**RNA-seq workshop BCBB information and links**

**Email**

BCBB bioinformatics collaboration or help request – [bioinformatics@niaid.nih.gov](http://bioinformatics@niaid.nih.gov)

NIH Locus account request - [NIAIDHPCSUPPORT@niaid.nih.gov](mailto:NIAIDHPCSUPPORT@niaid.nih.gov)

Brendan Jeffrey, Genomics specialist – [brendan.jeffrey@nih.gov](mailto:brendan.jeffrey@nih.gov)

Claire Wang, Statistics specialist - [qinlu.wang@nih.gov](http://qinlu.wang@nih.gov)

Jingwen Gu, Statistics specialist - [jingwen.gu@nih.gov](http://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>