

Last login: Tue Dec 12 21:18:18 on console
campus-024-044:~ susanmoenga\$ ssh smmoenga@farm.ucdavis.edu
ssh: Could not resolve hostname farm.ucdavis.edu: nodename nor servname provided
, or not known
campus-024-044:~ susanmoenga\$ ssh smmoenga@farm..cse.ucdavis.edu
ssh: Could not resolve hostname farm..cse.ucdavis.edu: nodename nor servname pro
vided, or not known
campus-024-044:~ susanmoenga\$ ssh smmoenga@farm.cse.ucdavis.edu
Welcome to Ubuntu 14.04.5 LTS (GNU/Linux 3.13.0-135-generic x86_64)

* Documentation: <https://help.ubuntu.com/>

2 packages can be updated.
0 updates are security updates.

New release '16.04.3 LTS' available.
Run 'do-release-upgrade' to upgrade to it.

*** System restart required ***
Timelimits are required now. This enabled much more efficient scheduling.
sbatch -t 10 gives you 10 minutes, sbatch -t 48:00:00 give you 2 days

Please do not run jobs on the head node.

A transfer node has been installed for scp, rsync, gzipping, please use port 202
2 to access this node. Ex: scp -P 2022 <username>@farm.cse.ucdavis.edu:file.

The cluster will be down the first Friday of October and April, please plan long
running jobs accordingly.

28TB of usable disk space may be purchased for \$3,000

Last login: Fri Dec 1 10:32:34 2017 from 2601:200:c000:bf93:459b:991b:a4ec:d119
Module slurm/16.05.8 loaded
Module openmpi/2.0.1 loaded
smmoenga@farm:~\$ ls
RNASeq suehist.txt tophat2.sh tophat3.sh tophat.sh
smmoenga@farm:~\$ cd RNASeq
smmoenga@farm:~/RNASeq\$ cd Seq_read_data/
smmoenga@farm:~/RNASeq/Seq_read_data\$ cd Susan_data/
smmoenga@farm:~/RNASeq/Seq_read_data/Susan_data\$ cd RNAseq_SM/
smmoenga@farm:~/RNASeq/Seq_read_data/Susan_data/RNAseq_SM\$ ls
05feiqp2xq
10.cxb
10_S42_L003
10_S42_L003.bam
10_S42_L003_cufflink
10_S42_L003_cuffquant
10_S42_L003_cuffquant1
10_S42_L003_cuffquant2
10_S42_L003_R1_001.fastq
10_S42_L003_R1_001.fastq_clean.fastq

10_S42_L003.sort_cufflink
10_S42_L003_stringtie.gtf
10_S42_L003_tophat
11.cxb
11_S43_L003
11_S43_L003.bam
11_S43_L003_cufflink
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11_S43_L003_cuffquant1
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16_S48_L004.bam
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16_S48_L004_cuffquant1
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31_S67_L005.bam
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31_S67_L005_R1_001.fastq_clean.fastq
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33_S69_L005_tophat
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34_S70_L005_cufflink
34_S70_L005_cuffquant
34_S70_L005_cuffquant2
34_S70_L005_R1_001.fastq
34_S70_L005_R1_001.fastq_clean.fastq
34_S70_L005_stringtie.gtf
34_S70_L005_tophat
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35_S71_L005.bam
35_S71_L005_cufflink
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35_S71_L005_cuffquant2
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35_S71_L005_tophat
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36_S72_L005
36_S72_L005.bam
36_S72_L005_cufflink
36_S72_L005_cuffquant
36_S72_L005_cuffquant2
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36_S72_L005_R1_001.fastq_clean.fastq
36_S72_L005_stringtie.gtf
36_S72_L005_tophat
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37_S73_L006.bam
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37_S73_L006_cuffquant

37_S73_L006_cuffquant2
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37_S73_L006_stringtie.gtf
37_S73_L006_tophat
38.cxb
38_S74_L006
38_S74_L006.bam
38_S74_L006_cufflink
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38_S74_L006_cuffquant2
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39.cxb
39_S75_L006
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3.cxb
3hkmu8tpe
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40_S76_L006_R1_001.fastq
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41.cxb
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41_S77_L006.bam
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41_S77_L006_R1_001.fastq
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41_S77_L006_stringtie.gtf
41_S77_L006_tophat
42.cxb
42_S78_L006
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42_S78_L006_R1_001.fastq
42_S78_L006_R1_001.fastq_clean.fastq
42_S78_L006_stringtie.gtf
42_S78_L006_tophat
43.cxb
43_S79_L006
43_S79_L006.bam
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43_S79_L006_R1_001.fastq_clean.fastq
43_S79_L006_stringtie.gtf
43_S79_L006_tophat
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44_S80_L006
44_S80_L006.bam
44_S80_L006_cufflink
44_S80_L006_cuffquant
44_S80_L006_cuffquant2
44_S80_L006_R1_001.fastq
44_S80_L006_R1_001.fastq_clean.fastq
44_S80_L006_stringtie.gtf
44_S80_L006_tophat
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45_S81_L006.bam
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45_S81_L006_cuffquant2
45_S81_L006_R1_001.fastq
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45_S81_L006_tophat
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46_S82_L006.bam
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46_S82_L006_cuffquant
46_S82_L006_cuffquant2
46_S82_L006_R1_001.fastq
46_S82_L006_R1_001.fastq_clean.fastq

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46_S82_L006_tophat
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47_S83_L006
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47_S83_L006_R1_001.fastq_clean.fastq
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47_S83_L006_tophat
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48_S84_L006.bam
48_S84_L006_cufflink
48_S84_L006_cuffquant
48_S84_L006_cuffquant2
48_S84_L006_R1_001.fastq
48_S84_L006_R1_001.fastq_clean.fastq
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8_S40_L003_R1_001.fastq
8_S40_L003_R1_001.fastq_clean.fastq
8_S40_L003_stringtie.gtf
8_S40_L003_tophat
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9_S41_L003_R1_001.fastq
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9_S41_L003_stringtie.gtf
9_S41_L003_tophat
alignstats.txt
Ballgown
blast2go
cov_refs_ball.txt
cov_refs.gtf
cov_refs.txt
cp.bam.sh
cp_for_cuffmerge
cp.sh
cuffcompare_out.combined.gtf
cuffcompare_out.cuffmerged2.gtf.refmap
cuffcompare_out.cuffmerged2.gtf.tmap
cuffcompare_out.cuffmerged.gtf.refmap
cuffcompare_out.cuffmerged.gtf.tmap
cuffcompare_out.loci
cuffcompare_out.stats
cuffcompare_out.tracking
cuffcomparerresult
cuffcompare.sh
cuffdiff2_14778.sh
cuffdiff2_8058.sh
cuffdiff2_Kalkan.sh

cuffdiff2_Savur.sh
cuffdiff2.sh
cuffdiff_out
cuffdiff_out2
cuffdiff_out2_14778
cuffdiff_out2_8058
cuffdiff_out2_Kalkan
cuffdiff_out2_Savur
cuffdiff.sh
cuffjob.sh
cufflinks2.sh
cufflinks.sh
cuffmerge2.sh
cuffmerged2.gtf
cuffmerged.gtf
cuffmerge_out
cuffmerge_out2
cuffmerge.sh
cuffmerge.sh!
cuffnorm2.sh
cuffnorm_geo_out
cuffnorm_quart_out
cuffnorm.sh
cuffout.cp.sh
cuffout.txt
cuffquant
cuffquant2.sh
cuffquant.sh
e2t.ctab
e_data.ctab
gene_abund_ball.tab
gene_abund.tab
genome.1.bt2
genome.1.ebwt
genome.2.bt2
genome.2.ebwt
genome.3.bt2
genome.3.ebwt
genome.4.bt2
genome.4.ebwt
genome.rev.1.bt2
genome.rev.1.ebwt
genome.rev.2.bt2
genome.rev.2.ebwt
gtf_cufflinks
gunzip.sh
history.txt
i2t.ctab
i_data.ctab
Kabuli_UWA-v2.6.3_Ca1-8Extracontigs.fasta
Kabuli_UWA-v2.6.3_Ca1-8Extracontigs.fasta.fai
Kabuli_UWA-v2.6.3_GeneModels-with-Annotations.gff

list
list2.txt
list.bam.txt
list.cufflink.txt
list.gtf_transcript.txt
list.newbam.txt
list.sam.txt
list.sort.bam.txt
list.stringtiegtf.txt
list.txt
newcuffmerge.sh
samtools.sort.sh
samtools.view.sh
skm7rrbvuw
slurm-17364261.out
slurm-17367857.out
slurm-17367895.out
slurm-17367897.out
slurm-17367898.out
slurm-17370366.out
slurm-17370368.out
slurm-17372006.out
slurm-17372027.out
slurm-17372590.out
slurm-17372591.out
slurm-17372592.out
slurm-17372597.out
slurm-17372613.out
slurm-17372614.out
slurm-17373446.out
slurm-17383780.out
slurm-17383781.out
slurm-17383783.out
slurm-17386175.out
slurm-17392423.out
slurm-17393739.out
slurm-17393783.out
slurm-17393793.out
slurm-17393797.out
slurm-17393812.out
slurm-17393857.out
slurm-17480383.out
slurm-17484101.out
slurm-17484102.out
slurm-17484103.out
slurm-17484113.out
slurm-17485516.out
slurm-17485554.out
slurm-17486933.out
slurm-17486935.out
slurm-17487218.out
slurm-17487219.out

