cd git clone https://github.com/ctb/2017-ucdavis-igg201b.git sudo Rscript --no-save ~/2017-ucdavis-igg201b/lab7/install-edgeR.R

cd curl -L -O https://github.com/COMBINE-lab/salmon/releases/download/v0.8.0/Salmon-0.8.0\_linux\_x86\_64.tar.gz tar xzf Salmon-0.8.0\_linux\_x86\_64.tar.gz export PATH=$PATH:$HOME/Salmon-latest\_linux\_x86\_64/bin

mkdir yeast cd yeast

curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR458/ERR458496/ERR458496.fastq.gz

curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR458/ERR458497/ERR458497.fastq.gz

curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR458/ERR458503/ERR458503.fastq.gz

curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR458/ERR458504/ERR458504.fastq.gz

curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR458/ERR458500/ERR458500.fastq.gz curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR458/ERR458501/ERR458501.fastq.gz curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR458/ERR458502/ERR458502.fastq.gz curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR458/ERR458493/ERR458493.fastq.gz curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR458/ERR458494/ERR458494.fastq.gz curl -O ftp://ftp.sra.ebi.ac.uk/vol1/fastq/ERR458/ERR458495/ERR458495.fastq.gz

curl –O http://downloads.yeastgenome.org/sequence/S288C\_reference/orf\_dna/orf\_coding.fasta.gz

salmon index --index yeast\_orfs --type quasi --transcripts orf\_coding.fasta.gz

for i in \*.fastq.gz do salmon quant -i yeast\_orfs --libType U -r $i -o $i.quant --seqBias --gcBias done

curl -L -O https://github.com/ngs-docs/2016-aug-nonmodel-rnaseq/raw/master/files/gather-counts.py python2 gather-counts.py

script --no-save ~/2017-ucdavis-igg201b/lab8/yeast.salmon.R

Conclusion

If we decide to choose FDR<0.05 for significantly by comparing the yeast-edgeR.csv from 10 libraries (HW3) by the yeast-edgeR.csv from 6 libraries (Lab8) we found about 430 differential expressed gene more in the yeast-edgeR.csv file with 10 libraries.

Maybe adding more biological replication increase number of the DEG

Also it depends on the FDR threshold that we choose