10/26/20  
DVAC November Workshop: Intro to R/ggplot2

Brainstorming

Goals/Key questions to answer

1. Why would I use R/ggplot at all?
2. How do I load and manipulate data?
3. How do I graph and customize a graph?
   1. How do I learn new things for R/ggplot?
4. How does this tie into using bash scripting?

General flow of the presentation:

1. Have people download R/Rstudio: R version 4.0.3 | RStudio version 1.3.1093
2. Data formats, loading data, manipulating data – Austin
3. Graphing data – Jess
   1. Using an Rscript from the command line

Workflow:

* We’ll each have our own slides if necessary 🡪 switch between slides and interactive coding
* Share our screens independently

Ideas:

* Include extra resources in a resources folder on the GitHub
  + One or two main ones and then a supplemental folder with LOTS for the people who want to exhaustively look through them
* Include sample biological data
  + What sorts of things do you do in the lab that you would make graphs for? What sorts of data would other folks generally acquire?
  + Data: Austin’s data to send | Jess Data
    - Histogram
      * Flow Data
    - Grouped Data
      * Between-groups
        + WB Quantification
      * Within-groups
        + Treatment of cells
    - Linear regression graphs
      * Protein contaminant data
      * ~~P-nitrophenol standard curves~~
    - Nonlinear regression graphs
      * Enzyme assay data – time series data
    - Volcano Plots
      * MEF data (downsize)
      * RNA-seq data (downsize)
    - Horizontal Dotplot/Barplot
      * MEF data
    - PCA
      * RNA seq data