slurm-17487220.out
slurm-17487222.out
slurm-17487224.out
slurm-17487932.out
slurm-17491983.out
slurm-17493570.out
slurm-17493575.out
slurm-17493576.out
slurm-17493578.out
slurm-17493671.out
slurm-17499399.out
slurm-17499438.out
slurm-17499442.out
slurm-17499452.out
slurm-17499577.out
slurm-17500619.out
slurm-17500741.out
slurm-17500782.out
slurm-17512913.out
slurm-17515814.out
slurm-17515816.out
slurm-17515821.out
slurm-17515823.out
slurm-17515824.out
sortbamfile
sortsamfile
stringcompare.sh
string_merge.sh
stringtie_ball
stringTieforBalgn.sh
stringtie_gtf.txt
stringtie_merged.gtf
stringTie_merged.sh
stringTie.sh
suehist.txt
t_data.ctab
tophat2.sh
tophat3.sh
tophat_out
tophat.sh
trimmomatic.sh
x_cov_refs_ball.txt
x_gene_abund_ball.tab
smmoenga@farm:~/RNASeq/Seq_read_data/Susan_data/RNAseq_SM\$ history
1 history
2 srun -p med -t 3 date
3 exit
4 mkdir RNASeq
5 cd RNASeq
6 cd RNASeq/
7 pwd
8 ls

```
9 cd Seq_read_data/
10 ls
11 cd Susan_data/
12 ls
13 cd RNAseq_SM/
14 LS
15 ls
16 TrimmomaticSE
17 vim trimmomatic.sh
18 cat trimmomatic.sh
19 echo "$PWD"
20 pwd
21 pwd >> trimmomatic.sh
22 cat trimmomatic.sh
23 vim trimmomatic.sh
24 cat trimmomatic.sh
25 awk '{print NR ":" length($0);}' 13_S45_L004_R1_001.fastq
26 awk '{print NR ":" length($0);}' trimmomatic.sh
27 cat trimmomatic.sh
28 ls
29 ls */*
30 ls */**
31 ls
32 ls 05feiqp2xq/05feiqp2xq/Unaligned/Project_DCSM_L4_SM_PoolB_13_24/
33 ls */**/*
34 for i in `ls */**/*/*.gz`; do echo $i; done
35 for i in `ls */**/*/*.gz`; do echo $i; done
36 for i in `ls */**/*/*.gz`; do echo $i; done
37 for i in `ls */**/*/*.gz`; do echo "mv $i ."; done
38 for i in `ls */**/*/*.gz`; do echo "cp $i ."; done
39 for i in `ls */**/*/*.gz`; do echo "cp $i ."; done > cp.sh
40 ls
41 head cp.sh
42 for i in `ls */**/*/*.gz`; do echo "cp $i ."; done >> cp.sh
43 wc -l cp.sh
44 wc cp.sh
45 tail cp.sh
46 bash cp.sh
47 ls
48 vim cp.sh
49 sbatch -p med -t 4800:00:00 --ntasks=1 cp.sh
50 queue | grep "smmoenga"
51 queue | grep "smmoenga"
52 ls
53 history
54 history > suehist.txt
55 cat suehist.txt
56 pwd
57 cd RNASeq
58 vim susan.text
59 cd RNASeq
60 ls
```

```
61 cd Seq_read_data/
62 ls
63 cd Susan_data/
64 ls
65 cd RNAseq_SM/
66 ls -F
67 ls
68 rm Undetermined_S0_L00*
69 ls
70 squeue|grep "smmoenga"
71 squeue
72 ls
73 ls *.gz
74 ls *.gz >list.txt
75 wc -l list.txt
76 vim gunzip.sh
77 pwd
78 pwd >> gunzip.sh
79 vim gunzip.sh
80 cat gunzip.sh
81 sbatch -p med -t 4800:00:00 --ntasks=1 gunzip.sh
82 squeue |grep "smmoenga"
83 squeue
84 ls *.fastq
85 ls *.fastq
86 ls *.fastq
87 ls *.fastq
88 ls *.fastq
89 ls *.fastq
90 ls *.fastq
91 ls *.fastq
92 ls *.fastq
93 squeue| grep "smmoenga"
94 squeue| grep "smmoenga"
95 ls *.fastq
96 vim trimmomatic.sh
97 ls *.fastq
98 cp list.txt list
99 tail list
100 perl -p -i -e "s/.gz//g" list
101 tail list
102 ls
103 cat trimmomatic.sh
104 sbatch -p med -t 4800:00:00 --ntasks=1 trimmomatic.sh
105 squeue |grep "smm"
106 ls
107 cat slurm-17367895.out
108 TrimmomaticSE
109 which TrimmomaticSE
110 vim trimmomatic.sh
111 sbatch -p med -t 4800:00:00 --ntasks=1 trimmomatic.sh
112 squeue |grep "smm"
```



```
113  queue |grep "smm"
114  ls
115  vim trimmomatic.sh
116  sbatch -p med -t 4800:00:00 --ntasks=1 trimmomatic.sh
117  queue |grep "smm"
118  vim trimmomatic.sh
119  queue |grep "smm"
120  ls
121  ls
122  queue |grep "smm"
123  ls
124  queue |grep "smm"
125  ls
126  queue |grep "smmoenga"
127  ls
128  history
129  history >suehist.txt
130  less suehist.txt
131  queue | grep "smm"
132  exit() q
133  quit
134  queue | grep "smm"
135  LS
136  ls
137  cd RNASeq/
138  ls
139  cd Seq_read_data/
140  ls
141  cd Susan_data/
142  ls
143  cd RNAseq_SM/
144  LS
145  ls
146  ls -hl
147  cat slurm-17367898.out
148  history
149  cat trimmomatic.sh
150  vim trimmomatic.sh
151  sbatch -p med -t 4800:00:00 --ntasks=6 trimmomatic.sh
152  vim trimmomatic.sh
153  sbatch -p med -t 4800:00:00 --ntasks=6 trimmomatic.sh
154  queue |grep "smm"
155  scancel 17370366
156  queue |grep "smm"
157  ls
158  head 10_S42_L003_R1_001.fastq
159  head 10_S42_L003_R1_001.fastq_clean.fastq
160  ls
161  ls
162  queue |grep "smm"
163  pwd
164  queue |grep "smm"
```

```
165  squeue |grep "srm"
166  squeue |grep "srm"
167  squeue | grep "srm"
168  squeue | grep "srm"
169  squeue | grep "srm"
170  ls
171  cd RNASeq/
172  ls
173  cd Seq_read_data/
174  ls
175  cd Susan_data/
176  ls
177  cd RNAseq_SM/
178  ls
179  squeue | grep "srm"
180  cd RNASeq/
181  cd Seq_read_data/
182  cd Susan_data/
183  cd RNAseq_SM/
184  ls
185  ls -hl
186  sl
187  cd RNASeq/
188  cd Seq_read_data/
189  cd Susan_data/
190  cd RNAseq_SM/
191  ls
192  ls -hl
193  ls *clean.fastq
194  ls *clean.fastq > list2.txt
195  cd RNASeq/
196  cd Seq_read_data/
197  cd Susan_data/
198  cd RNAseq_SM/
199  ls
200  vim tophat.sh
201  vim tophat.sh
202  ls
203  vim tophat.sh
204  cd RNASeq/
205  cd Seq_read_data/
206  cd Susan_data/
207  cd RNAseq_SM/
208  LS
209  ls
210  ls
211  tail list2.txt
212  vim tophat.sh
213  ls
214  ls Kabuli_UWA-v2.6.3_*
215  ls Kabuli_UWA-v2.6.3_* >> tophat.sh
216  vim tophat.sh
```

```
217 cat tophat.sh
218 bash tophat.sh
219 wc -l tophat.sh
220 vim tophat.sh
221 bash tophat.sh
222 vim tophat.sh
223 bash tophat.sh
224 vim tophat.sh
225 bash tophat.sh
226 ls
227 vim tophat
228 vim tophat.sh
229 vim tophat.sh
230 history
231 sbatch -p med -t 4800:00:00 --ntasks=8 tophat.sh
232 squeue |grep "smmoenga"
233 squeue |grep "smmoenga"
234 squeue |grep "smmoenga"
235 squeue |grep "smmoenga"
236 ls
237 ls -hl
238 cat slurm-17372006.out
239 vim tophat.sh
240 sbatch -p med -t 4800:00:00 --ntasks=8 tophat.sh
241 squeue |grep "smmoenga"
242 ls
243 vim tophat
244 cd S
245 ls
246 cd RNASeq/
247 cd Seq_read_data/
248 cd Susan_data/
249 cd RNAseq_SM/
250 ls
251 vim list2.txt
252 vim tophat.sh
253 pwd
254 pwd >> tophat.sh
255 head list2.txt
256 ls
257 bowtie2-build Kabuli_UWA-v2.6.3_Ca1-8Extracontigs.fasta genome
258 bowtie-build Kabuli_UWA-v2.6.3_Ca1-8Extracontigs.fasta genome
259 vim tophat.sh
260 cat tophat.sh
261 pwd >> tophat.sh
262 vim tophat.sh
263 vim tophat2.sh
264 vim tophat2.sh
265 vim tophat.sh
266 history
267 ls
268 cd RNASeq/
```

```
269 cd Seq_read_data/
270 cd Susan_data/
271 cd RNAseq_SM/
272 ls
273 cat tophat.sh
274 cd RNASeq/
275 cd Seq_read_data/
276 cd Susan_data/
277 cd RNAseq_SM/
278 vim tophat.sh
279 ls
280 cat tophat.sh
281 vim tophat.sh
282 history
283 sbatch -p med -t 36:00:00 -ntask 1 tophat.sh
284 history > history.txt
285 grep "sbatch" history.txt
286 sbatch -p med -t 36:00:00 --ntask=1 tophat.sh
287 sbatch -p med -t 36:00:00 --ntasks=1 tophat.sh
288 ls
289 squeue | grep "smm"
290 grep "squeue" history.txt
291 squeue |grep "smmoenga"
292 ls
293 cat slurm-17372027.out
294 ls
295 vim tophat.sh
296 bash tophat.sh
297 ls */*fastq
298 cp tophat.sh cp.sh
299 sbatch -p med -t 3600:00:00 --ntasks=1 cp.sh
300 squeue |grep "smmoenga"
301 squeue |grep "smmoenga"
302 vim cp.sh
303 sbatch -p med -t 3600:00:00 --ntasks=1 cp.sh
304 squeue |grep "smmoenga"
305 ls
306 cp tophat2.sh tophat.sh
307 cat tophat.sh
308 squeue |grep "smmoenga"
309 ls -hl */*fastq
310 ls -hl */*fastq
311 ls -hl */*fastq
312 ls -hl 10_S42_L003*
313 ls -hl */*fastq
314 ls -hl */*fastq
315 ls -hl */*fastq
316 cat cp.sh
317 cat tophat.sh
318 head list2.txt
319 tophat
320 tophat2
```

```
321 history
322 sbatch -p med -t 4800:00:00 --ntasks=8 tophat.sh
323 queue |grep "smm"
324 vim tophat.sh
325 cat cp.sh
326 tophat2
327 ls
328 cat cp.sh >> tophat2.sh
329 vim tophat2.sh
330 cat tophat2.sh
331 vim tophat2.sh
332 history
333 sbatch -p med -t 4800:00:00 --ntasks=1 tophat2.sh
334 queue |grep "smm"
335 queue |grep "smm"
336 queue |grep "smm"
337 cat cp.sh
338 tophat
339 queue |grep "smm"
340 cat slurm-17372597.out
341 cat tophat2.sh
342 cat tophat.s
343 cat tophat.sh
344 vim tophat.sh
345 vim tophat2.sh
346 cat cp.sh
347 vim tophat2.sh
348 sbatch -p med -t 4800:00:00 --ntasks=1 tophat2.sh
349 cat tophat.sh
350 vim tophat.sh
351 sbatch -p med -t 4800:00:00 --ntasks=8 tophat.sh
352 queue |grep "smm"
353 cat slurm-17372592.out
354 queue |grep "smm"
355 cat topha2.sh
356 cat tophat2.sh
357 queue |grep "smm"
358 queue |grep "smm"
359 cat slurm-17372614
360 cat slurm-17372614.out
361 man queue
362 queue |grep "smm"
363 scancel 17372594
364 queue |grep "smm"
365 cd RNASeq/Seq_read_data/Susan_data/RNAseq_SM/
366 ls
367 ls */*fastq
368 ls */*fastq
369 cp tophat.sh tophat2.sh
370 vim tophat2.sh
371 rm .tophat2.sh.swp
372 vim tophat2.sh
```

```
373 vim tophat2.sh
374 squeue |grep "smmoenga"
375 squeue
376 squeue |grep "smmoenga"
377 squeue |grep "smmoenga"
378 squeue
379 cd RNASeq/
380 cd Seq_read_data/
381 cd Susan_data/
382 cd RNAseq_SM/
383 squeue | "grep "smmo"
384 )
385 squeue | grep "smmoenga"
386 cat tophat2.sh
387 cd $dic
388 ls
389 cd RNASeq/
390 cd Seq_read_data/
391 cd Susan_data/
392 cd RNAseq_SM/
393 cd $dic
394 ls
395 pwd
396 cd ..
397 cd ..
398 cd ..
