

Replication Document

This document can be used to replicate the quantitative lithic analyses presented in the paper “Multiple hominin dispersals into Southwest Asia over the last 400,000 years” by Groucutt et al. 2020. All analyses were conducted in R.

Load libraries

First, we will load the psych library for convenient PCA-related tests, and the ggplot2 and ggpubr libraries for plotting results.

```
library(psych)
library(ggplot2)
library(ggpubr)
```

Data

Next, we load the lithic data as follows:

```
LP <- read.csv(file="./LP.csv")
MIS67 <- read.csv(file="./MIS67.csv")
```

These data sets come with several variables (columns). The Lower Palaeolithic data look like this:

```
head(LP)
```

##	ID	Assemblage	N..scars	Flaking.Length	Width.at.Midpoint	Proximal.Width
## 1	14	KAM-4 A.D	3	31.33	21.50	21.29
## 2	40	KAM-4 A.D	5	38.03	34.17	31.96
## 3	58	KAM-4 A.D	4	45.94	35.65	32.32
## 4	59	KAM-4 A.D	5	57.07	34.42	34.79
## 5	61	KAM-4 A.D	3	38.96	25.45	28.52
## 6	108	KAM-4 A.D	4	45.97	30.32	31.99

##	Distal.Width	Thickness.at.midpoint	Platform.Width	Platform.Thickness
## 1	12.76	5.76	18.05	4.87
## 2	23.17	7.95	26.32	4.47
## 3	26.41	12.43	29.02	12.18
## 4	6.41	9.36	36.18	7.72
## 5	2.18	5.83	29.80	5.26
## 6	3.44	7.84	29.78	8.89

The data from the transition between Marine Isotope Stage 6 and 7 (MIS67) look like this:

```
head(MIS67)
```

##	Assemblage	ID	N..scars	Flaking.Length	Width.at.Midpoint	Proximal.Width
## 1	KAM-4 A.C	61	6	46.27	41.22	25.09
## 2	KAM-4 A.C	5031	4	52.39	39.74	22.64
## 3	KAM-4 A.C	77	8	34.08	43.92	23.57

```
## 4 KAM-4 A.C 1427      4      41.68      24.16      24.01
## 5 KAM-4 A.C 1431      5      23.78      24.05      16.64
## 6 KAM-4 A.C 1455      3      30.16      32.35      28.43
##   Distal.Width Thickness.at.midpoint Platform.Width Platform.Thickness
## 1      38.77      7.95      25.18      3.34
## 2      27.48      7.99      19.28      7.45
## 3      20.64      9.74      24.30     10.16
## 4      18.35      7.18      21.56      5.87
## 5      14.62      6.81      19.06      3.27
## 6      26.15      7.04      26.55      4.88
```

PrePCA tests

Before running the analysis, we used a couple of simple preliminary tests to determine whether the variation in the data was sufficiently greater in at least one or more dimensions that sensible principle components could be extracted. One test involved the “Kaiser, Meyer, Olkin Measure of Sampling Adequacy”:

```
KMO(MIS67[,c(3:10)])
```

```
## Kaiser-Meyer-Olkin factor adequacy
## Call: KMO(r = MIS67[, c(3:10)])
## Overall MSA = 0.73
## MSA for each item =
##           N..scars      Flaking.Length      Width.at.Midpoint
##           0.39          0.56          0.76
##           Proximal.Width      Distal.Width Thickness.at.midpoint
##           0.76          0.54          0.84
##           Platform.Width      Platform.Thickness
##           0.76          0.87
```

```
KMO(LP[,c(3:10)])
```

```
## Kaiser-Meyer-Olkin factor adequacy
## Call: KMO(r = LP[, c(3:10)])
## Overall MSA = 0.78
## MSA for each item =
##           N..scars      Flaking.Length      Width.at.Midpoint
##           0.81          0.76          0.85
##           Proximal.Width      Distal.Width Thickness.at.midpoint
##           0.74          0.72          0.87
##           Platform.Width      Platform.Thickness
##           0.67          0.83
```

