 <- which.min(PC6)
extreme_max_PC6 <- which.max(PC6)

coords_min_PC6 <- as.data.frame(Slided_MorphoGeom_ALL_Rusa$coords[,,extreme_min_PC6])
coords_max_PC6 <- as.data.frame(Slided_MorphoGeom_ALL_Rusa$coords[,,extreme_max_PC6])
coords_min_PC6$landmark <- 1:nrow(coords_min_PC6)
coords_max_PC6$landmark <- 1:nrow(coords_max_PC6)

colnames(coords_min_PC6) <- c("x", "y", "landmark")
colnames(coords_max_PC6) <- c("x", "y", "landmark")
coords_min_PC6$group <- "Min PC6"
coords_max_PC6$group <- "Max PC6"

df_combined <- rbind(coords_min_PC6, coords_max_PC6)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on PC6", x = "X", y = "Y") +
  scale_color_manual(values = c("Min PC6" = "blue", "Max PC6" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```

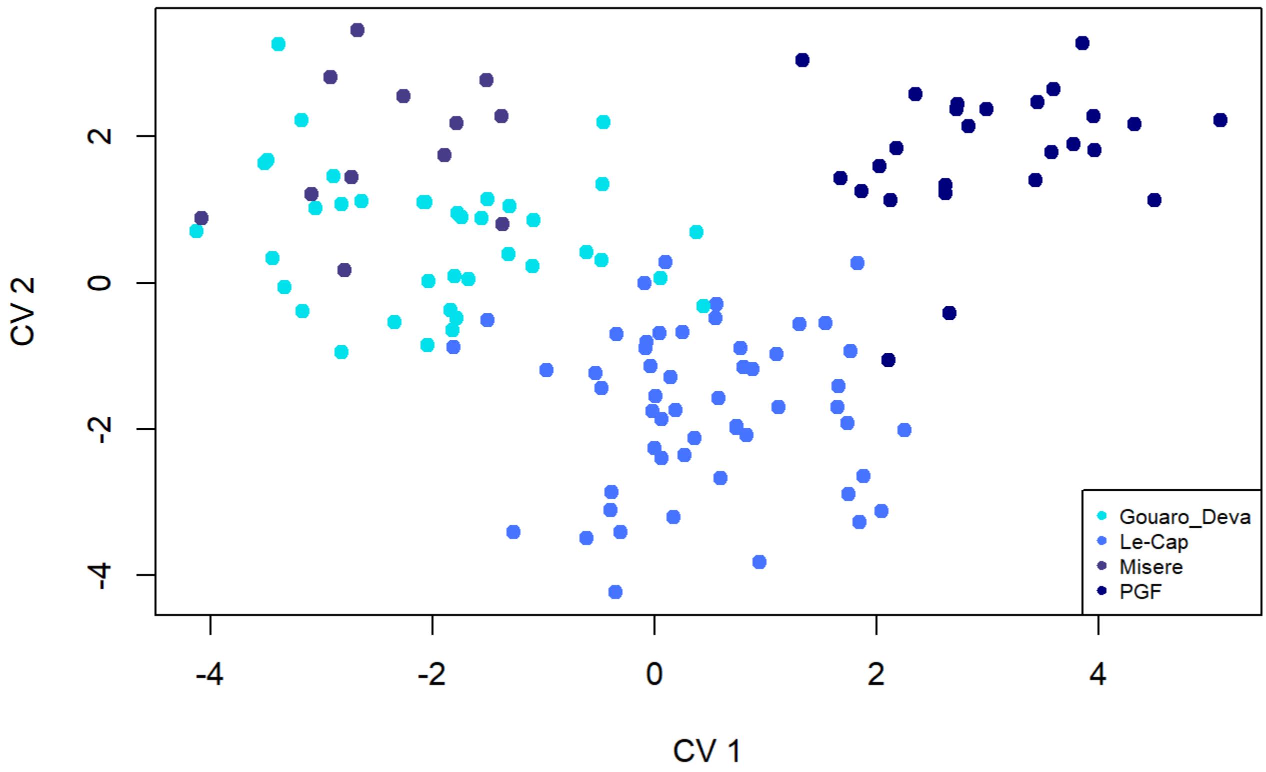


3.3.3 Canonical Variable Analysis (CVA):

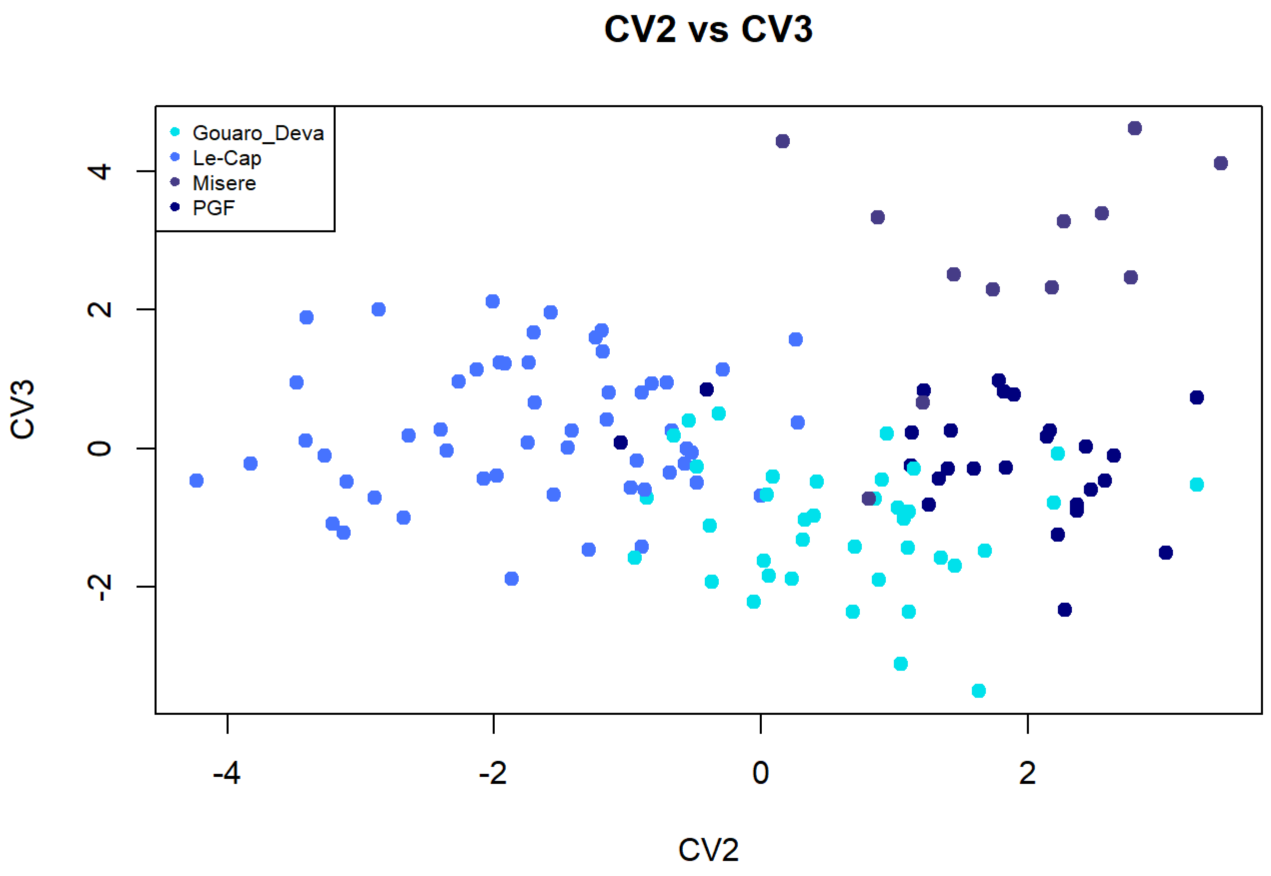
```
CVA_ALL_Rusa_pop <- CVA(Slided_MorphoGeom_ALL_Rusa$coords, ALL_Rusa_pop, rounds = 10000, p.adjust.method = "bonferroni")
```

```
## singular Covariance matrix: General inverse is used. Threshold for zero eigenvalue is 1e-10
```

```
plot(CVA_ALL_Rusa_pop$CVscores, col = Colors_ALL_Rusa_pop[ALL_Rusa_pop], pch = 19)
legend("bottomright", legend = names(Colors_ALL_Rusa_pop), col = Colors_ALL_Rusa_pop, pch = 19, cex= 0.65)
```



```
plot(CVA_ALL_Rusa_pop$CVscores[, 2], CVA_ALL_Rusa_pop$CVscores[, 3], col = Colors_ALL_Rusa_po
p[ALL_Rusa_pop], pch = 19, xlab = "CV2", ylab = "CV3", main = "CV2 vs CV3")
legend("topleft", legend = names(Colors_ALL_Rusa_pop), col = Colors_ALL_Rusa_pop, pch = 19, c
ex = 0.65)
```



```
CVA_ALL_Rusa_pop$Dist
```

```
## $GroupdistMaha
##          Gouaro_Deva   Le-Cap   Misere
## Le-Cap     3.630706
## Misere     4.083953 5.165858
## PGF        5.188260 4.366350 6.122453
##
## $GroupdistEuclid
##          Gouaro_Deva      Le-Cap      Misere
## Le-Cap 0.009061896
## Misere 0.012540112 0.008042877
## PGF    0.016735048 0.009874132 0.011282151
##
## $probsMaha
##          Gouaro_Deva     Le-Cap     Misere
## Le-Cap   0.00059994
## Misere   0.00059994 0.00059994
## PGF      0.00059994 0.00059994 0.00059994
##
## $probsEuclid
##          Gouaro_Deva     Le-Cap     Misere
## Le-Cap   0.20397960
## Misere   0.53454655 1.00000000
## PGF      0.00059994 0.24057594 1.00000000
##
## $p.adjust.method
## [1] "bonferroni"
```

```
CV_scores <- as.data.frame(CVA_ALL_Rusa_pop$CVscores)
view(CV_scores)
CV_scores$Pop <- ALL_Rusa_pop
CV1 <- CV_scores[,1]
CV2 <- CV_scores[,2]
CV3 <- CV_scores[,3]

anova_result_CV1 <- aov(CV1 ~ Pop, data = CV_scores)
summary(anova_result_CV1)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)    
## Pop           3  458.8   152.9   152.9 <2e-16 ***
## Residuals   126  126.0     1.0                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_result_CV2 <- aov(CV2 ~ Pop, data = CV_scores)
summary(anova_result_CV2)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)    
## Pop           3  297.5   99.16   99.16 <2e-16 ***
## Residuals   126  126.0    1.00                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova_result_CV3 <- aov(CV3 ~ Pop, data = CV_scores)
summary(anova_result_CV3)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)    
## Pop           3  143.8   47.92   47.92 <2e-16 ***
## Residuals   126  126.0    1.00                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

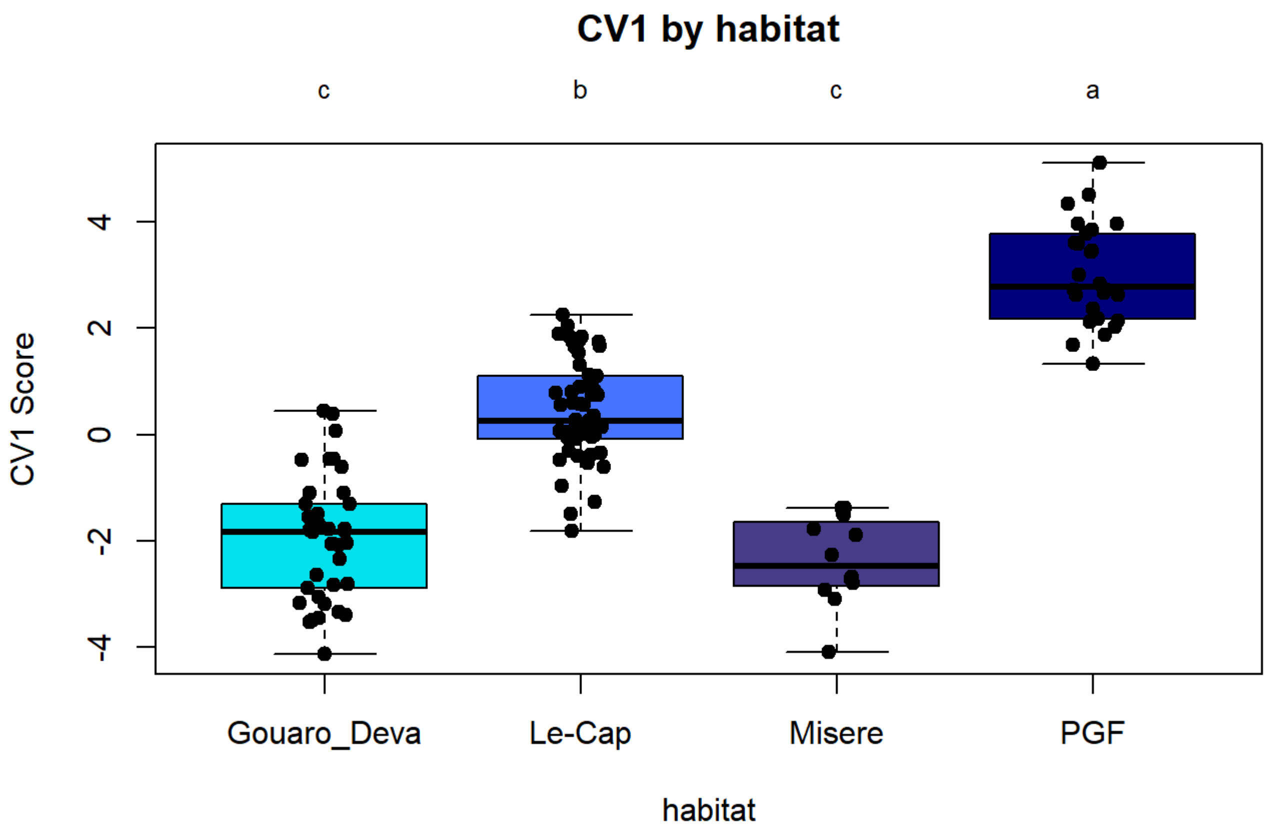
```
###Results ##############
# p-value <2e-16 : On CV1-3, significative differences between habitats
##########################

