Lab #10:

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

Please have lab submitted (whatever you have) before lab on Thursday, April 12th.

Get the CF qPCR dataset from here:

http://afodor.github.io/classes/stats2015/qPCRWithSampleDays.txt

(1) Plot the variable Log16S (total bacterial load as measured by qPCR primers targeting the 16S rRNA gene) vs. sampleDays. In your graph, give each of the 4 categorical variables in “treatmentStatus” a different color (see slide 39 of lecture #15 for hints as to how to do this).

(2) Consider three models to fit these data:

An 8 parameter model with separate slopes and intercepts for each treatment in treatmentStatus vs. time

A 5 parameter model with each treatment vs. time line having the same slope

A 2 parameter model with a single line for Log 16S vs. time.

Which model do you think is most appropriate (i.e. best describes the data with the fewest possible parameters)? Do you think that treatment had a statistically significant effect on the Log 16S variable?

Show your models with their R code to justify your answers with graphs or other evidence that you think is appropriate.