Lab #8:

Please e-mail code, graphs and answers to questions to [bsmit269@uncc.edu](mailto:bsmit269@uncc.edu) and [afodor@uncc.edu](mailto:afodor@uncc.edu)

Please have lab submitted (whatever you have) before class on Mon., March 30th.

(1) Consider the list price vs. best price of a new GMC pickup (data are from http://college.cengage.com/mathematics/brase/understandable\_statistics/7e/students/datasets/slr/frames/frame.html)

|  |  |
| --- | --- |
| ListPrice | BestPrice |
| 12.4 | 11.2 |
| 14.3 | 12.5 |
| 14.5 | 12.7 |
| 14.9 | 13.1 |
| 16.1 | 14.1 |
| 16.9 | 14.8 |
| 16.5 | 14.4 |
| 15.4 | 13.4 |
| 17 | 14.9 |
| 17.9 | 15.6 |
| 18.8 | 16.4 |
| 20.3 | 17.7 |
| 22.4 | 19.6 |
| 19.4 | 16.9 |
| 15.5 | 14 |
| 16.7 | 14.6 |
| 17.3 | 15.1 |
| 18.4 | 16.1 |
| 19.2 | 16.8 |
| 17.4 | 15.2 |
| 19.5 | 17 |
| 19.7 | 17.2 |
| 21.2 | 18.6 |

(You can copy this data in R with read.delim("clipboard") if you have the data in your clipboard).

Plot out the list price vs. the best price. Fit a linear model. What is the p-value for the null hypothesis that the two prices are not associated? What is the r-squared for the association?

(2) Consider the case-control file for the colorectal adenomas data set that is here:

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

A separate file gives obesity (BMI) data for these same subjects:

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

For each OTU in the spreadsheet, generate a p-value from linear regression comparing BMI to the relative abundance of each OTU. Graph out all the p-values. Do they appear uniformly distributed? Does the microbial community appear to be influencing body weight in this cohort? Are any of these associations significant at a 10% false discovery rate?

Hints: To lookup the ids in the BMI table, you will need to some processing on the “sample” column in the caseControl file. The following code will convert the a sampleID so that it will match the BMI file.

# remove case and control

key <- sub("case", "", sampleID)

key <- sub("control", "", key)

# remove extraneous information from the suffix

key <- strsplit( key, "\_")[[1]][1]

Also, to get the p-value out of the linear model try:

anova( myLm)$"Pr(>F)"

We’ll see why that work shortly in future lectures.