duncan_result_CV1 <- duncan.test(anova_result_CV1, "Pop", console = TRUE)
```

```
##
## Study: anova_result_CV1 ~ "Pop"
##
## Duncan's new multiple range test
## for CV1
##
## Mean Square Error:  1
##
## Pop,  means
##
##                    CV1       std  r       Min        Max
## Gouaro_Deva -1.9445639 1.1575841 38 -4.129571  0.4460721
## Le-Cap       0.4432213 0.9342616 54 -1.809093  2.2581292
## Misere      -2.3753003 0.8226665 12 -4.084109 -1.3739147
## PGF          3.0178109 0.9531970 26  1.331260  5.1032112
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                    CV1 groups
## PGF          3.0178109      a
## Le-Cap       0.4432213      b
## Gouaro_Deva -1.9445639      c
## Misere      -2.3753003      c
```

```
print(duncan_result_CV1)
```

```
## $statistics
##   MSerror  Df          Mean            CV
##         1 126 -1.879584e-13 -5.320326e+14
##
## $parameters
##     test name.t ntr alpha
##   Duncan    Pop   4  0.05
##
## $duncan
## NULL
##
## $means
##                    CV1       std  r       Min        Max         Q25        Q50
## Gouaro_Deva -1.9445639 1.1575841 38 -4.129571  0.4460721 -2.87433738 -1.8290538
## Le-Cap       0.4432213 0.9342616 54 -1.809093  2.2581292 -0.07927016  0.2604915
## Misere      -2.3753003 0.8226665 12 -4.084109 -1.3739147 -2.82622017 -2.4698145
## PGF          3.0178109 0.9531970 26  1.331260  5.1032112  2.22437599  2.7826467
##                   Q75
## Gouaro_Deva -1.305623
## Le-Cap       1.063550
## Misere      -1.714731
## PGF          3.735598
##
## $comparison
## NULL
##
## $groups
##                    CV1 groups
## PGF          3.0178109      a
## Le-Cap       0.4432213      b
## Gouaro_Deva -1.9445639      c
## Misere      -2.3753003      c
##
## attr(,"class")
## [1] "group"
```

```
duncan_labels_CV1 <- duncan_result_CV1$groups
duncan_labels_CV1 <- duncan_labels_CV1[order(rownames(duncan_labels_CV1)), ]
CV_scores$labels <- factor(duncan_labels_CV1$groups[match(CV_scores$Pop, rownames(duncan_labe
ls_CV1))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(CV1 ~ Pop, data = CV_scores, main = "CV1 by habitat", xlab = "habitat", ylab = "CV1 S
core", col = Colors_ALL_Rusa_pop)
stripchart(CV1 ~ Pop, data = CV_scores, vertical = TRUE, method = "jitter", add = TRUE, pch =
19, col = "black")
mtext(duncan_labels_CV1$groups, at = 1:length(duncan_labels_CV1$groups), side = 3, line = 1,
cex = 0.8)
```



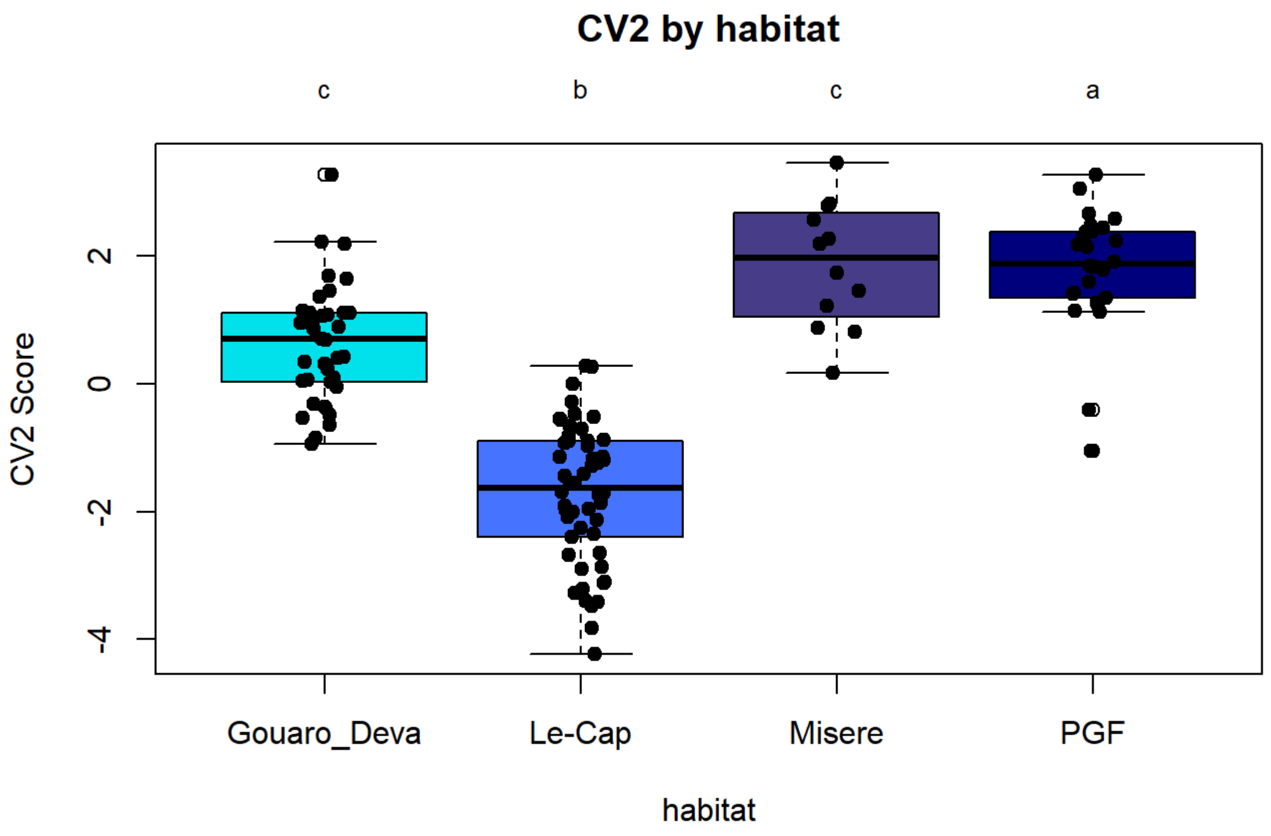
```
duncan_result_CV2 <- duncan.test(anova_result_CV2, "Pop", console = TRUE)
```

