Using Deseg counts walk through

Step 1) Copy our scripts

```
Log in to the super computer
Cd into the new directory
Make a directory /scratch/User/yourusername/day7/
Copy the two scripts we have provided in
/scratch/Shares/public/sread2021/scripts/day7/
```

```
[[maallen3@ip-172-31-38-192 ~]$ mkdir /scratch/Users/maallen3/day7/
[[maallen3@ip-172-31-38-192 ~]$ cd /scratch/Users/maallen3/day7/

[[maallen3@ip-172-31-38-192 day7]$ scp /scratch/Shares/public/sread2021/scripts/d]
ay7/* /scratch/Users/maallen3/day7/
[[maallen3@ip-172-31-38-192 day7]$ ls

DESeq2_example.R sr_deseq2.sbatch
[maallen3@ip-172-31-38-192 day7]$ 
[maallen3@ip-172-31-38-192 day7]$
```

Step 2) Edit Our scripts

In the R script Change your working directory
In the sbatch script change your email and error and output files
####Make sure the error and output directory exist before you run!!!!!!

```
[maallen3@ip-172-31-38-192 day7]$ vi DESeq2_example.R
[[maallen3@ip-172-31-38-192 day7]$ vi sr_deseq2.sbatch
```

```
# For more information see: http://www.bioconductor.org/help/workflows/rnaseqGen
e/
library("tidyverse")
library("DESeq2")
#set working dir
workdir <- '/scratch/Users/username/day7/'
dir.create(workdir, showWarnings = FALSE)
setwd(workdir)
getwd()
outdir <- paste(workdir, 'deseqresults', '/', sep='') ##naming our outdir
dir.create(outdir, showWarnings = FALSE) ###creating the directory
becomes</pre>
```

```
# For more information see: http://www.bioconductor.org/help/workflows/rnaseqGen
 e/
 library("tidyverse")
 library("DESeq2")
 #set working dir
 workdir <- '/scratch/Users/maallen3/day7/'</pre>
 dir.create(workdir, showWarnings = FALSE)
 setwd(workdir)
 qetwd()
 outdir <- paste(workdir, 'desegresults', '/', sep='') ##naming our outdir
 dir.create(outdir, showWarnings = FALSE) ###creating the directory
#!/bin/bash
#SBATCH --job-name=featurecounts
                                                        # Job name
#SBATCH --mail-type=ALL
                                          # Mail events (NONE, BEGIN, END, FAIL, ALL)
#SBATCH --mail-user=allenma@colorado.edu
                                                 # Where to send mail
#SBATCH --nodes=1
                                                # Number of cores job will run on
# Number of CPU (processers, tasks)
#SBATCH --ntasks=4
#SBATCH --time=2:00:00
                                                 # Time limit hrs:min:sec
#SBATCH --partition compute
                                                 # Job queue
#SBATCH --mem=4gb
                                                 # Memory limit
#SBATCH --output=/scratch/Users/maallen3/eofiles/%x_%j.out
#SBATCH --error=/scratch/Users/maallen3/eofiles/%x_%j.err
becomes
#!/bin/bash
#SBATCH --iob-name=featurecounts
                                                          # Job name
#SBATCH --mail-type=ALL
                                           # Mail events (NONE, BEGIN, END, FAIL, ALL)
#SBATCH --mail-user=username@email.edu
                                           # Where to send mail
#SBATCH --nodes=1
                                                   # Number of cores job will run on
#SBATCH --ntasks=4
                                                   # Number of CPU (processers, tasks)
#SBATCH --time=2:00:00
                                                   # Time limit hrs:min:sec
#SBATCH --partition compute
                                                    Job queue
#SBATCH --mem=4gb
                                                    Memory limit
#SBATCH --output=/scratch/Users/username/eofiles/%x_%j.out
#SBATCH --error=/scratch/Users/username/eofiles/%x_%j.err
Step 3) Submit the sbatch script to the queue
        The sbatch script runs the R script... how?
```

```
[maallen3@ip-172-31-38-192 day7]$ sbatch sr_deseq2.sbatch
```

Step 4) If it works you will end up with a directory named deseqresults in your working directory. In the deseqresults directory you will end up with two files. One is a MA plot. The other is the results table.

```
[[maallen3@ip-172-31-38-192 day7]$ ls

DESeq2_example.R deseqresults sr_deseq2.sbatch

[[maallen3@ip-172-31-38-192 day7]$ cd deseqresults/

[[maallen3@ip-172-31-38-192 deseqresults]$ ls

MA_ifn_vs_ctrl_DEA.pdf my_results.csv

[maallen3@ip-172-31-38-192 deseqresults]$ ls

MA_ifn_vs_ctrl_DEA.pdf my_results.csv

[[maallen3@ip-172-31-38-192 deseqresults]$ |

[[maallen3@ip-172-31-38-192 deseq
```