example_qsub.sh

```bash
#$ -S /bin/bash
#$ -l mfree=3G
#$ -l h_rt=8:0:0

for i in {1..10} ; do
        echo $i
        sleep 1
done
```

sci-RNA-seq.pipeline.elegans.sh

```bash
set -euo pipefail

WORKING_DIR=$HOME/output-clean
CONFIG_DIR=/net/gs/vol4/shared/trapnelllab/genome569A/scRNAseq-pipeline/config
SCRIPTS_DIR=./sci-RNA-seq-pipeline-scripts
READS_DIR=/net/gs/vol4/shared/trapnelllab/genome569A/scRNAseq-pipeline/reads
LOG_DIR=$WORKING_DIR/cluster-logs
DATAMASH_PATH=/net/gs/vol4/shared/trapnelllab/genome569A/scRNAseq-pipeline/datamash
```