# How to analyze RNA-seq data:

# All commands are for typing in Terminal

1. Download SRR:

wget ftp://ftp-trace.ncbi.nih.gov/sra/sra-instant/reads/ByRun/sra/SRR/SRR341/SRR3416290/SRR3416290.sra

# where SRR is the number of a given sample, repeat with all samples

2. Download annotation:

curl ftp://ftp.ensembl.org/pub/release-93/fasta/mus\_musculus/cdna/Mus\_musculus.GRCm38.cdna.all.fa.gz -o musculus.fa.gz

3. Run ./sra.sh to unpack sea files into fasted

4. Run ./run\_trimmo.sh to filter reads

5. Run ./run\_salmon to calculate transcript abundance

6. Proceed with instructions in RNA-seq-wicked-fast-pipeline-EZ.html

P.S. See also https://combine-lab.github.io/salmon/getting\_started/

*# DYLD\_FALLBACK\_LIBRARY\_PATH=/Users/zhivkopliasek/Desktop/RNAseq/Salmon-0.8.2\_macOX\_10.12/lib ~/Desktop/RNAseq/Salmon-0.8.2\_macOX\_10.12/bin/salmon – RUN Salmon on Mac*

*# Samples*

*SRR1030113 C57BL6J\_MOCK\_D2\_84*

*SRR1030115 C57BL6J\_MOCK\_D2\_92*

*SRR1030116 C57BL6J\_MOCK\_D4\_85*

*SRR1030118 C57BL6J\_MOCK\_D4\_96*

*SRR1030141 CAST\_MOCK\_D2\_100*

*SRR1030142 CAST\_MOCK\_D2\_107*

*SRR1030143 CAST\_MOCK\_D4\_104*

*SRR1030145 CAST\_MOCK\_D4\_111*