SRP Bioinformatics and Statistics Workshop
June 27-28, 2019

Software Requirements

Below is a list of software that will be necessary for participation in the hands-on sessions. Please follow the steps below prior to the workshop. Contact me if you have any problems or questions.

1. Download and install Firefox (https://www.mozilla.org/en-US/firefox/new/) **OR** Chrome internet browser (http://www.google.com/chrome/)
2. Make sure your Java (JVM) is up-to-date by downloading and installing from here: https://java.com/en/download/
3. Download and install Cytoscape 3.7.1 (https://cytoscape.org/download.html).
4. Download and R from http://cran.r-project.org/ (click on "R-3.6.0.pkg" to download). After download install R onto your computer. We've tested the workflow for the course on R version 3.6.0.
5. Download RStudio from http://www.rstudio.com/products/rstudio/download/ (select the free version of RStudio Desktop). Install RStudio onto your computer.
6. **If you are on a Windows PC (Mac users do not need to complete this step)**, download Rtools from https://cran.r-project.org/bin/windows/Rtools/ (download "Rtools35.exe"). Install Rtools onto your computer.

7. <u>Downloading and Installing R Packages</u>

    a. After installing, open RStudio, which opens an R session, and paste in the following commands into the Console window. Hitting enter will execute the lines.

    ```
    install.packages("BiocManager")
    BiocManager::install("minet")
    BiocManager::install("biomaRt")
    BiocManager::install("DESeq2")
    BiocManager::install("org.Dr.eg.db")
    BiocManager::install("topGO")
    BiocManager::install("tximport")
    BiocManager::install("org.Dr.eg.db")

    install.packages("devtools")
    devtools::install_github("hafen/trelliscopejs")

    install.packages("rbokeh")
    install.packages("readr")
    install.packages("rjson")
    install.packages("vegan")
    install.packages("ggplot2")
    install.packages("gplots")
    install.packages("cividis")
    ```

```
install.packages("igraph")
install.packages("tidyverse")
install.packages("purrr")
install.packages("dplyr")
install.packages("reshape2")
```

b. Once installed, scripts will be able to utilize the packages via loading which occurs each time you execute a given workflow or script. In our case, that environment loads in the following section (copy and paste these commands into the Console window):

```
library(minet)
library(biomaRt)
library(DESeq2)
library(org.Dr.eg.db)
library(topGO)
library(tximport)
library(org.Dr.eg.db)

library(trelliscopejs)
library(rbokeh)
library(readr)
library(rjson)
library(vegan)
library(ggplot2)
library(gplots)
library(cividis)
library(igraph)
library(tidyverse)
library(purrr)
library(dplyr)
library(reshape2)
```

c. These lines should execute without error. If you encounter an error like:

> Error in library("topGO") : there is no package called 'topGO'

Then that package failed to install and you can retry its installation command from above:

biocLite("topGO")

And read the console for any prompts.