399 cd ..
400 LS
401 ls
402 q
403 squeue |grep "smmoenga"
404 slurm-17372613.out
405 cat slurm-17372613.out
406 history
407 squeue
408 cd RNASeq/
409 cd Seq_read_data/
410 cd Susan_data/
411 cd RNAseq_SM/
412 cat slurm-17372613.out
413 ls
414 cd tophat_out
415 ls
416 cd logs
417 ls
418 cd ..
419 cd tmp
420 ls
421 cat tophat2.sh
422 cd ..
423 cd ..
424 cd tophat
```

```
425 cd _tophat
426 ls
427 cat tophat2.sh
428 cat 35_S70_L005
429 cat 34_S70_L005
430 cd 34_S70_L005
431 ls
432 cat tophat.sh
433 cd ..
434 cat tophat.sh
435 cat $dic
436 cd dic
437 ls
438 cat cp.sh
439 cd /home/smмоenga/RNASeq/Seq_read_data/Susan_data/RNAseq_SM/$dic
440 ls
441 cat cp.sh
442 cat tophat2.sh
443 queue |grep "smm"
444 cd "$dic"
445 ls
446 ls -ld "$dic"
447 ls -ld "$dic"_tophat
448 echo $dic
449 echo /home/smмоenga/RNASeq/Seq_read_data/Susan_data/RNAseq_SM/"$dic"_toph
at
450 ls
451 queue |grep "smm"
452 echo /home/smмоenga/RNASeq/Seq_read_data/Susan_data/RNAseq_SM/"$dic"_toph
at
453 cd tophat.out
454 cd tophat_out
455 ls
456 cdtmp
457 cd tmp
458 ls
459 cd ..
460 cd ..
461 cat tophat2.sh
462 queue
463 $dic
464 ls
465 queue | grep "smмоenga"
466 cp tophat.sh tophat3.sh
467 vim tophat3.sh
468 cat tophat.sh
469 cd RNASeq/
470 cd Seq_read_data/
471 cd Susan_data/
472 cd RNAseq_SM/
473 cp tophat.sh tophat3.sh
474 vim tophat3.sh
```

```
475 vim tophat3.sh
476 cat tophat3.sh
477 tophat
478 ls
479 history
480 sbatch -p med -t 4800:00:00 --ntasks=8 tophaht3.sh
481 sbatch -p med -t 4800:00:00 --ntasks=8 tophat3.sh
482 queue | grep "smm"
483 bash tophat3.sh
484 ls
485 ls *out
486 ls *tophat
487 cd 10_S42_L003_tophat
488 ls
489 tophat_out/
490 ls
491 cd tophat_out/
492 ls
493 cat align_summary.txt
494 cd ..
495 cd ..
496 ls
497 vim tophat2.sh
498 cd /home/ypgai/susan/tophat/
499 cat tophat.sh
500 cd ~/RNASeq/Seq_read_data/Susan_data/RNAseq_SM
501 ls
502 cat /home/ypgai/susan/tophat/tophat.sh
503 vim tophat2.sh
504 sbatch -p med -t 4800:00:00 --ntasks=8 tophat2.sh
505 queue | grep "smmoenga"
506 tophat
507 ls
508 scancel 17372614
509 queue | grep "smmoenga"
510 scancel 17373407
511 queue | grep "smmoenga"
512 queue | grep "smmoenga"
513 queue | grep "smmoenga"
514 queue | grep "smmoenga"
515 sbatch --help
516 sbatch --version
517 sexit
518 exit
519 queue
520 queue |grep "smmoenga"
521 queue
522 queue |grep "smmoenga"
523 htop
524 ranger
525 fortune
526 fg
```



```
527 count =1
528 squeue |grep "smmoenga"
529 cat tophat2.sh
530 cd RNASeq/
531 cd Seq_read_data/
532 cd Susan_data/
533 cd RNAseq_SM/
534 cat tophat2.sh
535 squeue |grep "smmoenga"
536 squeue |grep "smmoenga"
537 history
538 cd RNASeq/
539 cd Seq_read_data/
540 cd Susan_data/
541 cd RNAseq_SM/
542 ls *tophat
543 cd 10_S42_L003_tophat
544 ls
545 cd tophat_out/
546 ls
547 cat align_summary.txt
548 cat accepted_hits.bam
549 cat align_summary.txt
550 ls
551 cat prep_reads.info
552 squeue |grep "smmoenga"
553 squeue |grep "smmoenga"
554 squeue |grep "smmoenga"
555 cd RNASeq/
556 cd Seq_read_data/
557 cd Susan_data/
558 cd RNAseq_SM/
559 cat *tophat
560 ls *tophat
561 squeue |grep "smmoenga"
562 squeue |grep "smmoenga"
563 squeue |grep "smmoenga"
564 squeue |grep "smmoenga"
565 squeue |grep "smmoenga"
566 squeue |grep "smmoenga"
567 squeue |grep "smmoenga"
568 squeue |grep "smmoenga"
569 squeue |grep "smmoenga"
570 squeue |grep "smmoenga"
571 squeue |grep "smmoenga"
572 squeue |grep "smmoenga"
573 squeue |grep "smmoenga"
574 squeue |grep "smmoenga"
575 cd RNASeq/
576 cd Seq_read_data/
577 cd Susan_data/
578 cd RNAseq_SM/
```

```
579 ls
580 ls *tophat
581 cd tophat_out/
582 hist
583 history
584 cd tophat.out
585 cd tophat
586 ls *tophat
587 cd ..
588 ls *tophat_out
589 ls *tophat
590 ls *tophat_out
591 ls *tophat
592 cd 48_S84_L006
593 ls
594 cat 48_S84_L006_R1_001.fastq_clean.fastq
595 ls_tophat
596 ls *tophat
597 cd ..
598 ls *tophat
599 cd 8_S40_L003_tophat
600 ls
601 cd tophat_out/
602 ls
603 cat align_summary.txt
604 cd RNASeq/
605 cd Seq_read_data/
606 cd Susan_data/
607 cd RNAseq_SM/
608 ls
609 pwd
610 ls *tophat/
611 ls *tophat/tophat_out
612 ls *tophat/tophat_out/accepted_hits.bam
613 ls *tophat/tophat_out/accepted_hits.bam
614 ls *tophat/tophat_out/accepted_hits.bam > list.bam.txt
615 vim cp.bam.sh
616 pwd
617 pwd >> cp.bam.sh
618 vim cp.bam.sh
619 bash cp.bam.sh
620 vim cp.bam.sh
621 vim cp.bam.sh
622 bash cp.bam.sh
623 vim cp.bam.sh
624 bash cp.bam.sh
625 vim cp.bam.sh
626 bash cp.bam.sh
627 vim cp.bam.sh
628 bash cp.bam.sh
629 bash cp.bam.sh > com.cp.bam.sh
630 mv com.cp.bam.sh cmd.cp.bam.sh
```

```
631 vim cmd.cp.bam.sh
632 rm cmd.cp.bam.sh
633 cat cp.bam.sh
634 history
635 sbatch -p med -t 4800:00:00 --ntasks=1 cp.bam.sh
636 queue |grep "smmo"
637 cat slurm-17383780.out
638 ls
639 vim cp.bam.sh
640 sbatch -p med -t 4800:00:00 --ntasks=1 cp.bam.sh
641 queue |grep "smmo"
642 cat cp.bam.sh
643 history
644 cat cp.bam.sh
645 queue |grep "smmo"
646 queue |grep "smmo"
647 queue |grep "smmo"
648 vim samtools.sort.sh
649 pwd
650 vim samtools.sort.sh
651 queue |grep "smmo"
652 ls *.bam
653 queue |grep "smmo"
654 ls *.bam
655 queue |grep "smmo"
656 cat samtools.sort.sh
657 ls *.bam
658 ls *.bam > list.newbam.txt
659 sbatch -p med -t 4800:00:00 --ntasks=1 samtools.sort.sh
660 queue |grep "smmo"
661 ls
662 ls *tophat/tophat_out
663 cat ls *tophat/tophat_out/align_summary.txt
664 cat ls *tophat/tophat_out/align_summary.txt > alignstats.txt
665 cat ls *tophat/tophat_out/align_summary.txt > alignstats.txt
666 cat ls *tophat/tophat_out/align_summary.txt
667 cat *_tophat/tophat_out/align_summary.txt
668 queue |grep "smmo"
669 queue |grep "smmo"
670 cat slurm-17383783.out
671 queue |grep "smmo"
672 queue |grep "smmo"
673 queue |grep "smmo"
674 cat slurm-17383783.out
675 cat slurm-17383783.out
676 cd RNASeq/
677 cd Seq_read_data/
678 cd Susan_data/
679 cd RNAseq_SM/
680 cat slurm-17383783.out
681 ls
682 ls *.sort.bam
```

```
683 history
684 ls *.sort.bam > list.sort.bam.txt
685 cat list.sort.bam.txt
686 cd RNASeq/
687 cd Seq_read_data/
688 cd Susan_data/
689 cd RNAseq_SM/
690 cat trimmomatic.sh
691 trimmomatic
692 Trimmomatic
693 TrimmomaticSE
694 ls
695 ls *clean.fastq
696 cd 10_S42_L003_R1_001.fastq_clean.fastq
697 cd 10_S42_L003_R1_001.fastq
698 cd 9_S41_L003
699 ls
700 cat 9_S41_L003_R1_001.fastq_clean.fastq
701 cat trimmomatic.sh
702 cat trimmomatic.sh
703 cat trimmomatic.sh
704 cd ..
705 cat trimmomatic.sh
706 cat tophat.sh
707 history
708 cat tophat2.sh
709 ls
710 ls 44_S80_L006_tophat/tophat_out/align_summary.txt
711 head *_tophat/tophat_out/align_summary.txt
712 head list.sort.bam.txt
713 cp samtools.sort.sh samtools.view.sh
714 vim samtools.view.sh
715 cat samtools.view.sh
716 history
717 sbatch -p med -t 4800:00:00 --ntasks=1 samtools.view.sh
718 queue | grep "smm"
719 queue | grep "smm"
720 queue | grep "smm"
721 queue | grep "smm"
722 head *_tophat/tophat_out/align_summary.txt
723 head *_tophat/tophat_out/align_summary.txt > alignstats.txt
724 queue | grep "smm"
725 queue | grep "smm"
726 queue | grep "smm"
727 queue | grep "smm"
728 ls
729 queue | grep "smm"
730 cd RNASeq/
731 cd Seq_read_data/
732 cd Susan_data/
733 cd RNAseq_SM/
734 cat trimmomatic.sh
```

```
735 trimmomatic
736 Trimmomatic
737 TrimmomaticSE
738 ls
739 ls *clean.fastq
740 cd 10_S42_L003_R1_001.fastq_clean.fastq
741 cd 10_S42_L003_R1_001.fastq
742 cd 9_S41_L003
743 ls
744 cat 9_S41_L003_R1_001.fastq_clean.fastq
745 cat trimmomatic.sh
746 cat trimmomatic.sh
747 cat trimmomatic.sh
748 cd ..
749 cat trimmomatic.sh
750 cat tophat.sh
751 history
752 cat tophat2.sh
753 ls
754 ls 44_S80_L006_tophat/tophat_out/align_summary.txt
755 head *_tophat/tophat_out/align_summary.txt
756 head list.sort.bam.txt
757 cp samtools.sort.sh samtools.view.sh
758 vim samtools.view.sh
759 cat samtools.view.sh
760 history
761 sbatch -p med -t 4800:00:00 --ntasks=1 samtools.view.sh
762 queue | grep "srm"
763 queue | grep "srm"
764 queue | grep "srm"
765 queue | grep "srm"
766 head *_tophat/tophat_out/align_summary.txt
767 head *_tophat/tophat_out/align_summary.txt > alignstats.txt
768 queue | grep "srm"
769 queue | grep "srm"
770 queue | grep "srm"
771 queue | grep "srm"
772 cd RNASeq/
773 cd Seq_read_data/
774 cd Susan_data/
775 cd RNAseq_SM/
776 cat trimmomatic.sh
777 trimmomatic
778 Trimmomatic
779 TrimmomaticSE
780 ls
781 ls *clean.fastq
782 cd 10_S42_L003_R1_001.fastq_clean.fastq
783 cd 10_S42_L003_R1_001.fastq
784 cd 9_S41_L003
785 ls
786 cat 9_S41_L003_R1_001.fastq_clean.fastq
```

```
787 cat trimmomatic.sh
788 cat trimmomatic.sh
789 cat trimmomatic.sh
790 cd ..
791 cat trimmomatic.sh
792 cat tophat.sh
793 history
794 cat tophat2.sh
795 ls
796 ls 44_S80_L006_tophat/tophat_out/align_summary.txt
797 head *_tophat/tophat_out/align_summary.txt
798 head list.sort.bam.txt
799 cp samtools.sort.sh samtools.view.sh
800 vim samtools.view.sh
801 cat samtools.view.sh
802 history
803 sbatch -p med -t 4800:00:00 --ntasks=1 samtools.view.sh