```
##
## Study: anova_result_CV2 ~ "Pop"
##
## Duncan's new multiple range test
## for CV2
##
## Mean Square Error:  1
##
## Pop,  means
##
##                     CV2       std  r        Min       Max
## Gouaro_Deva  0.6245104 0.9174666 38 -0.9438001 3.2676299
## Le-Cap      -1.7122094 1.0813686 54 -4.2310832 0.2775483
## Misere       1.8585546 0.9797467 12  0.1676833 3.4493657
## PGF          1.7855868 0.9448919 26 -1.0519144 3.2731542
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                     CV2 groups
## Misere       1.8585546      a
## PGF          1.7855868      a
## Gouaro_Deva  0.6245104      b
## Le-Cap      -1.7122094      c
```

```
print(duncan_result_CV2)
```

```
## $statistics
##   MSerror  Df        Mean           CV
##         1 126 1.07114e-13 9.335852e+14
## 
## $parameters
##     test name.t ntr alpha
##   Duncan    Pop   4  0.05
## 
## $duncan
## NULL
## 
## $means
##                    CV2       std  r        Min       Max         Q25        Q50
## Gouaro_Deva  0.6245104 0.9174666 38 -0.9438001 3.2676299  0.02668344  0.6970901
## Le-Cap      -1.7122094 1.0813686 54 -4.2310832 0.2775483 -2.39075755 -1.6344511
## Misere       1.8585546 0.9797467 12  0.1676833 3.4493657  1.13143435  1.9621981
## PGF          1.7855868 0.9448919 26 -1.0519144 3.2731542  1.35459501  1.8707437
##                    Q75
## Gouaro_Deva  1.1068204
## Le-Cap      -0.8898868
## Misere       2.6131348
## PGF          2.3724039
## 
## $comparison
## NULL
## 
## $groups
##                    CV2 groups
## Misere       1.8585546      a
## PGF          1.7855868      a
## Gouaro_Deva  0.6245104      b
## Le-Cap      -1.7122094      c
## 
## attr(,"class")
## [1] "group"
```

```
duncan_labels_CV2 <- duncan_result_CV2$groups
duncan_labels_CV2 <- duncan_labels_CV2[order(rownames(duncan_labels_CV2)), ]
CV_scores$labels <- factor(duncan_labels_CV2$groups[match(CV_scores$Pop, rownames(duncan_labe
ls_CV2))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(CV2 ~ Pop, data = CV_scores, main = "CV2 by habitat", xlab = "habitat", ylab = "CV2 S
core", col = Colors_ALL_Rusa_pop)
stripchart(CV2 ~ Pop, data = CV_scores, vertical = TRUE, method = "jitter", add = TRUE, pch =
19, col = "black")
mtext(duncan_labels_CV1$groups, at = 1:length(duncan_labels_CV1$groups), side = 3, line = 1,
cex = 0.8)
```



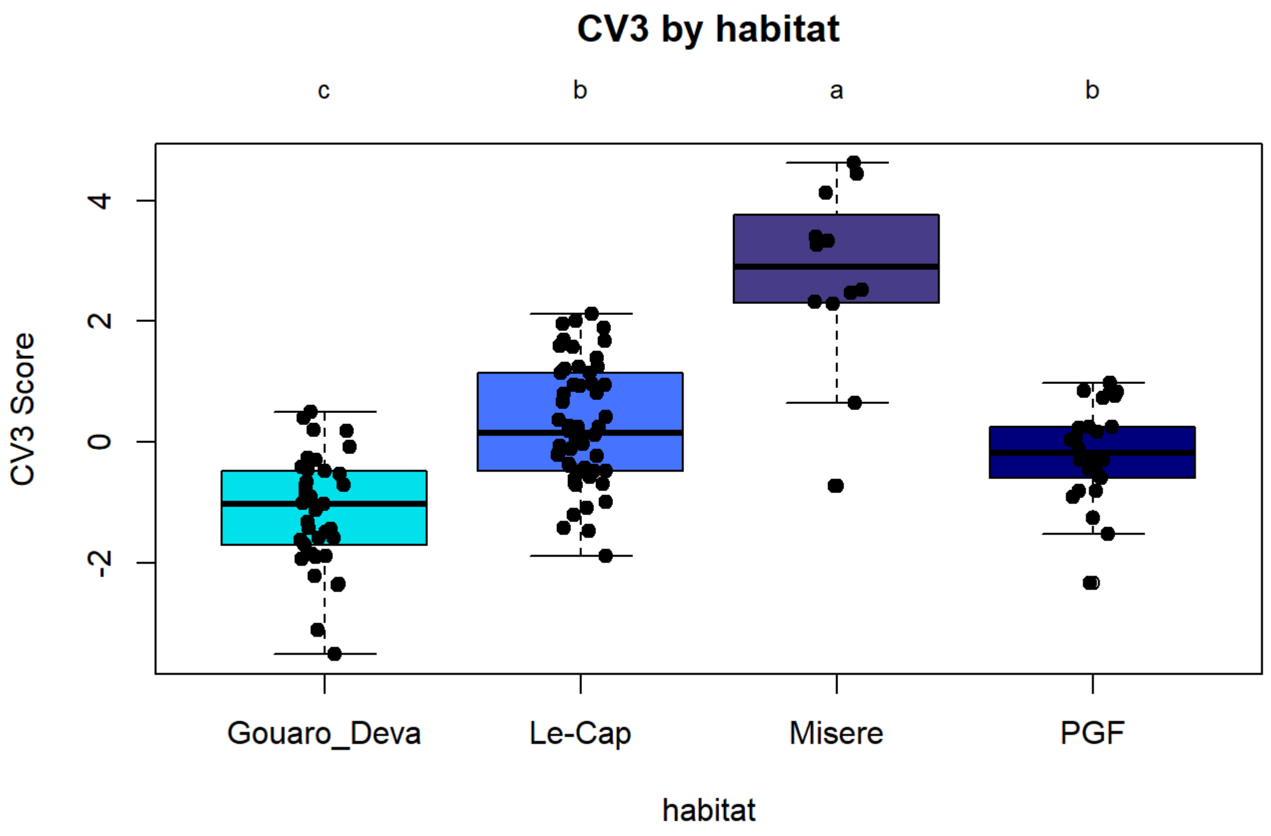
```
duncan_result_CV3 <- duncan.test(anova_result_CV3, "Pop", console = TRUE)
```

```
##
## Study: anova_result_CV3 ~ "Pop"
##
## Duncan's new multiple range test
## for CV3
##
## Mean Square Error:  1
##
## Pop,  means
##
##                     CV3       std  r        Min       Max
## Gouaro_Deva -1.1419598 0.9166229 38 -3.5130548 0.4940912
## Le-Cap       0.2793942 0.9938456 54 -1.8860759 2.1237122
## Misere       2.7271838 1.5466713 12 -0.7297914 4.6206768
## PGF         -0.1699623 0.8061994 26 -2.3436712 0.9820178
##
## Groups according to probability of means differences and alpha level( 0.05 )
##
## Means with the same letter are not significantly different.
##
##                     CV3 groups
## Misere       2.7271838      a
## Le-Cap       0.2793942      b
## PGF         -0.1699623      b
## Gouaro_Deva -1.1419598      c
```

