Lab #10:

Please e-mail code, graphs and answers to questions to [afodor@uncc.edu](mailto:afodor@uncc.edu) and msioda@uncc.edu. Please put Please put lab #10 in the subject line.

Please have lab submitted (whatever you have) before lab on Thursday., April 18th.

This week’s dataset is here:

<http://afodor.github.io/classes/stats2015/prePostPhylum.txt>

(This datset is described, albeit from a different analysis pipeline, in these papers:

<http://www.sciencemag.org/content/sci/338/6103/120.full.html>

and

<http://www.nature.com/ncomms/2014/140903/ncomms5724/full/ncomms5724.html>

Note that WT and IL10-/- animals are in different cages. So “Cage1\_WT” is a different cage from “Cage1\_10-/-“.

1. Download the dataset. Perform PCA ordination.

(For example:

rm(list=ls())

setwd("C:\\Users\\afodor\\git\\afodor.github.io\\classes\\stats2015\\")

inFileName <- paste("prePostPhylum.txt", sep ="")

myT <-read.table(inFileName,header=TRUE,sep="\t")

numCols <- ncol(myT)

myColClasses <- c(rep("character",4), rep("numeric", numCols-4))

myT <-read.table(inFileName,header=TRUE,sep="\t",colClasses=myColClasses)

myTData<-myT[,5:10]

myPCOA <- princomp(myTData)

1. Graph PCA1 vs. PCA2. Make three versions of the graph. One colored by genotype,

one colored by cage and one colored by timepoint (pre-vs-post)

(SEE NEXT PAGE)

1. Fill in the following table for p-values testing the null hypothesis for PCA 1 and 2. For cage, use a way one-ANOVA. For genotype and timepoint (“pre” vs “post”) use a t-test

|  |  |  |
| --- | --- | --- |
|  | PCA1 | PCA2 |
| Cage |  |  |
| Genotype |  |  |
| Time (pre vs. post) |  |  |