## PCA.R

## rob\_c

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```
# SUMMARY:
#### Al-Yotm distinct from Dead Sea and Kufranjah valley sites
#### Dead Sea and Kufranjah are different ON AVERAGE, but a lot of overlap

# ANALYSIS:
## Libraries
library(ggplot2)
library(ggfortify)

## Warning: package 'ggfortify' was built under R version 3.3.3
```

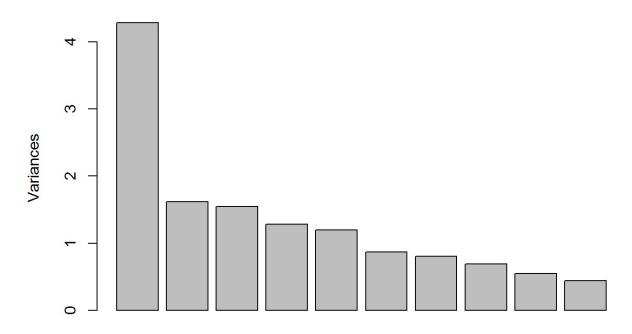
```
## Import Data
MorphData<-read.csv("MuhaidatEtAl_RawData.csv", header=T)
str(MorphData)</pre>
```

```
## 'data.frame': 57 obs. of 15 variables:
           : Factor w/ 3 levels "AlYotm", "DeadSea", ...: 3 3 3 3 3 3 3 3
## $ Loc
3 ...
## $ BLen
            : num 4.8 5 5.4 5.6 5.5 5.2 5.9 5.7 4.9 5.9 ...
## $ BWdth
             : num 0.4 0.5 0.4 0.4 0.4 0.5 0.4 0.5 0.4 0.5 ...
## $ BVeins : int 3 5 NA 3 3 3 5 3 5 ...
## $ BSpines : int 2 2 2 2 2 2 3 2 2 2 ...
             : num 1 1 1 1.2 1.1 0.9 0.9 1.3 1 1.5 ...
## $ SpLen
## $ NodeLen : num 1.3 1.6 1.5 1.6 1.3 1.8 1.8 1.6 1.6 2 ...
## $ LLen
            : num 7 7 9 8.5 7.5 10 8 8 9.1 10 ...
## $ LWdth : num 1 1 1.1 0.9 0.7 1.2 1 1.2 0.8 1.2 ...
## $ LTeeth : int 4 5 4 4 5 3 4 NA 5 4 ...
## $ ASFilLen : num 1.3 1.3 1.2 1.3 1.2 1.3 1.3 1.2 1.3 1.3 ...
## $ ASAnthLen: num 0.5 0.5 0.5 0.5 0.4 0.5 0.5 0.5 0.6 0.5 ...
## $ ASApenLen: num 0.5 0.5 0.6 0.5 0.5 0.6 0.5 0.6 0.5 ...
## $ PSFilLen : num 1.2 NA 1.1 1.2 1.1 1.1 1.1 1.4 1.2 1.2 ...
## $ PSAnthLen: num 0.5 0.5 0.5 0.5 0.5 NA 0.6 0.5 0.6 0.4 ...
```

```
## Recode integer as numeric
MorphData$BVeins<-as.numeric(MorphData$BVeins)</pre>
MorphData$BSpines<-as.numeric(MorphData$BSpines)</pre>
MorphData$LTeeth<-as.numeric(MorphData$LTeeth)</pre>
## Add midvalue for missing data
for (Row in 1:nrow (MorphData)) {
  for(Col in 2:ncol(MorphData)){
    if(is.na(MorphData[Row,Col])){
      MorphData[Row,Col] <-mean (MorphData[MorphData$Loc==MorphData$Loc[Row],Co
1],na.rm=T)
    }
  }
}
## Principal Components Analysis
PC<-prcomp (MorphData[,2:ncol(MorphData)],scale=T,center=T)</pre>
### Summary
summary(PC)
```

```
## Importance of components:
                           PC1 PC2 PC3
                                               PC4
##
                                                       PC5
## Standard deviation
                        2.0704 1.2724 1.2439 1.13256 1.09294 0.93352
## Proportion of Variance 0.3062 0.1156 0.1105 0.09162 0.08532 0.06225
## Cumulative Proportion 0.3062 0.4218 0.5323 0.62396 0.70928 0.77153
##
                            PC7
                                    PC8
                                           PC9
                                                 PC10 PC11
                                                                PC12
## Standard deviation
                        0.89550 0.82883 0.73852 0.66564 0.59368 0.42020
## Proportion of Variance 0.05728 0.04907 0.03896 0.03165 0.02518 0.01261
## Cumulative Proportion 0.82881 0.87788 0.91683 0.94848 0.97366 0.98627
##
                           PC13
                                PC14
                       0.35956 0.2509
## Standard deviation
## Proportion of Variance 0.00923 0.0045
## Cumulative Proportion 0.99550 1.0000
```

```
### ScreePlot
screeplot(PC)
```



```
### % Variation explained by PC1 alone
100*sum(summary(PC)[[1]][1])/sum(summary(PC)[[1]])
```

```
## [1] 16.56535
```

```
### % Variation explained by PC1 & PC2
100*sum(summary(PC)[[1]][1:2])/sum(summary(PC)[[1]])
```

