

RNA-seq workshop BCBB information and links

Email

BCBB bioinformatics collaboration or help request – bioinformatics@niaid.nih.gov

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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/>