```
print(duncan_result_CV3)
```

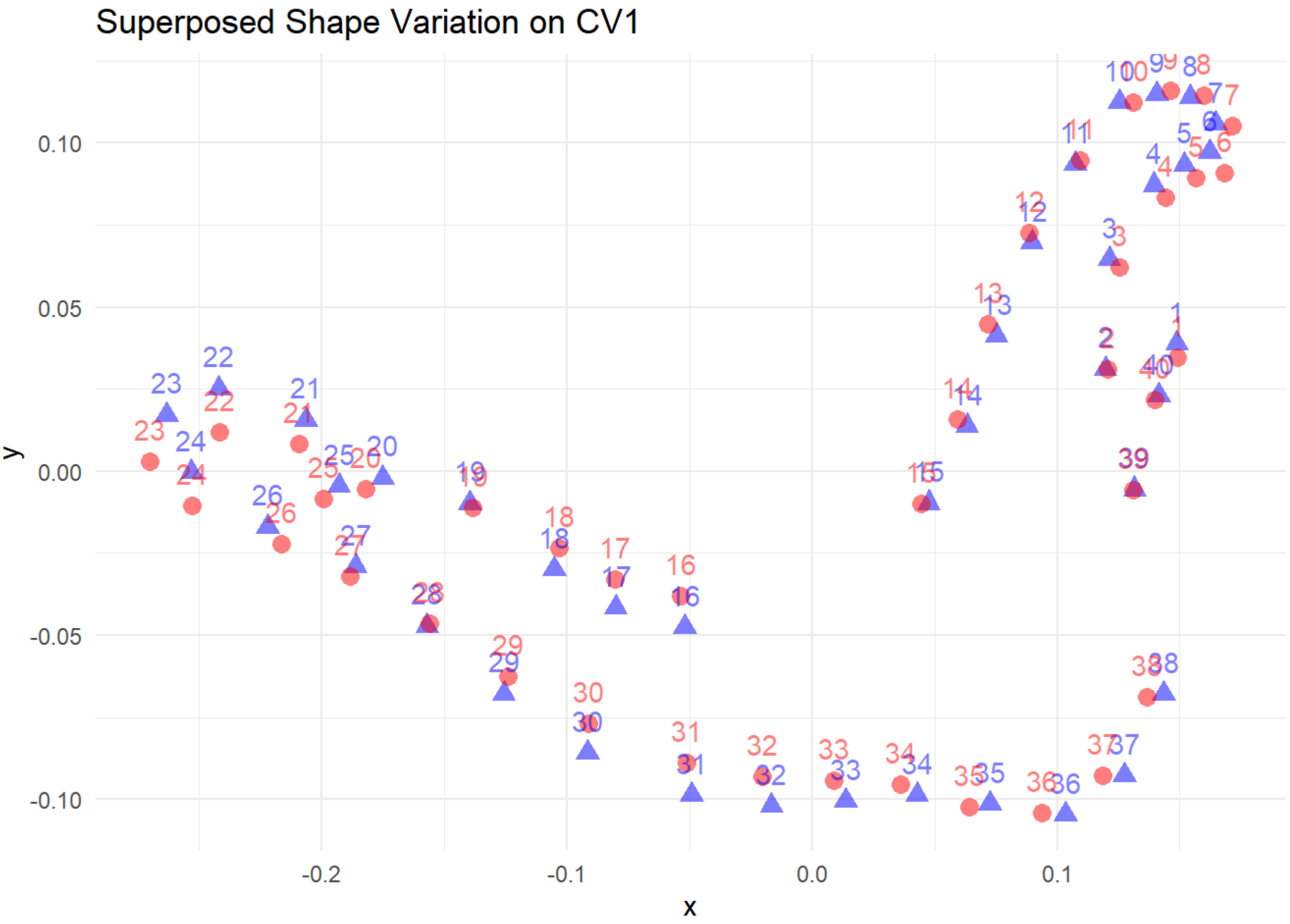
```
## $statistics
##   MSerror  Df         Mean           CV
##         1 126 1.854013e-13 5.393706e+14
## 
## $parameters
##     test name.t ntr alpha
##   Duncan    Pop   4  0.05
## 
## $duncan
## NULL
## 
## $means
##                    CV3       std  r        Min       Max        Q25        Q50
## Gouaro_Deva -1.1419598 0.9166229 38 -3.5130548 0.4940912 -1.6806025 -1.0227026
## Le-Cap       0.2793942 0.9938456 54 -1.8860759 2.1237122 -0.4656370  0.1479296
## Misere       2.7271838 1.5466713 12 -0.7297914 4.6206768  2.3139583  2.8948386
## PGF         -0.1699623 0.8061994 26 -2.3436712 0.9820178 -0.5689681 -0.1819872
##                    Q75
## Gouaro_Deva -0.4916538
## Le-Cap       1.0928278
## Misere       3.5827938
## PGF          0.2546068
## 
## $comparison
## NULL
## 
## $groups
##                    CV3 groups
## Misere       2.7271838      a
## Le-Cap       0.2793942      b
## PGF         -0.1699623      b
## Gouaro_Deva -1.1419598      c
## 
## attr(,"class")
## [1] "group"
```

```
duncan_labels_CV3 <- duncan_result_CV3$groups
duncan_labels_CV3 <- duncan_labels_CV3[order(rownames(duncan_labels_CV3)), ]
CV_scores$labels <- factor(duncan_labels_CV3$groups[match(CV_scores$Pop, rownames(duncan_labe
ls_CV3))])
par(mar = c(5, 4, 6, 2) + 0.1)
boxplot(CV3 ~ Pop, data = CV_scores, main = "CV3 by habitat", xlab = "habitat", ylab = "CV3 S
core", col = Colors_ALL_Rusa_pop)
stripchart(CV3 ~ Pop, data = CV_scores, vertical = TRUE, method = "jitter", add = TRUE, pch =
19, col = "black")
mtext(duncan_labels_CV3$groups, at = 1:length(duncan_labels_CV3$groups), side = 3, line = 1,
cex = 0.8)
```

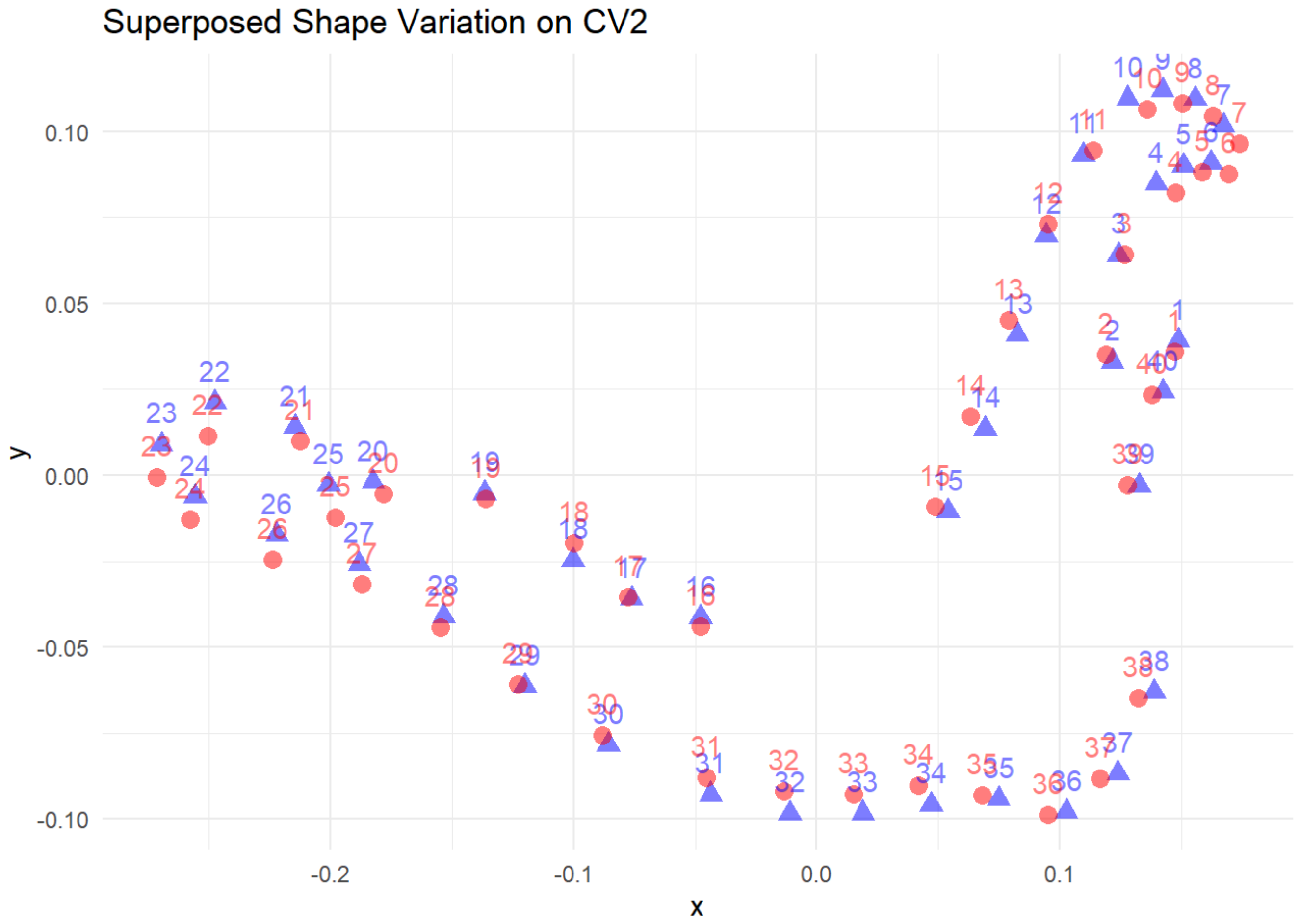


Visualize shape variation

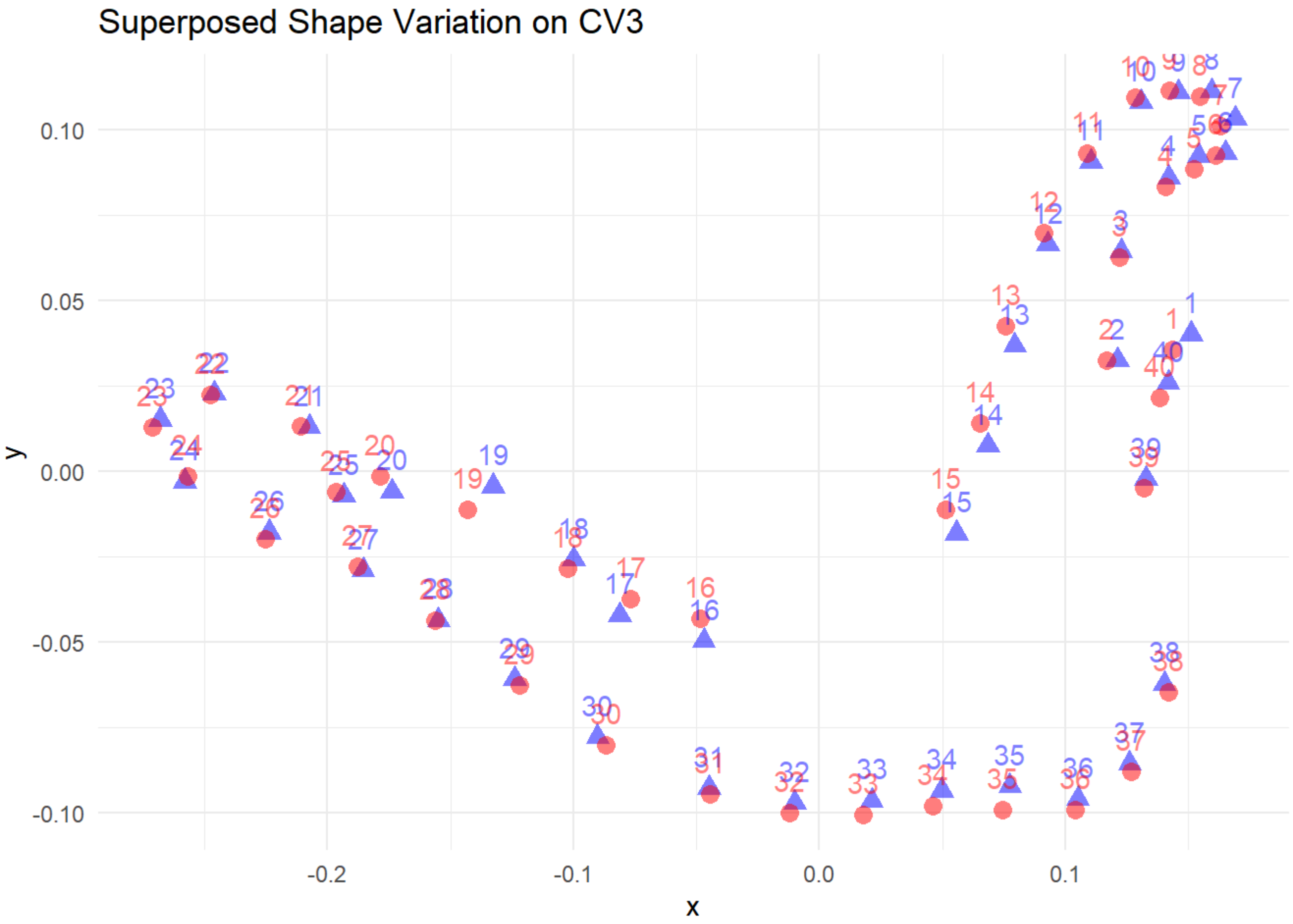
```
#Visualize shape variation on CV1
extreme_min_CV1 <- which.min(CV1)
extreme_max_CV1 <- which.max(CV1)