The other involved “Bartlett’s Test for Sphericity”,

```
cortest.bartlett(MIS67[,c(3:10)])
```

```
## R was not square, finding R from data
## $chisq
## [1] 396.6637
##
## $p.value
## [1] 9.26127e-67
##
## $df
```

```
## [1] 28
cortest.bartlett(LP[,c(3:10)])

## R was not square, finding R from data

## $chisq
## [1] 1673.095
##
## $p.value
## [1] 0
##
## $df
## [1] 28
```

PCA

Then, we can perform the simple PCA on the relevant lithic variables,

```
pca_MIS67 <- prcomp(
  x = MIS67[,c(3:10)],
  retx = T,
  center = T,
  scale = T)

pca_LP <- prcomp(
  x = LP[,c(3:10)],
  retx = T,
  center = T,
  scale = T)

LP_scores <- cbind(
  LP[,c(1:2)],
  pca_LP$x)

MIS67_scores <- cbind(
  MIS67[,c(1:2)],
  pca_MIS67$x)
```

Plotting

Lastly, we plot the results using ggplot2 as follows. The first plot will contain the results for the analysis of the LP data,

```
sample_name <- "LP"

p1 <- ggplot(
  data = get(paste(sample_name, "_scores", sep="")),
  mapping = aes(Assemblage, PC1, group = Assemblage)) +
  geom_boxplot(colour="darkgrey", fill="grey", alpha=0.8) +
  theme_minimal() +
  theme(text = element_text(family="Times", size=12),
        plot.title = element_text(face="bold", hjust=0.5, size=15),
```

```

        axis.text.x = element_blank(),
        axis.title.x = element_blank())

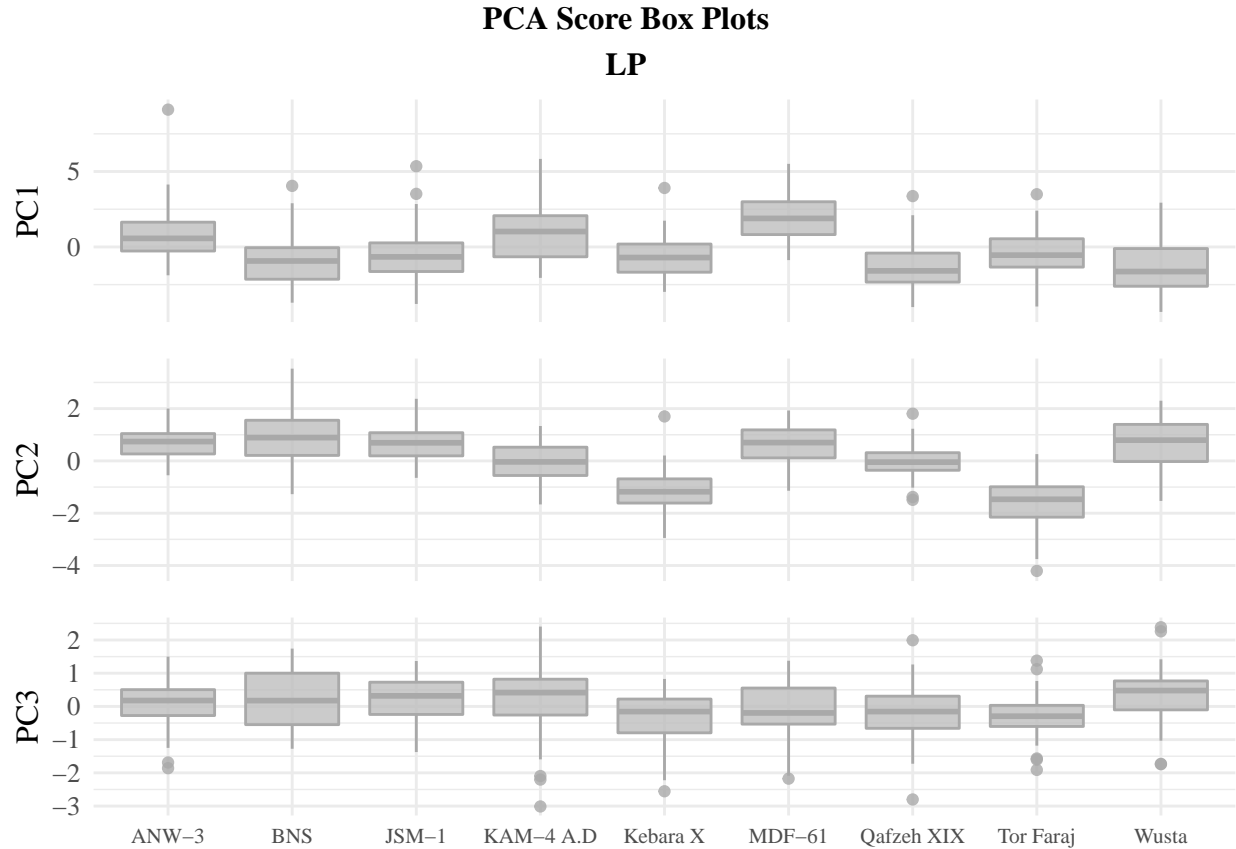
p2 <- ggplot(
  data = get(paste(sample_name, "_scores", sep="")),
  mapping = aes(Assemblage, PC2, group = Assemblage)) +
  geom_boxplot(colour="darkgrey", fill="grey", alpha=0.8) +
  theme_minimal() +
  theme(text = element_text(family="Times", size=12),
        plot.title = element_text(face="bold", hjust=0.5, size=15),
        axis.text.x = element_blank(),
        axis.title.x = element_blank())

p3 <- ggplot(
  data = get(paste(sample_name, "_scores", sep="")),
  mapping = aes(Assemblage, PC3, group = Assemblage)) +
  geom_boxplot(colour="darkgrey", fill="grey", alpha=0.8) +
  theme_minimal() +
  theme(text = element_text(family="Times", size=12),
        plot.title = element_text(face="bold", hjust=0.5, size=15),
        axis.text.x = element_text(size=8),
        axis.title.x = element_blank())

fig <- ggarrange(p1, p2, p3,
  ncol=1,
  nrow=3,
  align="v")

annotate_figure(fig,
  top = text_grob("PCA Score Box Plots\nLP",
    family="Times",
    face="bold"),
  fig.lab.pos = "top")

