Free resources for learning R:

<http://swirlstats.com/>

<https://www.coursera.org/learn/r-programming> (current course started March 27)

<https://www.datacamp.com/courses/free-introduction-to-r>

Non-free resources for learning R:

<https://leanpub.com/rprogramming>

R Graphics cookbook <http://shop.oreilly.com/product/0636920023135.do>

Free resources about ANOVA:

<https://www.sophia.org/tutorials/analysis-of-varianceanova--4>

<https://www.khanacademy.org/math/statistics-probability>

<http://onlinestatbook.com/2/analysis_of_variance/intro.html>

Free resources about ANOVA in R:

<https://www.datacamp.com/courses/intro-to-statistics-with-r-analysis-of-variance-anova>

<http://www.statmethods.net/stats/anova.html>

Goals of R analysis for Hyphal Waviness Project:

1. Set up R environment
   1. Recommend: R Studio, GitHub, and a consistent directory structure for your files
2. Read in data to R (BR\_JV\_ManualHyphalDat\_032817.csv)
3. Create a summary data frame (mean Phenotype within each PlateBlock)
4. Draw a bar graph with error bars (Phenotype +- Standard Error) [ggplot2::ggplot]
   1. OR Create a summary dataframe with: [plyr::ddply]
      1. Mean Phenotype per Isolate
      2. Standard deviation of Phenotype per Isolate
      3. Standard error of Phenotype per Isolate
      4. Then draw a bar graph
5. ANOVA of full data:
   1. Linear model: Phenotype = Isolate + PlateBlock + PlateBlock/DotRep + Date
   2. First check assumptions for ANOVA
      1. Are the data normally distributed? (Normality)
      2. Is N (replication) about equal for each isolate)? (Normality)
      3. Is the variance for each isolate homogenous? (Heteroscedasticity)
   3. Then test ANOVA of the linear model
6. Calculate least squared means from the linear model, to get 1 value per Isolate
7. Run bigRR GWA
   1. Use MAF > 20, try MAF > 10
   2. Try WITH and WITHOUT organic isolates
8. Draw Manhattan plots
9. Annotate genes for candidate loci
10. Draw summary plots