804 queue | grep "smm"
805 queue | grep "smm"
806 queue | grep "smm"
807 queue | grep "smm"
808 head *_tophat/tophat_out/align_summary.txt
809 head *_tophat/tophat_out/align_summary.txt > alignstats.txt
810 queue | grep "smm"
811 queue | grep "smm"
812 queue | grep "smm"
813 queue | grep "smm"
814 queue | grep "smm"
815 cd RNASeq/
816 cd Seq_read_data/
817 cd Susan_data/
818 cd RNAseq_SM/
819 ls
820 ls *.sam
821 ls *.sam > list.sam.txt
822 cat list.sam.txt
823 history
824 cp samtools.view.sh cufflinks.sh
825 vim cufflinks.sh
826 cufflinks
827 cd RNASeq/
828 cd Seq_read_data/
829 cd Susan_data/
830 cd RNAseq_SM/
831 vim cufflinks.sh
832 cat samtools.sh
833 ls
834 cat samtools.view.sh
835 gf
836 fg
837 fg
838 cat cufflinks.sh
```

```
839 sbatch -p med -t 4800:00:00 --ntasks=1 cufflink.sh
840 sbatch -p med -t 4800:00:00 --ntasks=1 cufflinks.sh
841 squeue|grep "smm"
842 squeue | grep "smm"
843 history
844 cat slurm-17392423.out
845 squeue | grep "smm"
846 cd RNASeq/
847 cd Seq_read_data/
848 cd Susan_data/
849 cd RNAseq_SM/
850 ls
851 cat slurm-17364261.out
852 cat slurm-17364261.out
853 squeue |grep "smm"
854 squeue |grep "smm"ls
855 cd RNASeq/
856 cd Seq_read_data/
857 cd Susan_data/
858 cd RNAseq_SM/
859 ls
860 ls *._cufflink
861 ls *.sort_cufflink
862 ls *.*_cufflink
863 cd 6_S38_L003.sort_cufflink
864 LS
865 ls
866 cd 6_S38_L003.sort.sam
867 cd ..
868 ls
869 cd 7_S39_L003.sort_cufflink
870 ls
871 cd ..
872 cat cufflinks.sh
873 ls
874 ls *.*_tophat
875 ls *.*_tophat
876 ls *._tophat
877 ls *.*_tophat
878 ls *_tophat
879 ls *.sort_cufflink
880 cat cufflinks.sh
881 ls *.sort_cufflink/
882 ls *.sort_cufflink/*/
883 ls *.sort_cufflink/*.sam
884 cat ls *.sort_cufflink/*.sam > cuffout.txt
885 history
886 cat *.sort_cufflink/*.sam > cuffout.txt
887 vim cuffout.cp.sh
888 fg
889 pwd
890 fg
```

```
891 vim cufflink2.sh
892 cd RNASeq/
893 cd Seq_read_data/
894 cd Susan_data/
895 cd RNAseq_SM/
896 cat cufflink.sh
897 cat cufflinks.sh
898 cp cufflinks.sh cufflinks2.sh
899 vim cufflinks2.sh
900 cat list.sam.txt
901 cat cufflinks2.sh
902 history
903 sbatch -p med -t 4800:00:00 --ntasks=1 cufflinks2.sh
904 cat slurm-17393739.out
905 cat cufflinks2.sh
906 cat vim cufflinks2.sh
907 vim cufflinks2.sh
908 sbatch -p med -t 4800:00:00 --ntasks=1 cufflinks2.sh
909 queue |grep "srm"
910 cat cufflinks.sh
911 cat cufflinks2.sh
912 vim cufflinks2.sh
913 cat cufflinks2.sh
914 sbatch -p med -t 4800:00:00 --ntasks=1 cufflinks2.sh
915 queue |grep "srm"
916 cat list.sam.txt
917 vim cufflinks2.sh
918 sbatch -p med -t 4800:00:00 --ntasks=1 cufflinks2.sh
919 queue |grep "srm"
920 cat slurm-17393797.out
921 vim cufflinks2.sh
922 vim cufflinks.sh
923 vim cufflinks2.sh
924 sbatch -p med -t 4800:00:00 --ntasks=1 cufflinks2.sh
925 queue |grep "srm"
926 queue |grep "srm"
927 queue |grep "srm"
928 cd RNASeq/
929 cd Seq_read_data/
930 cd Susan_data/
931 cd RNAseq_SM/
932 ls
933 cat slurm-17393812.out
934 vim cufflinks2.sh
935 ls
936 cat list.sort.bam.txt
937 fg
938 sbatch -p med -t 4800:00:00 --ntasks=1 cufflinks2.sh
939 queue |grep "srm"
940 cat slurm-17393857.out
941 cat slurm-17393857.out
942 cat slurm-17393857.out
```



```
943 cat slurm-17393857.out
944 scancel 17393857
945 squeue |grep "smm"
946 scancel 17393857
947 squeue |grep "smm"
948 history
949 cat cufflinks2.sh
950 cd RNASeq/
951 cd Seq_read_data/
952 cd Susan_data/
953 cd RNAseq_SM/
954 cat cufflinks2.sh
955 cd RNASeq/
956 cd
957 cd RNASeq/
958 cd Seq_read_data/
959 cd Susan_data/
960 cd RNAseq_SM/
961 ls
962 cd 10_S42_L003.sort_cufflink
963 ls
964 cat 10_S42_L003.sort.sam
965 cd ..
966 ls
967 rm *.sort_cufflink
968 cd 10_S42_L003.sort_cufflink/
969 ls
970 cd ..
971 cd 10_S42_L003_newcufflinks
972 cd 10_S42_L003_newcufflinks
973 ls
974 ls
975 cd ..
976 ls *newcufflinks
977 rm *newcufflinks
978 rm -R *newcufflinks
979 LS
980 ls
981 ls *newcufflinks
982 ls *_cufflinks
983 ls *.sort_cufflinks
984 ls
985 ls *._cufflink
986 ls *_cufflink
987 rm *_cufflink
988 rm -R *_cufflink
989 rm -r *_cufflink
990 rm -r *_cufflink/*/
991 rm -r *_cufflink/
992 ls
993 ls *.sort_cufflink
994 ls *.sort_cufflink
```

```
995 cd 10_S42_L003.sort_cufflink
996 ls
997 rm 10_S42_L003.sort_cufflink
998 cd ..
999 rm 10_S42_L003.sort_cufflink
1000 rm -r 10_S42_L003.sort_cufflink
1001 rm 10_S42_L003.sort_cufflink/
1002 ls
1003 cat cufflinks2.sh
1004 vim cufflinks2.sh
1005 vim cufflinks.sh
1006 vim cufflinks2.sh
1007 cat cufflinks2.sh
1008 history
1009 cat slurm-17393857.out
1010 cat slurm-17393857.out
1011 ls
1012 pwd
1013 mkdir sortbamfile
1014 cd sortbamfile/
1015 mv ../*.sort.bam .
1016 ls
1017 mkdir sortsamfile
1018 cd sortsamfile/
1019 cd ..
1020 cd ..
1021 mkdir sortsamfile
1022 cd sortsamfile/
1023 mv ../*.sort.sam .
1024 ls
1025 cd ..
1026 ls *.bam
1027 ls *.bam > list.bam.txt
1028 vim cufflinks2.sh
1029 cat cufflinks2.sh
1030 history
1031 sbatch -p med -t 4800:00:00 --ntasks=8 cufflinks2.sh
1032 queue | grep "smm"
1033 queue | grep "smm"
1034 queue | grep "smm"
1035 CD RNASeq/
1036 ls
1037 cd RNASeq/
1038 cd Seq_read_data/
1039 cd Susan_data/
1040 cd RNAseq_SM/
1041 ls
1042 queue | grep "smm"
1043 queue | grep "smm"
1044 queue | grep "smm"
1045 cd RNASeq/
1046 cd Seq_read_data/
```

```
1047 cd Susan_data/
1048 cd RNAseq_SM/
1049 ls
1050 history
1051 ls
1052 cat slurm-17480383.out
1053 ls
1054 cd 5_S37_L003_cufflink
1055 ls
1056 cat cufflinks2.sh
1057 cd ..
1058 cat cufflinks2.sh
1059 history
1060 ls *_cufflink
1061 ls *_cufflink >list.cufflink.txt
1062 cat cufflinks2.sh
1063 touch cuffquant.sh
1064 vim #!/bin/bash
1065 cuffquant
1066 cufflink
1067 cufflinks
1068 cuffquant
1069 cd 5_S37_L003_cufflink
1070 ls
1071 ls
1072 cat list.cufflink.txt
1073 cd ..
1074 cat list.cufflink.txt
1075 vim cuffquant1.sh
1076 ls
1077 rm cuffquant1.sh
1078 rm cuffquant.sh
1079 ls
1080 rm cuffmerge.sh
1081 ls
1082 mkdir gtf_cufflinks
1083 cd gtf_cufflinks/
1084 history
1085 cp ../*_cufflink/*.gtf .
1086 ls
1087 cd ..
1088 ls
1089 cd 37_S73_L006_cufflink
1090 ls
1091 cd ..
1092 cd gtf_cufflinks/
1093 ls
1094 rm *.gtf
1095 ls
1096 cp ../*_cufflink/*.gtf .
1097 ls
1098 rm *.gtf
```

```
1099 ls
1100 cd 37_S73_L006_cufflink
1101 cd ..
1102 cd 37_S73_L006_cufflink
1103 ls
1104 cd ..
1105 ls *_cufflink/
1106 ls *_cufflink/transcripts.gtf
1107 ls *_cufflink/transcripts.gtf > transcript_gtf.txt
1108 cat transcript_gtf.txt
1109 cd gtf_cufflinks/
1110 mv ../transcripts_gtf.txt .
1111 mv ../transcript_gtf.txt .
1112 mv ../transcript_gtf.txt .
1113 history
1114 mv ../transcript_gtf.txt .
1115 ls
1116 mv transcript_gtf.txt ..
1117 ls
1118 cd ..
1119 ls
1120 transcript_gtf.txt
1121 cat transcript_gtf.txt
1122 ls
1123 vim cp_for_cuffmerge
1124 gf
1125 fg
1126 fg
1127 vim cp_for_cuffmerge
1128 cat cuffmerge.sh
1129 cat cuffmerge.sh!
1130 rm cuffmerge.sh
1131 vim cuffmerge.sh!
1132 cat cuffmerge.sh
1133 cuffmerge
1134 sbatch -p med -t 4800:00:00 --ntasks=8 cuffmerge.sh
1135 queue | grep "smm"
1136 queue | grep "smm"
1137 queue | grep "smm"
1138 queue | grep "smm"
1139 queue | grep "smm"
1140 scancel 17484001
1141 queue | grep "smm"
1142 sbatch -p med -t 4800:00:00 --ntasks=1 cuffmerge.sh
1143 queue | grep "smm"
1144 scancel 17484005
1145 queue | grep "smm"
1146 vaim cuffmerge.sh
1147 vim cuffmerge.sh
1148 cat cuffmerge.sh
1149 sbatch -p med -t 4800:00:00 --ntasks=1 cuffmerge.sh
1150 queue | grep "smm"
```

```

1151  queue | grep "smm"
1152  queue | grep "smm"
1153  queue | grep "smm"
1154  ls
1155  cat transcript_gtf.txt
1156  pwd
1157  ls /home/smoeenga/RNASeq/Seq_read_data/Susan_data/RNAseq_SM/*_cufflink/*s
.gtf
1158  ls /home/smoeenga/RNASeq/Seq_read_data/Susan_data/RNAseq_SM/*_cufflink/*s
.gtf >list.gtf_transcript.txt
1159  cat list.gtf_transcript.txt
1160  queue | grep "smm"
1161  scancel 17484023
1162  queue | grep "smm"
1163  vim cuffmerge.sh
1164  sbatch -p med -t 4800:00:00 --ntasks=8 cuffmerge.sh
1165  queue | grep "smm"
1166  cat cuffmerge.sh
1167  queue | grep "smm"
1168  queue | grep "smm"
1169  cat cuffmerge.sh
1170  cuffmerge -o cuffmerge_out -p 8 -s Kabuli_UWA-v2.6.3_Ca1-8Extracontigs.fa
sta list.gtf_transcript.txt
1171  queue | grep "smm"
1172  vim cuffmerge.sh
1173  cat cuffmerge.sh
1174  sbatch -p med -t 4800:00:00 --ntasks=8 cuffmerge.sh
1175  queue | grep "smm"
1176  scancel 17484033
1177  queue | grep "smm"
1178  queue | grep "smm"
1179  queue | grep "smm"
1180  scancel 17484042
1181  queue | grep "smm"
1182  ls
1183  vim cuffmerge.sh
1184  cat cufflinks2.sh
1185  fg
1186  cuffmerge.sh
1187  sbatch -p med -t 4800:00:00 --ntasks=8 cuffmerge.sh
1188  queue | grep "smm"
1189  history
1190  queue | grep "smm"
1191  scancel 17484052
1192  queue | grep "smm"
1193  cuffmerge -o cuffmerge_out -p 8 -s Kabuli_UWA-v2.6.3_Ca1-8Extracontigs.fa
sta list.gtf_transcript.txt
1194  ls
1195  vim cuffmerge.sh
1196  sbatch -p med -t 4800:00:00 --ntasks=8 cuffmerge.sh
1197  queue | grep "smm"
1198  queue | grep "smm"

