RNA-seq workshop BCBB information and links

Email
BCBB bioinformatics collaboration or help request – bioinformatics@niaid.nih.gov
NIH Locus account request - NIAIDHPCSUPPORT@niaid.nih.gov
Brendan Jeffrey, Genomics specialist – brendan.jeffrey@nih.gov
Claire Wang, Statistics specialist - qinlu.wang@nih.gov
Jingwen Gu, Statistics specialist - jingwen.gu@nih.gov

Books, manuscripts, format descriptions, tutorials
Biometry: The Principles and Practices of Statistics in Biological Research -
https://www.amazon.com/Biometry-Principles-Practices-Statistics-Biological/dp/0716724111
Scotty, Power Analysis for RNA-seq experiments - http://scotty.genetics.utah.edu/
SAM/BAM format description - https://samtools.github.io/hts-specs/SAMv1.pdf
DESeq2 manuscript - https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4302049/
DESeq2 tutorial -
https://www.bioconductor.org/packages/devel/bioc/vignettes/DESeq2/inst/doc/DESeq2.html
HISAT, Stringtie, Ballgown manuscript - https://www.nature.com/articles/nprot.2016.095
RNA-seq tool comparison manuscripts –
https://www.ncbi.nlm.nih.gov/pubmed/27022035
https://www.ncbi.nlm.nih.gov/pubmed/28680106

Tools – Next Gen Sequencing Quality Control
FastQC Read QC overview – https://www.bioinformatics.babraham.ac.uk/projects/fastqc/
Trimmomatic- read trimming and adaptor removal –
http://www.usadellab.org/cms/?page=trimmomatic

Tools – Read mapping
Bowtie2 - http://bowtie-bio.sourceforge.net/bowtie2/index.shtml
HISAT2 - https://ccb.jhu.edu/software/hisat2/index.shtml
BWA-MEM - http://bio-bwa.sourceforge.net/
STAR - https://github.com/alexdobin/STAR
Kallisto - https://pachterlab.github.io/kallisto/
Salmon - https://combine-lab.github.io/salmon/

CLASS SURVEY! – please fill out if you can

https://tinyurl.com/yxw66ld3