coords_min_CV1 <- as.data.frame(Slided_MorphoGeom_ALL_Rusa$coords[,,extreme_min_CV1])
coords_max_CV1 <- as.data.frame(Slided_MorphoGeom_ALL_Rusa$coords[,,extreme_max_CV1])
coords_min_CV1$landmark <- 1:nrow(coords_min_CV1)
coords_max_CV1$landmark <- 1:nrow(coords_max_CV1)

colnames(coords_min_CV1) <- c("x", "y", "landmark")
colnames(coords_max_CV1) <- c("x", "y", "landmark")
coords_min_CV1$group <- "Min CV1"
coords_max_CV1$group <- "Max CV1"

df_combined <- rbind(coords_min_CV1, coords_max_CV1)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on CV1") +
  scale_color_manual(values = c("Min CV1" = "blue", "Max CV1" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



```
#Visualize shape variation on CV2
extreme_min_CV2 <- which.min(CV2)
extreme_max_CV2 <- which.max(CV2)

coords_min_CV2 <- as.data.frame(Slided_MorphoGeom_ALL_Rusa$coords[,,extreme_min_CV2])
coords_max_CV2 <- as.data.frame(Slided_MorphoGeom_ALL_Rusa$coords[,,extreme_max_CV2])
coords_min_CV2$landmark <- 1:nrow(coords_min_CV2)
coords_max_CV2$landmark <- 1:nrow(coords_max_CV2)

colnames(coords_min_CV2) <- c("x", "y", "landmark")
colnames(coords_max_CV2) <- c("x", "y", "landmark")
coords_min_CV2$group <- "Min CV2"
coords_max_CV2$group <- "Max CV2"

df_combined <- rbind(coords_min_CV2, coords_max_CV2)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on CV2") +
  scale_color_manual(values = c("Min CV2" = "blue", "Max CV2" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



```
#Visualize shape variation on CV3
extreme_min_CV3 <- which.min(CV3)
extreme_max_CV3 <- which.max(CV3)

coords_min_CV3 <- as.data.frame(Slided_MorphoGeom_ALL_Rusa$coords[,,extreme_min_CV3])
coords_max_CV3 <- as.data.frame(Slided_MorphoGeom_ALL_Rusa$coords[,,extreme_max_CV3])
coords_min_CV3$landmark <- 1:nrow(coords_min_CV3)
coords_max_CV3$landmark <- 1:nrow(coords_max_CV3)

colnames(coords_min_CV3) <- c("x", "y", "landmark")
colnames(coords_max_CV3) <- c("x", "y", "landmark")
coords_min_CV3$group <- "Min CV3"
coords_max_CV3$group <- "Max CV3"

df_combined <- rbind(coords_min_CV3, coords_max_CV3)

ggplot(df_combined, aes(x = x, y = y, color = group, shape = group)) +
  geom_point(size = 3, alpha = 0.5) +
  geom_text(aes(label = landmark), vjust = -1, alpha = 0.5) +
  labs(title = "Superposed Shape Variation on CV3") +
  scale_color_manual(values = c("Min CV3" = "blue", "Max CV3" = "red")) +
  theme_minimal() +
  theme(legend.position = "topright")
```



3.3.4 Role of mandible size and the influence of habitat in these variations:

```
# Procrust regression provides an overview, while PLS analysis allows us to focus on the specific influence of size.

# Procrust regression
# evaluate how shapes ( landmark coordinates) vary as a function of explanatory variables (size and habitat)
gdf <- geomorph.data.frame(Slided_MorphoGeom_ALL_Rusa, Habitat = Descriptive_ALL_Rusa$Pop,
                           Csize = Descriptive_ALL_Rusa$Centroid_Size)
fit.size <- procD.lm(coords ~ log(Csize) + Habitat, data = gdf, print.progress = FALSE)
summary(fit.size)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type I
## Effect sizes (Z) based on F distributions
##
##              Df       SS        MS     Rsq      F      Z Pr(>F)
## log(Csize)   1 0.004587 0.0045871 0.04368 5.9406 3.4309  0.001 ***
## Habitat      3 0.003917 0.0013058 0.03730 1.6911 1.8755  0.030 *
## Residuals  125 0.096521 0.0007722 0.91902
## Total      129 0.105026
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: procD.lm(f1 = coords ~ log(Csize) + Habitat, data = gdf, print.progress = FALSE)
```

```
# evaluate how shapes vary as a function of explanatory variables (size and habitat) on the a
xes with inter-habitat differences.
PC2 <- PC_scores_PCA_ALL_Rusa[, 2]
PC5 <- PC_scores_PCA_ALL_Rusa[, 5]
PC6 <- PC_scores_PCA_ALL_Rusa[, 6]

