

Pleistocene hunter-gatherer coastal adaptations in Atlantic Iberia

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## **Supplementary material**

R-code

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# Libraries
library(tidyverse)
library(readxl)
library(FactoMineR)
library(psych)
library(factoextra)

# Importing data and data wrangling
ArcheoBicho <- read_excel("~/ArcheoBicho2022.xlsx")
Archeo <- ArcheoBicho %>%
  replace(is.na(.), 0) %>%
  add_column(H, D1, D2, Hmax, J, E)

# PCA using package FactoMineR
arch.PCA <- PCA(Archeo[c(2:10)], graph = F)
print(arch.PCA)

# Bartlett's sphericity test and the KMO MSA index.
# Bartlett's sphericity test using library psych
cortest.bartlett(Archeo[c(2:10)])

# KMO Measure of Sampling Adequacy (MSA)
# using function from package psych for overall and partial KMO:
KMO(R)

# Detailed results of the PCA
arch.PCA$eig # component eigenvalues
arch.PCA$var # variables (artifacts and proxies)
arch.PCA$ind # sites

kbl(arch.PCA$var$contrib) %>%

```

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kable_classic(full_width = F, html_font = "helvetica") %>%
  add_header_above(c(" " = 1, "Coordinates" = 5, "Correlation" = 5,
"cos2" = 5, "Contribution" = 5))

# variables in PCA
fviz_eig(arch.PCA, addlabels = TRUE, ylim = c(0, 75))

# PCA plot of variables (based on quality of representation cos2 i.e.
# a high cos2 indicates a good representation of the variable on the
# principal component.

# In this case the variable is positioned close to the circumference
# of the correlation circle.

# A low cos2 indicates that the variable is not perfectly represented
# by the PCs. In this case the variable is close to the center of the
# circle.)

# Figures
fviz_pca_var(arch.PCA, col.var = "cos2",
             gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),
             repel = TRUE # Avoid text overlapping)
)

fviz_pca_var(arch.PCA, col.var = "cos2", axes = c(3:4),
             gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),
             repel = TRUE # Avoid text overlapping)
)

# Idem but based on contribution (i.e. The larger the value of the
# contribution, the more the variable contributes to the component.)
fviz_pca_var(arch.PCA, col.var = "contrib",
             gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"))
)

fviz_pca_var(arch.PCA, col.var = "contrib", axes = c(3,4),
             gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"))
)

```

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# Dimension description

res.desc <- dimdesc(arch.PCA, axes = c(1,2), proba = 0.05) #
Description of dimension 1

# Description of Dim.1 and Dim.2

res.desc$Dim.1

res.desc$Dim.2

# Description of dimensions 3 and 4

res.desc34 <- dimdesc(arch.PCA, axes = c(3,4), proba = 0.05)
res.desc34$Dim.3
res.desc34$Dim.4

# individuals in PCA

fviz_pca_ind(arch.PCA,
              geom.ind = "point",
              pointshape = 21,
              pointsize = 2,
              #fill.ind = Archeo$Dist,
              col.ind = "black",
              palette = "jco",
              addEllipses = TRUE,
              label = "var",
              col.var = "black",
              repel = TRUE,
              legend.title = "Treatment") +
  ggtitle("PCA individuals") +
  theme(plot.title = element_text(hjust = 0.5))

# Plot of individuals

fviz_pca_ind(arch.PCA,
              col.ind = "contrib",
              gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07")) +
  ggtitle("PCA individuals") +
  theme(plot.title = element_text(hjust = 0.5))

```

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# Total contribution of individuals on PC1 and PC2
fviz_contrib(arch.PCA, choice = "ind", axes = 1:2)
fviz_contrib(arch.PCA, choice = "ind", axes = 3:4)

# PCA Biplot
fviz_pca_biplot(arch.PCA, repel = F,
                 col.var = "#2E9FDF", # Variables color
                 col.ind = "#696969" # Individuals color)
)

fviz_pca_biplot(arch.PCA, axes=c(3,4), repel = F,
                 col.var = "#2E9FDF", # Variables color
                 col.ind = "#696969" # Individuals color)
)

# Accessing PCA results
# Eigenvalues
eig.val <- get_eigenvalue(arch.pca)
eig.val

# Results for Variables
res.var <- get_pca_var(arch.pca)
res.var$coord          # Coordinates
res.var$contrib         # Contributions to the PCs
res.var$cos2            # Quality of representation

# Results for individuals
res.ind <- get_pca_ind(arch.pca)
res.ind$coord          # Coordinates
res.ind$contrib         # Contributions to the PCs
res.ind$cos2            # Quality of representation

```