Below is a list of software that will be necessary for participation in the hands-on sessions.  Please follow the steps below (#1-3) prior to the workshop.  Contact me if you have any problems or questions.

1.  Download the software below to your laptop:

| | |
|---|---|
| R (workflow tested in version 3.6.0) | http://cran.r-project.org/ |
| RStudio | http://www.rstudio.com/products/rstudio/download/ |
| Cytoscape 3.5.1 | http://www.cytoscape.org/download.php |
| Tm4 Multi-Experiment Viewer (MeV) v. 4.9 | https://sourceforge.net/projects/mev-tm4/ |
| Firefox or Chrome internet browser | https://www.mozilla.org/en-US/firefox/new/ <br> http://www.google.com/chrome/ |
| Java (JVM) (make sure up-to-date) | https://java.com/en/download/ |

2.  After installing R/Rstudio, please go to the following link (https://figshare.com/articles/Workshop/5378317) to download additional course material for the hands-on sessions in R.
3.  Scroll all the way down to the bottom of the figshare site (from #2 above) and follow the instructions for installing and testing the necessary tools in R.

**Software Requirements**

You will need to install R from http://cran.r-project.org/ onto your computer. We've tested the workflow on R version 3.4.1.

You will also need RStudio from http://www.rstudio.com/products/rstudio/download/.

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.


```
source("https://bioconductor.org/biocLite.R")
biocLite("biomaRt")
biocLite("DESeq2")
biocLite("org.Dr.eg.db")
biocLite("topGO")
biocLite("tximport")
install.packages("rbokeh")
install.packages("readr")
install.packages("rjson")
```


Once installed, scripts will be able to utilize the libraries via loading which occurs each time you execute a given workflow or script. In our case, that environment loads in the following section:

```
library("readr")
library("rjson")
library("tximport")
library("DESeq2")
library("biomaRt")
library("rbokeh")
library("topGO")
library("org.Dr.eg.db")
```

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 from above:

biocLite("topGO")

And read the console for any prompts.

**Other Downloads**

Download the osu-workshop.zip file and extract. This contains the data, some intermediate data, our working examples for this workshop. The hands-on portion will be going through the DE.Rmd document in RStudio.