```

```
1199 rm transcript_gtf.txt
1200 cat list.gtf_transcript.txt
1201 /home/smмоenga/RNASeq/Seq_read_data/Susan_data/RNAseq_SM/9_S41_L003_cuffl
ink
1202 cd /home/smмоenga/RNASeq/Seq_read_data/Susan_data/RNAseq_SM/9_S41_L003_cu
fflink
1203 ls
1204 queue | grep "smm"
1205 queue | grep "smm"
1206 queue | grep "smm"
1207 queue | grep "smm"
1208 cat cuffmerge.sh
1209 cd ..
1210 cat cuffmerge.sh
1211 cat list.gtf_transcript.txt
1212 queue | grep "smm"
1213 cat cuffmerge.sh
1214 pwd
1215 cat cufflinks2.sh
1216 cp cufflinks2.sh cuffquant.sh
1217 vim cuffquant.sh
1218 bash cuffquant.sh
1219 vim cuffquant.sh
1220 sbatch -p med -t 480:00:00 --ntasks=1 cuffquant.sh
1221 queue | grep "smm"
1222 module avail
1223 vim cuffquant.sh
1224 sbatch -p med -t 480:00:00 --ntasks=1 cuffquant.sh
1225 queue | grep "smm"
1226 scancel 17484064
1227 queue | grep "smm"
1228 sbatch -p med -t 480:00:00 --ntasks=1 cuffmerge.sh
1229 queue | grep "smm"
1230 queue | grep "smm"
1231 queue | grep "smm"
1232 history
1233 queue | grep "smm"
1234 cat cuffmerge.sh
1235 cp cuffmerge.sh newcuffmerge.sh
1236 vim newcuffmerge.sh
1237 bash newcuffmerge.sh
1238 history > history.txt
1239 grep "cuffmerge" history.txt
1240 queue | grep "smm"
1241 queue | grep "smm"
1242 queue
1243 queue | grep "smm"
1244 queue | grep "smm"
1245 queue | grep "smm"
1246 cat slurm-17484103.out
1247 ls
1248 cd cuffmerge_out
```

```
1249 ls
1250 cat cuffquant.sh
1251 cat cuffquant.sh
1252 cd ..
1253 cat cuffquant.sh
1254 cp cuffquant.sh cuffquant2.sh
1255 cd cuffmerge_out/
1256 mv ./merged.gtf ..
1257 ls
1258 cd ..
1259 ls
1260 vim cuffquant2.sh
1261 cat cuffquant2.sh
1262 squeue |grep "smmoen"
1263 sbatch -p med -t 4800:00:00 --ntasks=1 cuffquant2.sh
1264 squeue |grep "smmoen"
1265 cat slurm-17484102.out
1266 squeue |grep "smmoen"
1267 ls
1268 squeue |grep "smmoen"
1269 cd 10_S42_L003_cuffquant
1270 ls
1271 cd ..
1272 squeue |grep "smmoen"
1273 squeue |grep "smmoen"
1274 squeue |grep "smmoen"
1275 squeue |grep "smmoen"
1276 squeue |grep "smmoen"
1277 squeue |grep "smmoen"
1278 cd RNASeq/
1279 cd Seq_read_data/
1280 cd Susan_data/
1281 cd RNAseq_SM/
1282 ls
1283 cd 10_S42_L003_cuffquant
1284 ls
1285 squeue |grep "smmoen"
1286 cd RNASeq/
1287 cd Seq_read_data/
1288 cd Susan_data/
1289 cd RNAseq_SM/
1290 ls
1291 squeue |grep "smmoen"
1292 cd RNASeq/
1293 cd Seq_read_data/
1294 cd Susan_data/
1295 cd RNAseq_SM/
1296 ls
1297 squeue |grep "smmoen"
1298 squeue |grep "smmoen"
1299 ls
1300 cd 15_S47_L004_cuffquant2
```

