Final Project - EEB590C

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Homework 3

This assignment is due prior to the last day class. You are to self-select and work in groups: 2-3 in a group. For the assignment below submit one R-script. Annotations via comments are highly encouraged. The script should run!

Assignment:

1: Obtain a dataset. This may be one of your own, a dataset from DRYAD, or some other source. Identify hypotheses for this dataset and analyze patterns in the data. You may use any methods learned during the semester, but at least one analysis must come from material learned in weeks 11-13.

USE COMMENTS IN THE R CODE to describe what the patterns you find represent.

```
setwd("D:/Documents/BoxSync/Classes_Spring2021/Advanced_Biostatistics_EEB590C/Homework/Final_EEB590")
#load appropriate libraries
library(knitr)
library(geomorph)
library(tidyverse)
library(readxl)
library(ade4)
library(vegan)
library(mice)
```

Intro

TODO

Preprocessing

Read in data

```
#READ IN DATA AS DATAFRAME
mydata<-read_excel(path="data/TransformGuaduaSet.xlsx", col_names = TRUE, na="x")</pre>
```

Remove Column V and Y

Remove column V and Y, because there is missing data and we cannot impute the data because it just doesn't make sense to attempt to predict these columns.

V. Adaxial: Frequency of stomates if present on the adaxial surface of foliage leaf blades: 0 = common; 1 = infrequent. Y. Adaxial: Papillae on long cells of the intercostal zone adjacent to the stomates: 0 = not overarching the stomates; 1 = overarching the stomates.

```
to_drop<-c("Adaxial: Papillae on long cells of the intercostal zone adjacent to the stomates: 0 = not
df=data.frame(mydata[,!( names(mydata) %in% to_drop)],stringsAsFactors = TRUE)</pre>
```

Set columns to factors

##

```
df<-data.frame(lapply(df,as.factor))
```

Imputation of missing data

In the last three columns, in some species the papillae of the cells adjacent to the stomata obscured the shape of the subsidiary cells. Therefore, the shapes of these subsidiary cells resulted in missing data that we imputed using the MICE package's logistic regression method.

```
init = mice(df,maxit=0)
meth = init$method
predM=init$predictorMatrix
meth[c(colnames(df[,7:length(df)]))]<-"logreg"</pre>
set.seed(183)
imputed <-mice(df, method = meth, predictorMatrix = predM, m=5, printFlag = FALSE)
## Warning: Number of logged events: 90
imputed<-complete(imputed)</pre>
sapply(imputed,function(x) sum(is.na(x))) #double check to make sure there are no more NA
##
##
##
##
##
##
##
##
##
##
##
##
##
                                 Abaxial.papillae.on.the.long.cells.in.the.stomatal.zone.0...absent.1...
##
##
                        Abaxial.papillae.on.the.long.cells.in.the.interstomatal.zone...0...absent..1...p
##
##
                                                                 Abaxial..Prickle.hairs..0...absent..1...
##
##
                                                         Abaxial..Bicellular.microhairs..0...absent..1...
##
##
                                                                     Abaxial..Macrohairs..0...absent..1...
##
                      Abaxial..Dumbbell.shaped.silica.bodies.in.the.intercostal.zone...0...present..1..
##
##
                         Abaxial..Saddle.shaped.silica.bodies.in.the.intercostal.zone...0...present..1..
##
##
##
                 Abaxial..Crenate..elongated..silica.bodies.in.the.intercostal.zone...0...present..1...
```

```
##
                           Abaxial..Dumbbell.shaped.silica.cells.in.the.costal.zone...0...present..1....
##
##
                             Abaxial..Saddle.shaped.silica.cells.in.the.costal.zone...0...present..1...
##
##
                       Abaxial..Crenate..elongated..silica.cells.in.the.costal.zone...0...present..1...
##
                                          Abaxial..Triangular.stomata.subsidiary.cells..0...absent..1...
##
##
##
                                         Abaxial..Dome.shaped.stomata.subsidiary.cells..0...absent..1...
##
##
                                      Abaxial..Parallel.sided.stomata.subsidiary.cells..0...absent..1...
##
##
                    Adaxial..stomates.on.the.adaxial.surface.of.foliage.leaf.blades...0...absent..1...p
##
## Adaxial.papillae.on.the.long.cells.in.the.stomatal.zone.exclusive.of.bulliform.cells.0...absent.1...
##
                       Adaxial.papillae.on.the.long.cells.in.the.interstomatal.zone...0...absent..1...p
##
##
##
                                             Adaxial.papillae.on.the.bulliform.cells...0...absent..1...p
##
##
                                                                Adaxial..Prickle.hairs..0...absent..1...
##
##
                                                        Adaxial..Bicellular.microhairs..0...absent..1...
##
##
                                                                   Adaxial..Macrohairs..0...absent..1...
##
                      Adaxial..Dumbbell.shaped.silica.bodies.in.the.intercostal.zone...0...present..1..
##
##
                        Adaxial..Saddle.shaped.silica.bodies.in.the.intercostal.zone...0...present..1..
##
##
##
                 Adaxial..Crenate..elongated..silica.bodies.in.the.intercostal.zone...0...present..1...
##
##
                           Adaxial..Dumbbell.shaped.silica.cells.in.the.costal.zone...0...present..1...
##
                             Adaxial..Saddle.shaped.silica.cells.in.the.costal.zone...0...present..1...
##
##
##
                       Adaxial..Crenate..elongated..silica.cells.in.the.costal.zone...0...present..1....
##
                                          Adaxial..Triangular.stomata.subsidiary.cells..0...absent..1...
##
##
                                         Adaxial..Dome.shaped.stomata.subsidiary.cells..0...absent..1...
##
##
                                      Adaxial..Parallel.sided.stomata.subsidiary.cells..0...absent..1...;
##
##
```

Analysis

PCOA

```
#TODO
?dist.binary() #Distance matrix for binary is simple matching coefficient
```

starting httpd help server ... done

STICK PLOT of PCOA

```
#TODO
#example
#screeplot(pca.bumpus,bstick = TRUE)
```

FACTORIAL ANOVA

#TODO

INTERACTIONS

#TODO

Group VS country
Group vs habitat

MODEL COMPARISON USING LIKELIHOOD RATIO TEST (LTR)

#TODO