DELLA

ssh vonholdt@della.princeton.edu

Managing scripts:
to_run_mapping.sh
to_run_methylCall.sh
to_run_qseq2fastq.sh

cd /tigress/VONHOLDT
cd /tigress/vonholdt

to_run_qseq2fastq.sh

```
### Job Name
#PBS -N qseq2fastq
#PBS  -l nodes=1;ppn=1;walltime=0:10:00
#PBS -M vonholdt@princeton.edu
#PBS -m abe

cd /tigress/VONHOLDT/scripts
./batchqseq2fastq.sh
```

ssh netID@della.princeton.edu

Managing scripts:
to_run_parser.sh
to_run_R_library1.sh

cd /tigress/VONHOLDT
cd /tigress/netID

ssh netID@della.princeton.edu

Managing scripts:
to_run_dmrAnalysis.sh
to_run_plotDMR.sh

cd /tigress/VONHOLDT
cd /tigress/netID

TIGRESS

/tigress/vonholdt
/tigress/netID1
/tigress/netID2

/tigress/VONHOLDT # this is the shared folder!
/tigress/VONHOLDT/data # do not move/edit this data
You must know the path of the data files so you can direct your script.sh (in /tigress/VONHOLDT/scripts) to the right input file and write your output to the correct place.

Example: /tigress/VONHOLDT/data contains
maleWolf.qseq
femaleWolf.qseq

/tigress/VONHOLDT/scripts # these are the working scripts
Store all of your scripts here and call them in a batch.sh file, analogous to a pipeline. Then point your to_run.sh to this batch.sh which actually contains all of your real commands.

Example: I want to run a perl script that converts the two qseq files to the fastq format. So I write a batch.sh file that is:

batchqseq2fastq.sh

```
#!/bin/bash

./qseq2fastq.pl <maleWolf.qseq
./qseq2fastq.pl <femaleWolf.qseq

exit 0;
```