[illegible]


```
1353 ls
1354 squeue |grep "smmo"
1355 ls
1356 stringTie
1357 module avail
1358 cp cuffquant.sh stringTie.sh
1359 vim stringTie.sh
1360 cat stringTie.sh
1361 squeue |grep "smmoe"
1362 sbatch -p med -t 4800:00:00 -ntasks=1 stringTie.sh
1363 sbatch -p med -t 4800:00:00 --ntasks=1 stringTie.sh
1364 squeue |grep "smmoe"
1365 ls
1366 ls *_cuffquant2
1367 squeue |grep "smmoe"
1368 squeue |grep "Q0SGrpMe"
1369 squeue |grep "smmoe"
1370 squeue |grep "Q0SGrpMe"
1371 squeue |grep "smmoe"
1372 cat cuffmerge2.sh
1373 squeue |grep "smmoe"
1374 squeue |grep "Q0SGrpMe"
1375 squeue |grep "smmoe"
1376 squeue |grep "smmoe"
1377 squeue |grep "Q0SGrpMe"
1378 squeue |grep "Q0SGrpMe"
1379 squeue |grep "Q0SGrpMe"
1380 squeue |grep "Q0SGrpMe"
1381 cuffnorm
1382 load module cufflinks/2.2.1
1383 module avail
1384 load module cufflinks/2.2.1
1385 cufflinks/2.2.1
1386 module cufflinks/2.2.1
1387 cd RNASeq/
1388 cd Seq_read_data/
1389 cd Susan_data/
1390 cd RNAseq_SM/
1391 ls
1392 cat cuffquant.sh
1393 module load cufflinks/2.2.1
1394 cufflinks history
1395 history
1396 cuffdiff
1397 cd RNASeq/
1398 cd Seq_read_data/
1399 cd Susan_data/
1400 cd RNAseq_SM/
1401 ls *_cuffquant2
1402 cat cuffquant2.sh
1403 ls
1404 squeue |grep "smmo"
```

```
1405 cat stringTie.sh
1406 cuffnorm
1407 cuffnorm
1408 module load cufflinks/2.21
1409 history
1410 module load cufflinks/2.2.1
1411 cuffnorm
1412 ls
1413 less -S merged.gtf
1414 cd cuffmerge_out
1415 ls
1416 cd cuffmerge_out2
1417 cd ..
1418 cd cuffmerge_out2
1419 ls
1420 less -S merged.gtf
1421 cd ..
1422 cat cuffmerge.sh
1423 cat cuffmerge2.sh
1424 queue |grep "smmo"
1425 ls *_cuffquant2
1426 ls
1427 touch cuffjob.sh
1428 vim cuffjob.sh
1429 bash cuffjob.sh
1430 vim cuffjob.sh
1431 bash cuffjob.sh
1432 ls
1433 touch cuffnorm.sh
1434 vim cuffnorm.sh
1435 ls *.cxb
1436 fg
1437 fg
1438 cd cuffmerge_out
1439 mv ../merged.gtf .
1440 ls
1441 cd ..
1442 ls
1443 cd cuffmerge2_out
1444 cd cuffmerge_out2
1445 ls
1446 mv merged.gtf merged2.gtf
1447 ls
1448 mv ./merged2.gtf ..
1449 ls
1450 cd ..
1451 gf
1452 fg
1453 cat cuffnorm.sh
1454 sbatch -p med -t 4800:00:00 --ntasks=1 cuffnorm.sh
1455 queue
1456 queue |grep "smm"
```

```
1457  squeue |grep "Q0SGrpMemLimit"
1458  cp cuffnorm.sh cuffnorm2.sh
1459  vim cuffnorm2.sh
1460  sbatch -p med -t 4800:00:00 --ntasks=1 cuffnorm2.sh
1461  squeue |grep "smm"
1462  squeue |grep "smm"
1463  squeue |grep "smm"
1464  cd RNASeq/
1465  cd Seq_read_data/
1466  cd Susan_data/
1467  cd RNAseq_SM/
1468  ls
1469  squeue |grep "smmo"
1470  cat slurm-17485554.out
1471  squeue |grep "smmo"
1472  ls
1473  cat slurm-17486933.out
1474  vim cuffnorm.sh
1475  sbatch -p med -t 4800:00:00 --ntasks=1 cuffnorm.sh
1476  vim cuffnorm2.sh
1477  slurm-17486935.out
1478  cat slurm-17486935.out
1479  sbatch -p med -t 4800:00:00 --ntasks=1 cuffnorm2.sh
1480  cat slurm-17485516.out
1481  cat cuffmerge2.sh
1482  cat cuffmerge.sh
1483  cat cuffmerge2.sh
1484  cat cuffquant2.sh
1485  vim cuffquant2.sh
1486  cat cuffquant2.sh
1487  ls
1488  sbatch -p med -t 4800:00:00 --ntasks=1 cuffquant2.sh
1489  squeue |grep "smmo"
1490  ls
1491  cat slurm-17487218.out
1492  vim cuffnorm.sh
1493  sbatch -p med -t 4800:00:00 --ntasks=1 cuffnorm.sh
1494  vim cuffnorm2.sh
1495  squeue |grep "smmo"
1496  sbatch -p med -t 4800:00:00 --ntasks=1 cuffnorm2.sh
1497  squeue |grep "smmo"
1498  squeue |grep "Q0SGrpMemLimit"
1499  cat slurm-17485516.out
1500  cat slurm-17485554.out
1501  cat stringTie.sh
1502  squeue |grep "smmo"
1503  rm *_cuffquant2
1504  rm -R *_cuffquant2
1505  ls
1506  less -S cov_refs.gtf
1507  squeue |grep "smmo"
1508  squeue |grep "smmo"
```

```
1509  squeue |grep "smmo"
1510  cd RNASeq/
1511  cd Seq_read_data/
1512  cd Susan_data/
1513  cd RNAseq_SM/
1514  ls
1515  ls *.cxb
1516  ls
1517  ls *_cuffquant2
1518  squeue |grep "smmo"
1519  ls *_cuffquant1
1520  cat stringTie.sh
1521  cat slurm-17486933.out
1522  cat slurm-17485554.out
1523  vim stringTie.sh
1524  sbatch -p med -t 4800:00:00 --ntasks=1 stringTie.sh.sh
1525  sbatch -p med -t 4800:00:00 --ntasks=1 stringTie.sh
1526  squeue |grep "smmo"
1527  mkdir cuffquant
1528  ls *_cuffquant
1529  history
1530  cd cuffquant
1531  cp ../*_cuffquant/*.cxb .
1532  cp ../*_cuffquant/ .
1533  ls
1534  cp ../*_cuffquant .
1535  ls
1536  cd ..
1537  ls
1538  cd 36_S72_L005_cuffquant
1539  ls
1540  ls *_cuffquant
1541  cd ..
1542  ls *_cuffquant
1543  cd cuffquant/
1544  cp ..ls *_cuffquant .
1545  cp ../ls *_cuffquant .
1546  cp -R ../*_cuffquant .
1547  ls
1548  rm abundances.cxb
1549  ls
1550  cd 9_S41_L003_cuffquant/
1551  ls
1552  cd ..
1553  ls *_cuffquant1
1554  cd ..
1555  ls *_cuffquant1
1556  squeue |grep "smm"
1557  squeue |grep "sQ0SG"
1558  squeue |grep "SQ0SG"
1559  squeue |grep "Q0SG"
1560  ls
```

```
1561 cp cuffnorm.sh cuffdiff.sh
1562 vim cuffdiff.sh
1563 squeue |grep "smmoe"
1564 cat cuffdiff.sh
1565 sbatch -p med -t 4800:00:00 --ntasks=1 cuffdiff.sh
1566 squeue |grep "smmoe"
1567 squeue |grep "smmoe"
1568 ls *_cuffquant1
1569 ls *_cuffquant1
1570 squeue |grep "smmoe"
1571 cd RNASeq/
1572 cd Seq_read_data/
1573 cd Susan_data/
1574 cd RNAseq_SM/
1575 ls
1576 squeue |grep "smmo"
1577 squeue |grep "Q0SG"
1578 squeue |grep "smmo"
1579 ls
1580 cat samtools.sort.sh
1581 cat tophat2.sh
1582 ls
1583 cat cuffquant2.sh
1584 cd 9_S41_L003.bam
1585 cat samtools.sort.sh
1586 cat samtools.view.sh
1587 cat samtools.sort.sh
1588 squeue |grep "smmo"
1589 cat stringTie.sh
1590 cat cuffquant.sh
1591 squeue |grep "smmo"
1592 ls
1593 ls *_cuffquant1
1594 squeue |grep "smmoe"
1595 squeue |grep "smmoe"
1596 cd RNASeq/
1597 cd Seq_read_data/
1598 cd Susan_data/
1599 cd RNAseq_SM/
1600 ls
1601 squeue |grep "smmoe"
1602 squeue |grep "PD"
1603 cd RNASeq/
1604 cd Seq_read_data/
1605 cd Susan_data/
1606 cd RNAseq_SM/
1607 ls
1608 squeue |grep "smmo"
1609 cd RNASeq/
1610 cd Seq_read_data/
1611 cd Susan_data/
1612 squeue |grep "PD"
```

```
1613  squeue |grep "smm"
1614  squeue |grep "smm"
1615  cd RNASeq/
1616  cd Seq_read_data/
1617  cd Susan_data/
1618  cd RNAseq_SM/
1619  ls *cuffquant1
1620  cd RNAseq_SM/
1621  cd RNAseq
1622  cd RNAseq
1623  cd RNASeq/
1624  cd Seq_read_data/
1625  CD
1626  cd Susan_data/
1627  cd RNAseq_SM/
1628  ls *cuffquant1
1629  squeue |grep "smm"
1630  squeue |grep "Q0S"
1631  squeue |grep "Q0S"
1632  squeue |grep "Q0S"
1633  squeue |grep "smm"
1634  cd RNASeq/
1635  cd Seq_read_data/
1636  cd Susan_data/
1637  cd RNAseq_SM/
1638  ls
1639  ls *_cuffquant
1640  ls *_cuffquant1
1641  ls *_cuffquant1
1642  squeue |grep "smm"
1643  squeue |grep "smm"
1644  squeue |grep "Q0SG"
1645  squeue |grep "Q0SG"
1646  squeue |grep "smm"
1647  cd RNASeq/