```



The second plot contains the results pertaining to the MIS67 data,

```
sample_name <- "MIS67"
```

```
p1 <- ggplot(
  data = get(paste(sample_name, "_scores", sep="")),
  mapping = aes(Assemblage, PC1, group = Assemblage)) +
  geom_boxplot(colour="darkgrey", fill="grey", alpha=0.8) +
  theme_minimal() +
  theme(text = element_text(family="Times", size=12),
    plot.title = element_text(face="bold", hjust=0.5, size=15),
    axis.text.x = element_blank(),
    axis.title.x = element_blank())

p2 <- ggplot(
  data = get(paste(sample_name, "_scores", sep="")),
  mapping = aes(Assemblage, PC2, group = Assemblage)) +
  geom_boxplot(colour="darkgrey", fill="grey", alpha=0.8) +
  theme_minimal() +
  theme(text = element_text(family="Times", size=12),
    plot.title = element_text(face="bold", hjust=0.5, size=15),
    axis.text.x = element_blank(),
    axis.title.x = element_blank())

p3 <- ggplot(
  data = get(paste(sample_name, "_scores", sep="")),
  mapping = aes(Assemblage, PC3, group = Assemblage)) +
```

```

geom_boxplot(colour="darkgrey",fill="grey",alpha=0.8) +
theme_minimal() +
theme(text = element_text(family="Times", size=12),
      plot.title = element_text(face="bold",hjust=0.5,size=15),
      axis.text.x = element_text(size=8),
      axis.title.x = element_blank())

fig <- ggarrange(p1,p2,p3,
  ncol=1,
  nrow=3,
  align="v")

annotate_figure(fig,
  top = text_grob("PCA Score Box Plots\nMIS67",
    family="Times",
    face="bold"),
  fig.lab.pos = "top")

```