fit.size.PC2 <- procD.lm(PC2 ~ log(gdf$Csize) + gdf$Habitat)
fit.size.PC5 <- procD.lm(PC5 ~ log(gdf$Csize) + gdf$Habitat)
fit.size.PC6 <- procD.lm(PC6 ~ log(gdf$Csize) + gdf$Habitat)
summary(fit.size.PC2)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type I
## Effect sizes (Z) based on F distributions
##
##                  Df        SS          MS     Rsq      F      Z Pr(>F)
## log(gdf$Csize)   1 0.0011340 0.00113399 0.06674 9.4779 2.5316  0.004 **
## gdf$Habitat      3 0.0009007 0.00030023 0.05301 2.5093 1.6043  0.055 .
## Residuals      125 0.0149556 0.00011965 0.88025
## Total          129 0.0169903
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: procD.lm(f1 = PC2 ~ log(gdf$Csize) + gdf$Habitat)
```

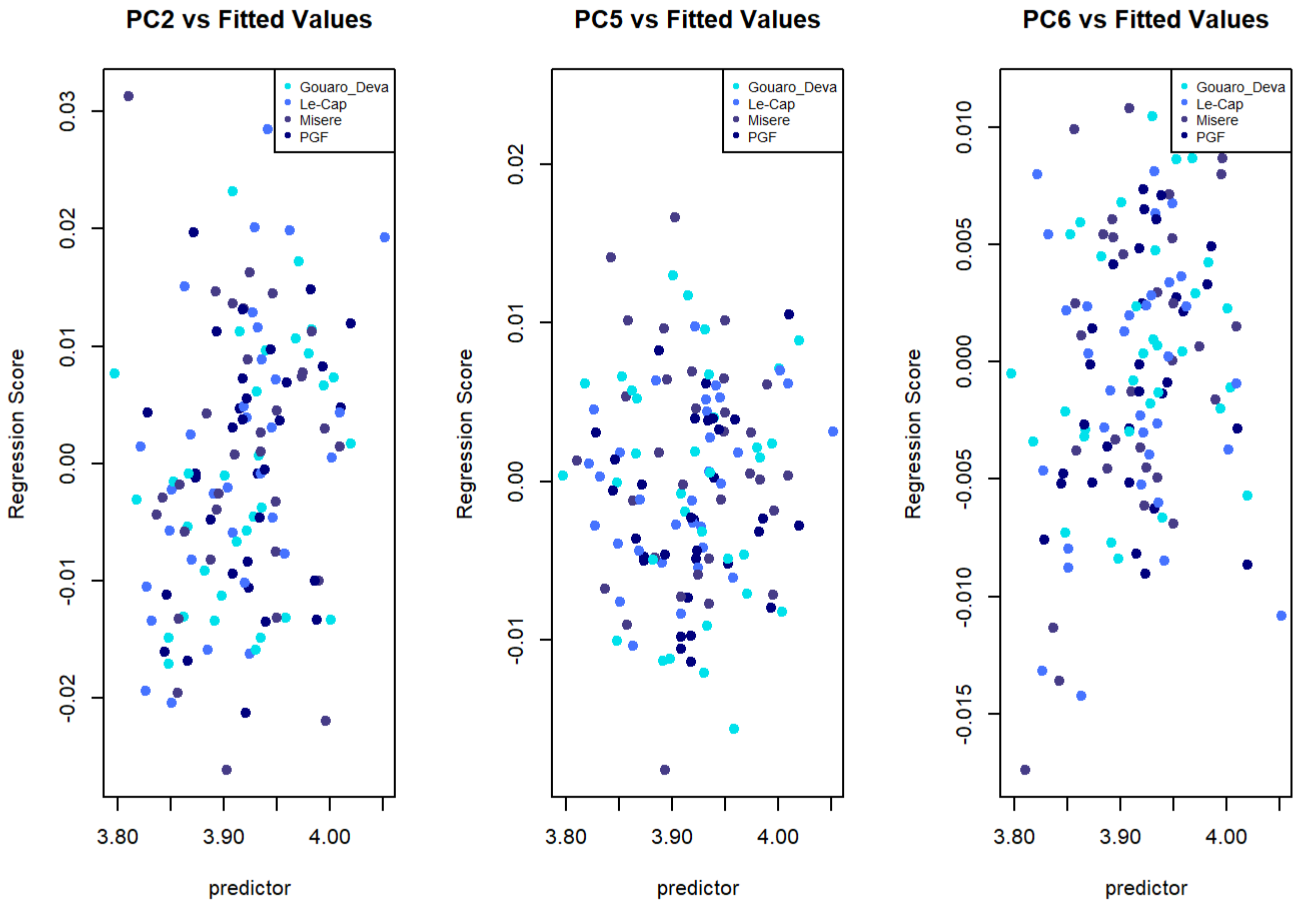
```
summary(fit.size.PC5)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type I
## Effect sizes (Z) based on F distributions
##
##                  Df        SS         MS     Rsq      F       Z Pr(>F)
## log(gdf$Csize)   1 0.0000458 4.5799e-05 0.00766 1.1089 0.63276  0.276
## gdf$Habitat      3 0.0007678 2.5593e-04 0.12847 6.1966 3.06262  0.002 **
## Residuals      125 0.0051628 4.1302e-05 0.86386
## Total          129 0.0059764
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: procD.lm(f1 = PC5 ~ log(gdf$Csize) + gdf$Habitat)
```

```
summary(fit.size.PC6)
```

```
##
## Analysis of Variance, using Residual Randomization
## Permutation procedure: Randomization of null model residuals
## Number of permutations: 1000
## Estimation method: Ordinary Least Squares
## Sums of Squares and Cross-products: Type I
## Effect sizes (Z) based on F distributions
##
##                  Df        SS         MS     Rsq       F       Z Pr(>F)
## log(gdf$Csize)   1 0.0003701 0.00037005 0.07985 11.2692 2.65349  0.002 **
## gdf$Habitat      3 0.0001599 0.00005329 0.03450  1.6229 0.86258  0.199
## Residuals      125 0.0041047 0.00003284 0.88566
## Total          129 0.0046346
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Call: procD.lm(f1 = PC6 ~ log(gdf$Csize) + gdf$Habitat)
```

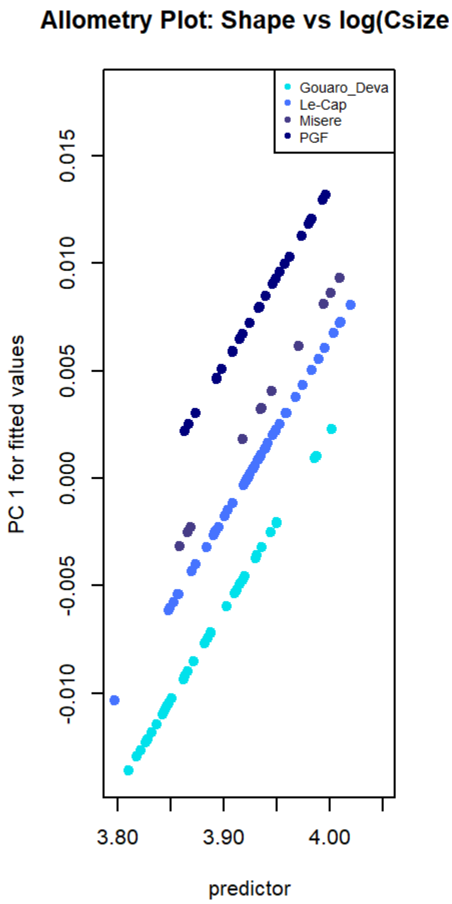
```
par(mfrow = c(1, 3))

# Graphic "PC2 vs Csize"
plot(fit.size.PC2, type = "regression", predictor = log(gdf$Csize), reg.type = "RegScore", pc
h = 19, col = Colors_ALL_Rusa_pop, main = "PC2 vs Fitted Values")
legend("topright", legend = names(Colors_ALL_Rusa_pop), col = Colors_ALL_Rusa_pop, pch = 19,
cex= 0.65)
# Graphic "PC5 vs Fitted Values"
plot(fit.size.PC5, type = "regression", predictor = log(gdf$Csize), reg.type = "RegScore", pc
h = 19, col = Colors_ALL_Rusa_pop, main = "PC5 vs Fitted Values")
legend("topright", legend = names(Colors_ALL_Rusa_pop), col = Colors_ALL_Rusa_pop, pch = 19,
cex= 0.65)
# Graphic "PC6 vs Fitted Values"
plot(fit.size.PC6, type = "regression", predictor = log(gdf$Csize), reg.type = "RegScore", pc
h = 19, col = Colors_ALL_Rusa_pop, main = "PC6 vs Fitted Values")
legend("topright", legend = names(Colors_ALL_Rusa_pop), col = Colors_ALL_Rusa_pop, pch = 19,
cex= 0.65)
```

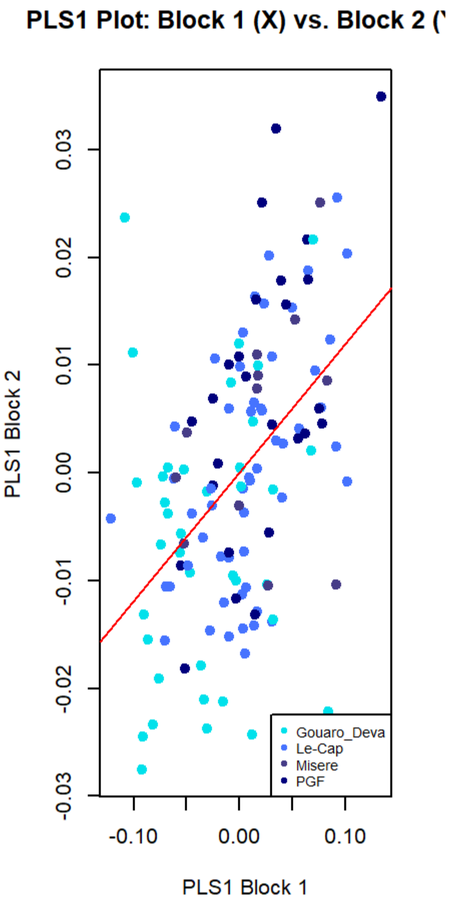


```
###Results ###############
# PC2 : size effect (p-value <0.05; R²: 6.7%) : landmark coordinates (shape) change according to the centroid size
# PC5 : habitat effect (p-value <0.05; R²: 12.8%): landmark coordinates (shape) change according to the type of habitat
# PC6: size effect (p-value <0.05; R²: 8%) : landmark coordinates (shape) change according to the centroid size
##########################

# Plot Allometry
# Allometry is the study of differential growth relationships between different parts of an organism.
plotAllometry(fit.size, size = gdf$Csize, logsz = TRUE, method = "PredLine", col = Colors_ALL_Rusa_pop[ALL_Rusa_pop], pch = 19)
legend("topright", legend = names(Colors_ALL_Rusa_pop), col = Colors_ALL_Rusa_pop, pch = 19, cex= 0.65)
title("Allometry Plot: Shape vs log(Csize)")

# Partial Least Squares : explore the relationship between the logarithmic centroid size and the coordinates of the landmarks. PLS analysis seeks to maximise the covariance between centroid size and landmark coordinates. r-PLS² gives an estimate of the proportion of variance in landmark coordinates that is explained by centroid size alone.
PLS <- two.b.pls(log(gdf$Csize), gdf$coords, print.progress = FALSE)
PLS # (r-PLS varies between -1 and 1; 0 = no correlation)
```

```
##
## Call:
## two.b.pls(A1 = log(gdf$Csize), A2 = gdf$coords, print.progress = FALSE)
##
##
##
## r-PLS: 0.465
##
## Effect Size (Z): 3.957
##
## P-value: 0.001
##
## Based on 1000 random permutations
```

```
plot(PLS, col = Colors_ALL_Rusa_pop[ALL_Rusa_pop], pch = 19)
legend("bottomright", legend = names(Colors_ALL_Rusa_pop), col = Colors_ALL_Rusa_pop, pch = 19, cex= 0.65)