1648  cd Seq_read_data/
1649  cd Susan_data/
1650  cd RNAseq_SM/
1651  ls
1652  cat slurm-17491983.out
1653  vim cuffdiff.sh
1654  sbatch -p med -t 4800:00:00 --ntasks=1 cuffdiff.sh
1655  ls
1656  cat slurm-17491983.out
1657  cat slurm-17487932.out
1658  vim stringTie.sh
1659  cat cuffquant.sh
1660  vim stringTie.sh
1661  fg
1662  cat stringTie.sh
1663  sbatch -p med -t 4800:00:00 --ntasks=1 stringTie.sh
1664  ls
```

```
1665 cat slurm-17487224.out
1666 vim cuffnorm2.sh
1667 sbatch -p med -t 4800:00:00 --ntasks=1 cuffnorm2.sh
1668 cat slurm-17487222.out
1669 vim cuffnorm.sh
1670 sbatch -p med -t 4800:00:00 --ntasks=1 cuffnorm.sh
1671 squeue |grep "smm"
1672 ls *cuffquant1
1673 squeue |grep "smm"
1674 ls *cuffdiff
1675 ls
1676 squeue |grep "smm"
1677 ls
1678 cat slurm-17493575.out
1679 ls
1680 squeue |grep "smm"
1681 cat slurm-17493570.out
1682 sbatch -p med -t 4800:00:00 --ntasks=8 cuffdiff.sh
1683 squeue |grep "smm"
1684 squeue |grep "smm"
1685 ls
1686 cat samtools.sh
1687 cat samtools.sort.sh
1688 squeue |grep "smm"
1689 ls
1690 cat slurm-17493578.out
1691 ls
1692 squeue |grep "smm"
1693 cat slurm-17493576.out
1694 ls
1695 squeue |grep "smm"
1696 cat slurm-17493576.out
1697 squeue
1698 squeue | grep "smmoenga"
1699 squeue | ls
1700 cat slurm-17493578.out
1701 cat cuffnorm.sh
1702 ls
1703 cd cuffnorm_geo_out
1704 ls
1705 cat slurm-17493576.out
1706 cat slurm-17493576.out
1707 cat slurm-17493575.out
1708 squeue | grep "smmoenga"
1709 cat slurm-17493570.out
1710 cat slurm-17493578.out
1711 cd ..
1712 cat slurm-17493575.out
1713 squeue | grep "smmoenga"
1714 cd cuffnorm_quart_out/
1715 ls
1716 cd ..
```

```
1717  squeue | grep "smmoenga"
1718  cat stringTie.sh
1719  cat cov_refs.txt
1720  ls *str
1721  ls
1722  ls *str
1723  ls *.gtf
1724  ls *gene_abund.ta
1725  cat gene_abund.tab
1726  cat stringTie.sh
1727  squeue | grep "smmoenga"
1728  ls
1729  cp stringTie.sh stringtie_merge.sh
1730  vim stringtie_merge.sh
1731  ls *tie.gtf
1732  ls *tie.gtf > list.stringtiegtf.txt
1733  fg
1734  cat cuffmerge.sh
1735  cat list.gtf_transcript.txt
1736  cat cuffmerge.sh
1737  stringtie
1738  stringTie
1739  cat stringTie.sh
1740  module load stringtie
1741  squeue | grep "smmoenga"
1742  squeue | grep "smmoenga"
1743  cd RNASeq/
1744  cd Seq_read_data/
1745  cd Susan_data/
1746  cd RNAseq_SM/
1747  ls
1748  cat slurm-17493671.out
1749  ls *_cuffquant1
1750  ls *_cuffquant1
1751  squeue | grep "smmoenga"
1752  cd RNASeq/
1753  cd Seq_read_data
1754  cd Susan_data/
1755  cd RNAseq_SM/
1756  ls *_cuffquant1
1757  cd RNASeq/
1758  cd Seq_read_data/
1759  cd Susan_data/
1760  cd RNAseq_SM/
1761  ls
1762  cd RNAseq_SM/
1763  ls
1764  ls
1765  ls
1766  ls
1767  cd RNASeq/
1768  cd Seq_read_data/
```



```
1769 cd Susan_data/
1770 cd RNAseq_SM/
1771 ls *_cuffquant1
1772 cat cuffnorm2.sh
1773 cat stringTie.sh
1774 cp stringTie.sh string_merge.sh
1775 vim string_merge.sh
1776 cd RNASeq/
1777 cd Seq_read_data/
1778 cd Susan_data/
1779 cd RNAseq_SM/
1780 vim string_merge.sh
1781 ls
1782 vim string_merge.sh
1783 stringtie_merge.sh
1784 vim stringtie_merge.sh
1785 cat cuffnorm.sh
1786 cat cuffmerge.sh
1787 vim stringtie_merge.sh
1788 ls
1789 ls *tie.gtf
1790 ls *tie.gtf>stringtie_gtf.txt
1791 cat stringtie_gtf.txt
1792 fg
1793 ls
1794 rm stringtie_merge.sh
1795 rm string_merge.sh
1796 ls
1797 cp stringTie.sh string_merge.sh
1798 vim string_merge.sh
1799 vim string_merge.sh
1800 vim string_merge.sh
1801 vim string_merge.sh
1802 vim string_merge.sh
1803 fg
1804 cat stringTie_merged.sh
1805 sbatch -p med -t 4800:00:00 --ntasks=1 stringTie_merged.sh
1806 queue |grep "smm"
1807 ls *merge
1808 ls *.gtf
1809 cd cuffmerge_out
1810 ls
1811 mv merged.gtf cuffmerged.gtf
1812 ls
1813 mv ./cuffmerged.gtf ..
1814 ls
1815 cd ..
1816 ls *ed.gtf
1817 mv merged2.gtf cuffmerged2.gtf
1818 vim cuffcompare.sh
1819 cd RNASeq/
1820 cd Seq_read_data/
```

```
1821 cd Susan_data/
1822 cd RNAseq_SM/
1823 ls
1824 pwd
1825 vim cuffcompare.sh
1826 rm cuffcompare.sh.swp
1827 vim -r cuffcompare.sh
1828 cat stringTie.sh
1829 cat cuffnorm.sh
1830 fg
1831 cat cuffcompare.sh
1832 sbatch -p med -t 4800:00:00 -ntasks=1 cuffcompare.sh
1833 sbatch -p med -t 4800:00:00 --ntasks=1 cuffcompare.sh
1834 squeue |grep "smm"
1835 ls
1836 ls
1837 squeue |grep "smm"
1838 cat slurm-17493671.out
1839 ls
1840 cat slurm-17499438.out
1841 vim cuffcompare.sh
1842 rm *.swp
1843 ls -a
1844 rm *.swp
1845 rm .stringtie_merge.sh.swn
1846 rm .stringtie_merge.sh.swo
1847 rm .stringtie_merge.sh.swp
1848 ls -a
1849 rm .string_merge.sh.swp
1850 rm .cuffcompare.sh.swo
1851 rm .cuffcompare.sh.swp
1852 cat cuffcompare.sh
1853 vim cuffcompare.sh
1854 sbatch -p med -t 4800:00:00 --ntasks=1 cuffcompare.sh
1855 squeue |grep "smm"
1856 squeue |grep "smm"
1857 cat slurm-17499442.out
1858 ls
1859 ls cuffcompare_*
1860 mkdir cuffcompare_output
1861 cd cuffcompare_output/
1862 mv ../cuffcompare_* .
1863 cd ..
1864 rm cuffcompare_output/
1865 rm -r cuffcompare_output/
1866 mkdir cuffcompare_result
1867 cd cuffcompare_result/
1868 mv ../cuffcompare_* .
1869 cd ..
1870 mv cuffcompare_result cuffcompareresult
1871 cd cuffcompareresult/
1872 mv ../cuffcompare_* .
```

```
1873 ls
1874 mv ../cuffcompare_out.* .
1875 cd ..
1876 ls cuffcompare_out.*
1877 ls cuffcompare_out*
1878 ls cuffcompare_*
1879 ls cuffcompare_out*
1880 ls cuffcompare_out*
1881 ls
1882 cd cuffcompareresult/
1883 ls
1884 sbatch -p med -t 4800:00:00 --ntasks=1 cuffcompare.sh
1885 cat cuffcompare.sh
1886 ls -a
1887 cd .
1888 ls
1889 cd ..
1890 ls
1891 ls -a
1892 cat cuffcompare.sh
1893 sbatch -p med -t 4800:00:00 --ntasks=1 cuffcompare.sh
1894 queue|grep "smmoenga"
1895 queue|grep "smmoenga"
1896 ls
1897 cd cuffdiff_out
1898 ls
1899 cd RNASeq/
1900 CD
1901 cd Seq_read_data/
1902 cd Susan_data/
1903 cd RNAseq_SM/
1904 queue |grep "smm"
1905 ls
1906 queue |grep "smm"
1907 ls *cuffquant1
1908 queue |grep "smm"
1909 ls
1910 cat slurm-17499452.out
1911 cat slurm-17487220.out
1912 vim cuffquant2.sh
1913 sbatch -p med -t 4800:00:00 --ntasks=1 cuffquant2.sh
1914 queue |grep "smm"
1915 queue |grep "smm"
1916 ls
1917 queue|grep "smmoenga"
1918 cd RNASeq/
1919 cd Seq_read_data/
1920 cd Susan_data/
1921 cd RNAseq_SM/
1922 ls *cuffquant2
1923 ls
1924 ls *cuffquant2
```

```
1925  squeue|grep "smmoenga"
1926  ls *.cuffquant2
1927  ls *_cuffquant2
1928  ls *_cuffquant2
1929  ls
1930  cat cuffdiff.sh
1931  cd cuffdiff_out/
1932  ls
1933  cat genes.fpkms_tracking
1934  squeue |grep "smm"
1935  cd RNASeq/
1936  cd Seq_read_data/
1937  cd Susan_data/
1938  cd RNAseq_SM/
1939  ls
1940  cat cuffdiff.sh
1941  cd RNASeq/
1942  cd Seq_read_data/
1943  ls
1944  cd Susan_data/
