Environment setup

Login to Hydra and install R libraries

```
$ ssh <username>@hydra-login01.si.edu
```

Now load the R module and open R

```
$ module load tools/R/3.4.1
```

```
$ R
```

Now we are going to install bioconductor packages that we will use during the differential expression portion of the analysis.

```
> source("http://bioconductor.org/biocLite.R")
```

Warning message:

> >source("http://bioconductor.org/biocLite.R") Warning in install.packages("BiocInstaller", repos = a["BioCsoft", "URL"]) : 'lib = "/share/apps/tools/R/gcc/4.9.2/3.4.1/lib64/R/library"' is not writable Would you like to use a personal library instead? (y/n)

```
Reply "y"
```

Warning Message:

> Would you like to create a personal library ~/R/x86_64-pc-linux-gnu-library/3.4 to install packages into? (y/n)

```
Reply "y"
```

Then Continue:

```
> biocLite()
```

```
> biocLite('edgeR')
```

```
> biocLite('ctc')
```

```
> biocLite('Biobase')
```

```
> biocLite('ape')
```

```
> install.packages('gplots')
```

Exit R

```
> quit()
```

When prompted to save your workspace image, reply 'n' and press enter:

```
Save workspace image? [y/n/c]: n
```