###Results ###############
#There is a moderate (r-PLS= 0.465; less than for Cervus) and statistically significant (P-value = 0.001 ) correlation between centroid size and mandible shape. The variance explained by size is R²≈(r-PLS)²=0.216, indicating that 22% of the variation in shape is due to size, while 78% is explained by other factors.
# Effect Size (Z): 3.957 : Indicates a significant difference between the observed correlation and the null distribution, suggesting a significative correlation between shape and size.
##########################
```





#

List all the packages used in this study:

```
knitr::purl("MorphoGeom_cervids.Rmd", output = "MorphoGeom_cervids_code.R", quiet = TRUE)
```

```
## [1] "MorphoGeom_cervids_code.R"
```

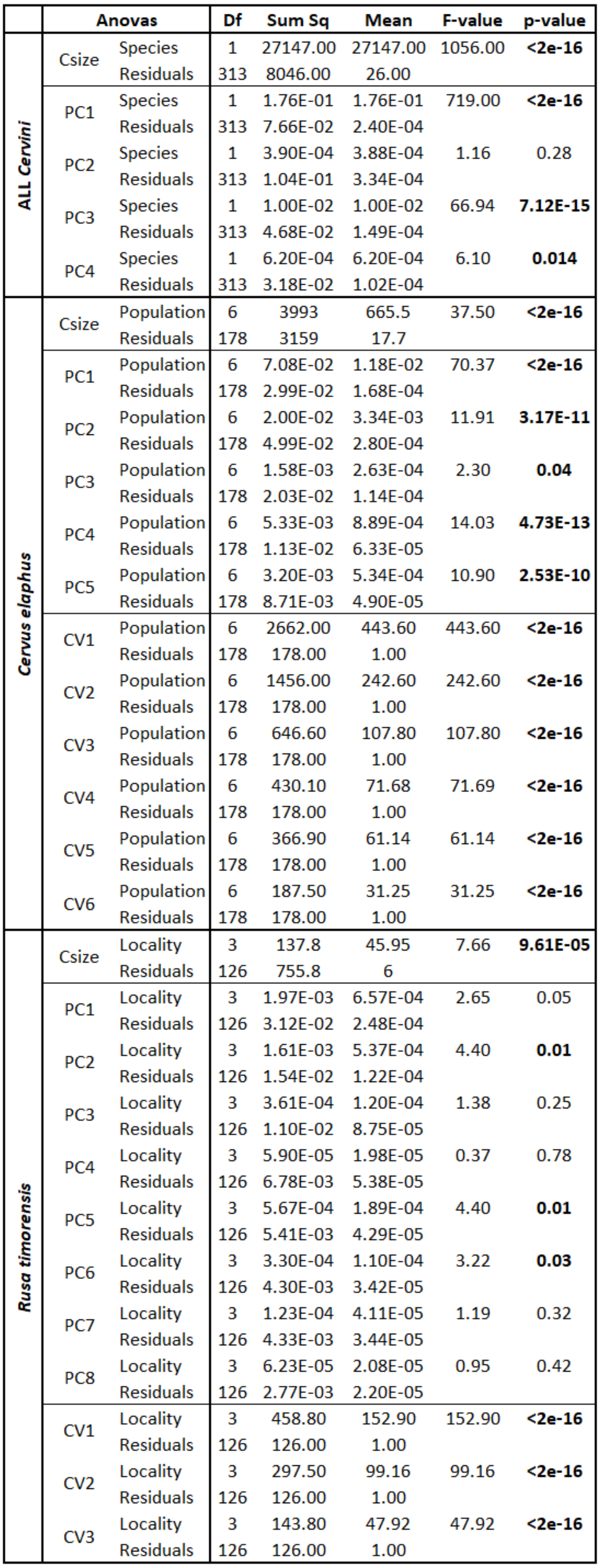
```
deps <- renv::dependencies("MorphoGeom_cervids_code.R")
```