1945  cd RNAseq_SM/
1946  ls
1947  cd RNASeq/
1948  cd Seq_read_data/
1949  cd Susan_data/
1950  cd RNAseq_SM/
1951  ls *_cuffquant2
1952  ls *_cuffquant2
1953  cd RNASeq/
1954  cd Seq_read_data/
1955  cd Susan_data/
1956  cd RNAseq_SM/
1957  ls *_cuffquant2
1958  cp cuffdiff.sh cuffdiff2.sh
1959  vim cuffdiff2.sh
1960  vim cuffdiff2.sh
1961  sbatch -p med -t 4800:00:00 --ntasks=8 cuffdiff2.sh
1962  squeue |grep "smmoenga"
1963  scancel 17500617
1964  squeue |grep "smmoenga"
1965  sbatch -p med -t 4800:00:00 --ntasks=1 cuffdiff2.sh
1966  squeue |grep "smmoenga"
1967  squeue |grep "smmoenga"
1968  squeue |grep "smmoenga"
1969  squeue |grep "smmoenga"
1970  squeue |grep "smmoenga"
1971  squeue |grep "smmoenga"
1972  squeue |grep "smmoenga"
1973  squeue |grep "smmoenga"
1974  cd RNASeq/
1975  cd Seq_read_data/
1976  cd Susan_data/
```

```
1977 cd RNAseq_SM/
1978 ls
1979 cat slurm-17500619.out
1980 sbatch -p med -t 4800:00:00 --ntasks=4 cuffdiff2.sh
1981 squeue |grep "smmoenga"
1982 ls
1983 squeue |grep "smmoenga"
1984 squeue |grep "smmoenga"
1985 squeue |grep "smmoenga"
1986 cat stringTie.sh
1987 cp stringTie.sh stringTieforBalgn.sh
1988 vim stringTieforBalgn.sh
1989 ls
1990 fg
1991 sbatch -p med -t 4800:00:00 --ntasks=4 stringTieforBalgn.sh
1992 squeue |grep "smmoenga"
1993 squeue |grep "smmoenga"
1994 squeue |grep "smmoenga"
1995 squeue |grep "smmoenga"
1996 squeue |grep "smmoenga"
1997 ls
1998 squeue |grep "smmoenga"
1999 squeue |grep "smmoenga"
2000 squeue |grep "smmoenga"
2001 ls
2002 squeue |grep "smmoenga"
2003 squeue |grep "smmoenga"
2004 gffcompare
2005 module load stringTie
2006 cat stringTie.sh
2007 module load stringtie/1.3.2d
2008 gffcompare
2009 cp stringTie.sh sringcompare.sh
2010 rm sringcompare
2011 rm sringcompare.sh
2012 cp stringTie.sh stringcompare.sh
2013 vim stringcompare.sh
2014 modules
2015 module load
2016 ls
2017 history
2018 module avail
2019 vim stringcompare.sh
2020 module load conda3/1.0
2021 gffcompare
2022 samtools
2023 gffcompare
2024 gffcompare() quit(r)
2025 module load cufflinks
2026 gffcompare
2027 cat stringcompare.sh
2028 module load gffcompare/0.9.8
```

```
2029 module avail
2030 squeue |grep "smmoenga"
2031 ls
2032 squeue |grep "smmoenga"
2033 cat slurm-17500782.out
2034 cat stringTieforBalgn.sh
2035 ls *_stringtie_ball.gtf
2036 mkdir stringtie_ball
2037 cd stringtie_ball/
2038 cd ..
2039 pwd
2040 mv *_stringtie_ball.gtf ~/home/smmoenga/RNASeq/Seq_read_data/Susan_data/R
NAseq_SM/stringtie_ball
2041 cd stringtie_ball/
2042 cd ..
2043 ls -l | grep "stringtie_ball.gtf" | xargs -i mv {} /home/smmoenga/RNASeq/
Seq_read_data/Susan_data/RNAseq_SM/stringtie_ball
2044 cd stringtie_ball/
2045 ls
2046 cd ..
2047 ls *cuffquant2
2048 ls
2049 cat stringTie.sh
2050 cat stringTieforBalgn.sh.sh
2051 cat stringTieforBalgn.sh
2052 squeue |grep "smmoenga"
2053 ls
2054 squeue |grep "smmoenga"
2055 ls
2056 cat stringTieforBalgn.sh
2057 cat list.bam.txt
2058 ls -a
2059 cd 13_S45_L004
2060 ls
2061 cd .
2062 ls
2063 cd ..
2064 vim stringTie.sh
2065 vim stringTieforBalgn.sh
2066 cd RNASeq/
2067 cd Seq_read_data/
2068 cd Susan_data/
2069 cd RNAseq_SM/
2070 ls
2071 cd RNASeq/
2072 CD
2073 cd Seq_read_data/
2074 cd Susan_data/
2075 cd RNAseq_SM/
2076 ls
2077 squeue | grep "smm"
2078 squeue | grep "smm"
```

```
2079 cd RNASeq/
2080 cd Seq_read_data/
2081 cd Susan_data/
2082 cd RNAseq_SM/
2083 ls
2084 squeue | grep "smm"
2085 cd RNASeq/
2086 cd Seq_read_data/
2087 cd Susan_data/
2088 cd RNAseq_SM/
2089 ls
2090 cat stringTie.sh
2091 cat stringTieforBalgn.sh
2092 cd 7_S39_L003
2093 ls
2094 cd 48_S84_L006_stringtie.gtf
2095 cat stringTieforBalgn.sh
2096 cd ..
2097 cat stringTieforBalgn.sh
2098 vim stringTieforBalgn.sh
2099 cd ballgown
2100 mkdir Ballgown
2101 fg
2102 cat tophat.sh
2103 cat trimmomatic.sh
2104 fg
2105 fg
2106 fg
2107 rm stringbad
2108 vim stringTieforBalgn.sh
2109 sbatch -p med -t 4800:00:00 --ntasks=8 cat list.bam.txt | while read i; d
o x=${i/.bam/}; stringtie $i -e -B -p 8 -G stringtie_merged.gtf -o /home/smмоeng
a/RNASeq/Seq_read_data/Susan_data/RNAseq_SM/Ballgown/"$x"/"$x"_stringtie_ball.gt
f --rf -A "x"_gene_abund_ball.tab -C "x"_cov_refs_ball.txt; done
2110 sbatch -p med -t 4800:00:00 --ntasks=8 stringTieforBalgn.sh
2111 squeue |grep "smm"
2112 squeue |grep "smm"
2113 squeue |grep "smm"
2114 ls
2115 cd Ballgown/
2116 ls
2117 cd 10_S42_L003/
2118 ls
2119 cd ..
2120 ls
2121 cd..
2122 cd ..
2123 ls
2124 cd Ballgown/
2125 ls
2126 cd 10_S42_L003
2127 ls
```

```
2128 cd .. ..
2129 cd ..
2130 cat cuffdiff2.sh
2131 cat cuffdiff.sh
2132 vim cuffdiff2.sh
2133 cat cuffquant
2134 cat cuffquant.sh
2135 cat cuffnorm.sh
2136 cd Ballgown
2137 ls
2138 cd RNASeq/
2139 cd Seq_read_data/
2140 cd Susan_data/
2141 cd RNAseq_SM/
2142 cd Ballgown/
2143 ls
2144 squeue |"smmoenga"
2145 squeue |grep "sm"
2146 squeue |grep "smm"
2147 cd ..
2148 ls
2149 cat cuffcompare.sh
2150 cat cuffmerged2.sh
2151 cat cuffmerge.sh
2152 cat cuffmerge2.sh
2153 vim cuffmerge.sh
2154 squeue |grep "smmoenga"
2155 ls
2156 history
2157 history
2158 history
2159 ls
2160 cat x_cov_refs_ball.txt
2161 ls
2162 ls
2163 cd 36_S72_L005_cuffquant2
2164 ls
2165 history
2166 cd ..
2167 ls
2168 ls
2169 cat cuffdiff2.sh
2170 ls
2171 cd RNASeq/
2172 cd Seq_read_data/
2173 cd Susan_data/
2174 cd RNAseq_SM/
2175 ls
2176 cd RNASeq/
2177 cd Seq_read_data/
2178 cd Susan_data/
2179 cd RNAseq_SM/
```



```
2180 ls
2181 cd RNASeq/
2182 cd RNASeq/
2183 cd Seq_read_data/
2184 cd Susan_data/
2185 cd RNASeq/
2186 cd RNAseq_SM/
2187 LS
2188 ls
2189 ls
2190 ls
2191 ls
2192 ls
2193 ls
2194 ls
2195 ls
2196 ls
2197 ls
2198 ls
2199 ls
2200 ls
2201 cd RNASeq/
2202 cd Seq_read_data/
2203 cd Susan_data/
2204 cd RNAseq_SM/
2205 ls
2206 cp cuffdiff2.sh cuffdiff_Kalkan.sh
2207 vim cuffdiff_kalkan.sh
2208 rm cuffdiff_kalkan.sh
2209 vim cuffdiff_Kalkan.sh
2210 mkdir cuffdiff_out2_kalkan
2211 cat cuffdiff2_Kalkan.sh
2212 mv cuffdiff_Kalkan.sh cuffdiff2_Kalkan.sh
2213 cat cuffdiff2_Kalkan.sh
2214 mkdir cuffdiff_out2_Kalkan
2215 sbatch -p -med t 4800:00:00 --ntasks = 4 cuffdiff2_Kalkan.sh
2216 sbatch -p med t 4800:00:00 --ntasks = 4 cuffdiff2_Kalkan.sh
2217 sbatch -p med -t 4800:00:00 --ntasks = 4 cuffdiff2_Kalkan.sh
2218 sbatch -p med -t 4800:00:00 --ntasks=4 cuffdiff2_Kalkan.sh
2219 cp cuffdiff2.sh cuffdiff2_Savur.sh
2220 squeue |grep "smmoeng"
2221 ls
2222 cat slurm-17515814.out
2223 vim cuffdiff2_Kalkan.sh
2224 sbatch -p med -t 4800:00:00 --ntasks=4 cuffdiff2_Kalkan.sh
2225 squeue |grep "smmoeng"
2226 vim cuffdiff2_Savur.sh
2227 squeue |grep "smmoeng"
2228 rm cuffdiff2_kalkan
2229 rm -R cuffdiff2_kalkan
2230 mkdir cuffdiff_out2_Savur
2231 cat cuffdiff2_Savur.sh
```