```
## [1] 26.74563
```

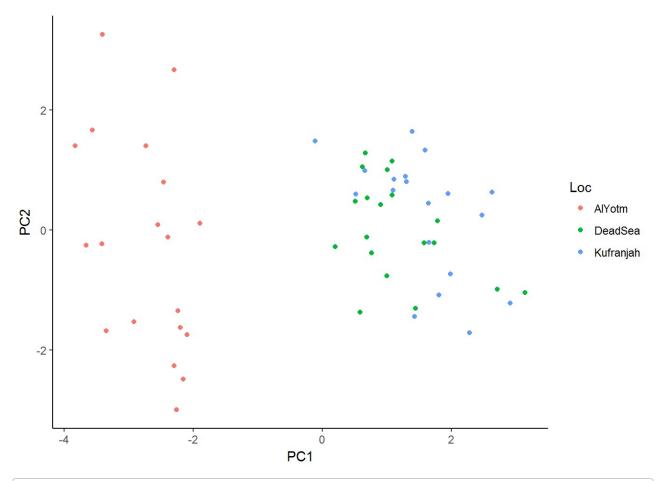
```
### % Variation explained by first n PCs
n<-10
100*sum(summary(PC)[[1]][1:n])/sum(summary(PC)[[1]])</pre>
```

```
## [1] 87.00394
```

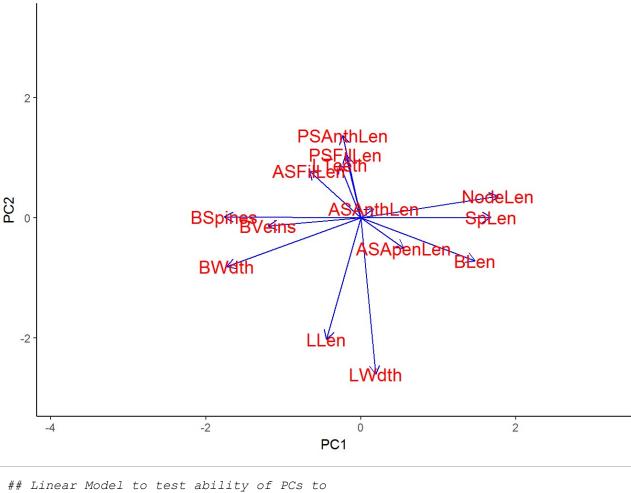
```
### Factor Loadings
PC$Rotation
```

```
## NULL
```

```
### Plot of PC1 & 2
#### Individuals
autoplot(PC,data=MorphData,colour="Loc",scale=0)+theme_classic()
```



## Warning: Removed 57 rows containing missing values (geom point).



```
## Linear Model to test ability of PCs to
MorphPCs<-cbind(MorphData,PC$x)
anova(lm(PC1 ~ Loc,data=MorphPCs)) ## PC1 only significant factor</pre>
```

```
anova(lm(PC2 ~ Loc, data=MorphPCs))
```

```
## Analysis of Variance Table
##
## Response: PC2
##
           Df Sum Sq Mean Sq F value Pr(>F)
          2 2.448 1.2240 0.7493 0.4776
## Residuals 54 88.213 1.6336
anova(lm(PC3 ~ Loc, data=MorphPCs))
## Analysis of Variance Table
##
## Response: PC3
          Df Sum Sq Mean Sq F value Pr(>F)
## Loc 2 1.970 0.98523 0.6283 0.5373
## Residuals 54 84.672 1.56800
anova(lm(PC4 ~ Loc, data=MorphPCs))
## Analysis of Variance Table
##
## Response: PC4
## Df Sum Sq Mean Sq F value Pr(>F)
            2 2.401 1.2006 0.9338 0.3993
## Loc
## Residuals 54 69.429 1.2857
anova(lm(PC5 ~ Loc,data=MorphPCs))
## Analysis of Variance Table
##
## Response: PC5
     Df Sum Sq Mean Sq F value Pr(>F)
## Loc 2 0.658 0.32906 0.2683 0.7657
## Residuals 54 66.234 1.22656
anova(lm(PC6 ~ Loc, data=MorphPCs))
## Analysis of Variance Table
##
## Response: PC6
          Df Sum Sq Mean Sq F value Pr(>F)
## Loc 2 0.180 0.08992 0.0999 0.9051
## Residuals 54 48.622 0.90040
```

```
anova(lm(PC7 ~ Loc, data=MorphPCs))
## Analysis of Variance Table
##
## Response: PC7
           Df Sum Sq Mean Sq F value Pr(>F)
## Loc 2 1.067 0.53371 0.6574 0.5223
## Residuals 54 43.840 0.81186
anova(lm(PC8 ~ Loc, data=MorphPCs))
## Analysis of Variance Table
## Response: PC8
           Df Sum Sq Mean Sq F value Pr(>F)
## Loc 2 3.192 1.5958 2.4427 0.09648 .
## Residuals 54 35.278 0.6533
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
anova(lm(PC9 ~ Loc, data=MorphPCs))
## Analysis of Variance Table
## Response: PC9
## Df Sum Sq Mean Sq F value Pr(>F)
         2 0.0355 0.01777 0.0315 0.969
## Residuals 54 30.5074 0.56495
anova(lm(PC10 ~ Loc, data=MorphPCs))
## Analysis of Variance Table
##
## Response: PC10
           Df Sum Sq Mean Sq F value Pr(>F)
          2 0.8703 0.43516 0.9815 0.3813
## Loc
## Residuals 54 23.9420 0.44337
```