```
## Finding R package dependencies ... Done!
```

```
unique(deps$Package)
```

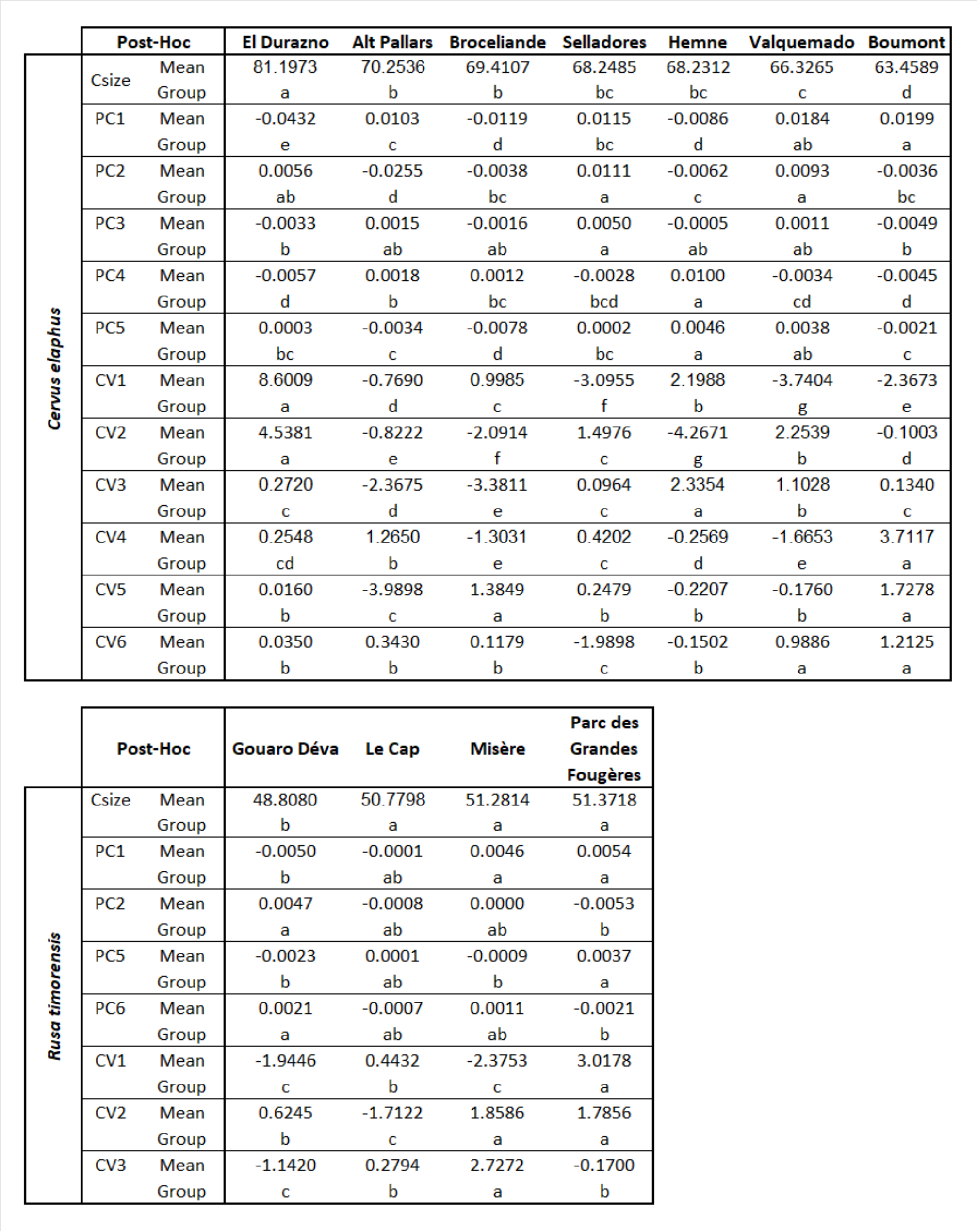
```
##  [1] "agricolae"    "broom"        "car"          "caret"        "dplyr"       
##  [6] "factoextra"   "FactoMineR"   "geomorph"     "knitr"        "ltm"         
## [11] "Morpho"       "multcompView" "performance"  "readxl"       "renv"        
## [16] "RRPP"         "shapes"       "tidyverse"
```

Table S 1 Results of ANOVA analyses (p-values)



	Anovas		Df	Sum Sq	Mean	F-value	p-value
ALL Cervini	Csize	Species	1	27147.00	27147.00	1056.00	**<2e-16**
		Residuals	313	8046.00	26.00		
	PC1	Species	1	1.76E-01	1.76E-01	719.00	**<2e-16**
		Residuals	313	7.66E-02	2.40E-04		
	PC2	Species	1	3.90E-04	3.88E-04	1.16	0.28
		Residuals	313	1.04E-01	3.34E-04		
	PC3	Species	1	1.00E-02	1.00E-02	66.94	**7.12E-15**
		Residuals	313	4.68E-02	1.49E-04		
	PC4	Species	1	6.20E-04	6.20E-04	6.10	**0.014**
		Residuals	313	3.18E-02	1.02E-04		
Cervus elaphus	Csize	Population	6	3993	665.5	37.50	**<2e-16**
		Residuals	178	3159	17.7		
	PC1	Population	6	7.08E-02	1.18E-02	70.37	**<2e-16**
		Residuals	178	2.99E-02	1.68E-04		
	PC2	Population	6	2.00E-02	3.34E-03	11.91	**3.17E-11**
		Residuals	178	4.99E-02	2.80E-04		
	PC3	Population	6	1.58E-03	2.63E-04	2.30	**0.04**
		Residuals	178	2.03E-02	1.14E-04		
	PC4	Population	6	5.33E-03	8.89E-04	14.03	**4.73E-13**
		Residuals	178	1.13E-02	6.33E-05		
	PC5	Population	6	3.20E-03	5.34E-04	10.90	**2.53E-10**
		Residuals	178	8.71E-03	4.90E-05		
	CV1	Population	6	2662.00	443.60	443.60	**<2e-16**
		Residuals	178	178.00	1.00		
	CV2	Population	6	1456.00	242.60	242.60	**<2e-16**
		Residuals	178	178.00	1.00		
	CV3	Population	6	646.60	107.80	107.80	**<2e-16**
		Residuals	178	178.00	1.00		
	CV4	Population	6	430.10	71.68	71.69	**<2e-16**
		Residuals	178	178.00	1.00		
	CV5	Population	6	366.90	61.14	61.14	**<2e-16**
		Residuals	178	178.00	1.00		
	CV6	Population	6	187.50	31.25	31.25	**<2e-16**
		Residuals	178	178.00	1.00		
Rusa timorensis	Csize	Locality	3	137.8	45.95	7.66	**9.61E-05**
		Residuals	126	755.8	6		
	PC1	Locality	3	1.97E-03	6.57E-04	2.65	0.05
		Residuals	126	3.12E-02	2.48E-04		
	PC2	Locality	3	1.61E-03	5.37E-04	4.40	**0.01**
		Residuals	126	1.54E-02	1.22E-04		
	PC3	Locality	3	3.61E-04	1.20E-04	1.38	0.25
		Residuals	126	1.10E-02	8.75E-05		
	PC4	Locality	3	5.90E-05	1.98E-05	0.37	0.78
		Residuals	126	6.78E-03	5.38E-05		
	PC5	Locality	3	5.67E-04	1.89E-04	4.40	**0.01**
		Residuals	126	5.41E-03	4.29E-05		
	PC6	Locality	3	3.30E-04	1.10E-04	3.22	**0.03**
		Residuals	126	4.30E-03	3.42E-05		
	PC7	Locality	3	1.23E-04	4.11E-05	1.19	0.32
		Residuals	126	4.33E-03	3.44E-05		
	PC8	Locality	3	6.23E-05	2.08E-05	0.95	0.42
		Residuals	126	2.77E-03	2.20E-05		
	CV1	Locality	3	458.80	152.90	152.90	**<2e-16**
		Residuals	126	126.00	1.00		
	CV2	Locality	3	297.50	99.16	99.16	**<2e-16**
		Residuals	126	126.00	1.00		
	CV3	Locality	3	143.80	47.92	47.92	**<2e-16**
		Residuals	126	126.00	1.00		

Table S 2 Results of Duncan post-hoc tests



	Post-Hoc		El Durazno	Alt Pallars	Broceliande	Selladores	Hemne	Valquemado	Boumont
Cervus elaphus	Csize	Mean	81.1973	70.2536	69.4107	68.2485	68.2312	66.3265	63.4589
		Group	a	b	b	bc	bc	c	d
	PC1	Mean	-0.0432	0.0103	-0.0119	0.0115	-0.0086	0.0184	0.0199
		Group	e	c	d	bc	d	ab	a
	PC2	Mean	0.0056	-0.0255	-0.0038	0.0111	-0.0062	0.0093	-0.0036
		Group	ab	d	bc	a	c	a	bc
	PC3	Mean	-0.0033	0.0015	-0.0016	0.0050	-0.0005	0.0011	-0.0049
		Group	b	ab	ab	a	ab	ab	b
	PC4	Mean	-0.0057	0.0018	0.0012	-0.0028	0.0100	-0.0034	-0.0045
		Group	d	b	bc	bcd	a	cd	d
	PC5	Mean	0.0003	-0.0034	-0.0078	0.0002	0.0046	0.0038	-0.0021
		Group	bc	c	d	bc	a	ab	c
	CV1	Mean	8.6009	-0.7690	0.9985	-3.0955	2.1988	-3.7404	-2.3673
		Group	a	d	c	f	b	g	e
	CV2	Mean	4.5381	-0.8222	-2.0914	1.4976	-4.2671	2.2539	-0.1003
		Group	a	e	f	c	g	b	d
	CV3	Mean	0.2720	-2.3675	-3.3811	0.0964	2.3354	1.1028	0.1340
		Group	c	d	e	c	a	b	c
	CV4	Mean	0.2548	1.2650	-1.3031	0.4202	-0.2569	-1.6653	3.7117
		Group	cd	b	e	c	d	e	a
	CV5	Mean	0.0160	-3.9898	1.3849	0.2479	-0.2207	-0.1760	1.7278
		Group	b	c	a	b	b	b	a
	CV6	Mean	0.0350	0.3430	0.1179	-1.9898	-0.1502	0.9886	1.2125
		Group	b	b	b	c	b	a	a

	Post-Hoc		Gouaro Déva	Le Cap	Misère	Parc des Grandes Fougères
Rusa timorensis	Csize	Mean	48.8080	50.7798	51.2814	51.3718
		Group	b	a	a	a
	PC1	Mean	-0.0050	-0.0001	0.0046	0.0054
		Group	b	ab	a	a
	PC2	Mean	0.0047	-0.0008	0.0000	-0.0053
		Group	a	ab	ab	b
	PC5	Mean	-0.0023	0.0001	-0.0009	0.0037
		Group	b	ab	b	a
	PC6	Mean	0.0021	-0.0007	0.0011	-0.0021
		Group	a	ab	ab	b
	CV1	Mean	-1.9446	0.4432	-2.3753	3.0178
		Group	c	b	c	a
	CV2	Mean	0.6245	-1.7122	1.8586	1.7856
		Group	b	c	a	a
	CV3	Mean	-1.1420	0.2794	2.7272	-0.1700
		Group	c	b	a	b

Table S 3 Results of procrust regressions evaluating how mandible shape vary as a function of size and species (for Cervini), population (for C. elaphus) and habitat (for R. timorensis).

Procrust regression results :

		Df	**SS**	**MS**	**R^2**	**F**	**Z**	**Pr(>F)**
Cervini	log(Csize)	1	0.1877	0.1877	**0.3369**	173.0420	6.9378	**0.0010**
	Species	1	0.0311	0.0311	**0.0558**	28.6410	6.2224	**0.0010**
	Residuals	312	0.3385	0.0011	0.6074			
	Total	314	0.5572					
Cervus elaphus	log(Csize)	1	0.0377	0.0377	**0.1396**	43.6740	5.1801	**0.0010**
	Pop	6	0.0794	0.0132	**0.2945**	15.3510	10.1882	**0.0010**
	Residuals	177	0.1526	0.0009	0.5659			
	Total	184	0.2697					
Rusa timorensis	log(Csize)	1	0.0046	0.0046	**0.0437**	5.9406	3.4309	**0.0010**
	Habitat	3	0.0039	0.0013	**0.0373**	1.6911	1.8755	**0.0300**
	Residuals	125	0.0965	0.0008	0.9190			
	Total	129	0.1050					

Table S 4 Results of procrust regressions (p-values and R²) for each axis of PCA carrying significant interpopulation and inter-habitat differences.

Procrust regression results per axis of the PCA with significant differences:

		Df	SS	MS	R^2	F	Z	Pr(>F)
Cervus elaphus	log(Csize)	1	0.0315	0.0315	**0.3125**	187.0540	6.0920	**0.0010**
	Pop	6	0.0395	0.0066	**0.3919**	39.0950	10.0250	**0.0010**
	Residuals	177	0.0298	0.0000				
	Total	184	0.1007					
	log(Csize)	1	0.0037	0.0037	**0.0528**	15.4030	2.9396	**0.0010**
	Pop	6	0.0238	0.0040	**0.3399**	16.5150	7.4453	**0.0010**
	Residuals	177	0.0425	0.0002	**0.6072**			
	Total	184	0.0699					
	log(Csize)	1	0.0001	0.0001	**0.0027**	0.5212	0.1576	0.4480
	Pop	6	0.0015	0.0003	**0.0696**	2.2132	1.7163	**0.0450**
	Residuals	177	0.0203	0.0001	**0.9277**			
	Total	184	0.0219					
	log(Csize)	1	0.0005	0.0005	**0.0290**	9.1848	2.4425	**0.0030**
	Pop	6	0.0069	0.0011	**0.4128**	21.8160	7.9325	**0.0010**
	Residuals	177	0.0093	0.0001	**0.5582**			
	Total	184	0.0166					
	log(Csize)	1	0.0003	0.0003	**0.0273**	6.9244	2.0620	**0.0120**
	Pop	6	0.0033	0.0005	**0.2742**	11.5819	5.7118	**0.0010**
	Residuals	177	0.0083	0.0000	**0.6985**			
	Total	184	0.0119					
Rusa timorensis	log(Csize)	1	0.0011	0.0011	**0.0667**	9.4779	2.5316	**0.0040**
	Habitat	3	0.0009	0.0003	**0.0530**	2.5093	1.6043	0.0550
	Residuals	125	0.0150	0.0001	**0.8803**			
	Total	129	0.0170					
	log(Csize)	1	0.0000	0.0000	**0.0077**	1.1089	0.6328	0.2760
	Habitat	3	0.0008	0.0003	**0.1285**	6.1966	3.0626	**0.0020**
	Residuals	125	0.0052	0.0000	**0.8639**			
	Total	129	0.0060					
	log(Csize)	1	0.0004	0.0004	**0.0799**	11.2692	2.6535	**0.0020**
	Habitat	3	0.0002	0.0001	**0.0345**	1.6229	0.8626	0.1990
	Residuals	125	0.0041	0.0000	**0.8857**			
	Total	129	0.0046					

Table S 5 Results of Partial Least Squares

Partial Least Squares :

	r-PLS	**Effect size (Z)**	**p-value**
Cervus elaphus	0.6410	6.2082	0.0010
Rusa timorensis	0.4650	3.9570	0.0010