READ ME for files created by Neptune & Company, Inc., September, 2016

(1) You will have to set your working directory at the beginning of most of the files.

Eg) setwd("~/repos/Phytoplankton-DataAnalysis/gitAnalysisFiles/analysis")

(2) If the big algae file is updated, you should start by re-running the code chunks in **Phytoplankton\_DataAnalysis.Rmd**. This code will create .Rdata files that are used in other .Rmd files. The Rdata files will then be loaded at the beginning of other .Rmd files.

(3) Because there were field duplicates in the first few data sets we were working with, there are still response variable names to indicate this and they are denoted with and \_Ravg at the end, or an \_Rmax at the end indicating whether it was created by averaging the field duplicates or taking the maximum. Now that there are no duplicates (and assuming that continues to be the case) it does not matter which one you use because they will be the same.

(3) Here is a list of the other files and a very brief description of each, though the file names are meant to be informative and these are not in any particular order. (Yellow highlighting means I still need to look through them one more time to possibly take out some code that is not needed.)

* **ExploratoryPlotsForOneLake.Rmd** - plots to make for a single lake where you tell the file what reservoir you are interested in at the beginning
* **SummerMaxInvestigation.Rmd** – Creates plots to explore the use of the summer maximum for total cell density and these also include the horizontal lines for the EPA health
* **SummerMaxInvestigation\_biovolume.Rmd –**Same as SummerMaxInvesigation.Rmd, but for biovolume instead of cell density. The two could easily be combined because they load the same data sets and use essentially the same plotting code (just response variable name differs).
* **CompareMeasures.Rmd –** Compares total cell density, total biovolume, and proportions for all taxa, cyanobacteria, and toxin producing. These plots provide a good check of the cyanobacteria data because toxin producing should be a subset of cyanobacteria.