

NGS DATA ANALYSIS SOFTWARE TOOLS FOR UBUNTU

(DNA-SEQ | RNA-SEQ | CHIP-SEQ | META-SEQ)

G LAKSHMAN TEJA
Genomics Data Scientist
laksmanteja@gmail.com
+91 9590743777

GETTING READ FILES FROM NCBI-SRA

=> sratoolkit.2.9.0 (<https://www.ncbi.nlm.nih.gov/sra/docs/toolkitsoft/>)

RAW-READS QUALITY CONTROL TOOLS

=> NGSQCToolkit_v2.3.3 (<http://www.nipgr.res.in/ngsqctoolkit.html>)

=> FastQC (<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>)

=> FASTX-Toolkit (http://hannonlab.cshl.edu/fastx_toolkit/)

=> Cutadapt (<https://pypi.org/project/cutadapt/#files>)

=> Seq_Crumbs-0.1.9 (https://bioinf.comav.upv.es/seq_crumbs/)

GENOME ASSEMBLY TOOLS

General/DNA-SEQ:

=> ABySS-2.0.2 (<http://www.bcgsc.ca/platform/bioinfo/software/abyss>)

=> SPAdes-3.11.1 (<http://cab.spbu.ru/software/spades/>)

=> SOAPdenovo2 (<http://soap.genomics.org.cn/soapdenovo.html>)

=> Velvet_1.2.10 (<https://www.ebi.ac.uk/~zerbino/velvet/>)

=> Ray (<http://sebhtml.github.io/Ray.web/download.html>)

RNA-SEQ:

=> Trinity_RNA_Seq (<https://github.com/trinityrnaseq/trinityrnaseq/releases>)

=> Cufflinks (<http://cole-trapnell-lab.github.io/cufflinks/install/>)

=> TopHat-2.1.1 (<https://ccb.jhu.edu/software/tophat/index.shtml>)

META-SEQ:

=> MetaVelvet-1.2.02 (<http://metavelvet.dna.bio.keio.ac.jp/src/>)

=> MEGAHIT (<http://www.metagenomics.wiki/tools/assembly/megahit>)

=> IDBA-UD (https://i.cs.hku.hk/~alse/hkubrg/projects/idba_ud/index.html)

=> MetaAMOS (<http://metamos.readthedocs.io/en/v1.5rc3/content/>)

SCAFFOLING TOOLS

=> SSPACE-3.0

(<https://www.baseclear.com/services/bioinformatics/basetools/>)

=> SeqTK (<https://github.com/lh3/seqtk>)

K-MER GENERATION

=> kmergenie-1.7048 (<http://kmergenie.bx.psu.edu>)

GENOME ASSEMBLY ASSESSMENT TOOLS

=> QUAST-4.6.3 (<https://sourceforge.net/projects/quast/files/>)

=> GAGE (<http://gage.cbc.umd.edu/results/index.html>)

=> BUSCO-v3 (<http://busco.ezlab.org>)

META GENOME BINNING

=> MetaBIN (<http://metabin.riken.jp/download>)

=> MetaBAT (<https://bitbucket.org/berkeleylab/metabat>)

=> MEGAN6 (<http://ab.inf.uni-tuebingen.de/software/megan6/>)

TAXONOMIC PROFILING

=> Kraken (<https://ccb.jhu.edu/software/kraken/>) ** Need more of Disk space

=> Centrifuge (<https://github.com/infphilo/centrifuge>)

=> KronaTools (<https://github.com/marbl/Krona/wiki/KronaTools>)

=> MetaPhlAn2 (<http://segatalab.cibio.unitn.it/tools/metaphlan2/>)

GENOME ALIGNMENT TOOLS

=> Bowtie2-2.3.4.1 (<http://bowtie-bio.sourceforge.net/bowtie2/index.shtml>)

=> BWA-0.7.17 (<https://sourceforge.net/projects/bio-bwa/files/>)

=> minimap2 (<https://github.com/lh3/minimap2>)

=> Picard (<https://broadinstitute.github.io/picard/>)

=> Tablet Viewer (<https://ics.hutton.ac.uk/tablet/download-tablet/>)

CHIP-SEQ TOOLS

=> MACS-1.4.2 (<http://liulab.dfci.harvard.edu/MACS/>)

=> PeakAnalyzer_1.4 (<https://www.ebi.ac.uk/research/bertone/software>)

=> NGS-QC (<http://www.ngs-qc.org/index.php>)

GENE PREDICTION TOOLS

Eukaryotics

=> Augustus-3.3.1 (<http://bioinf.uni-greifswald.de/augustus/binaries/>)

Prokaryotics

=> Prodigal.v2_50 (<https://github.com/hyattpd/Prodigal/wiki/installation>)

=> Glimmer-v.3.02 (<https://ccb.jhu.edu/software/glimmer/>)

GENE ANNOTATION (NCBI-BLAST)

=> NCBI-BLAST (<ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/>)

GENE ONTOLOGY

=> BLAST2GO (<https://www.blast2go.com>)

SNP CALLING

=> GATK-4.0.4.0 (<https://software.broadinstitute.org/gatk/download/>)

=> SAMtools-1.8 (<http://samtools.sourceforge.net>)

=> FreeBayes (<https://github.com/ekg/freebayes>)

=> VarScan-v2.4 (<http://varscan.sourceforge.net>)

=> Vcftools-v0.1.15 (<https://vcftools.github.io/downloads.html>)

=> SnpSift (<http://snpeff.sourceforge.net/SnpSift.html>)

=> BEDtools (<http://bedtools.readthedocs.io/en/latest/>)

=> MISA (<http://pgrc.ipk-gatersleben.de/misa/misa.html>)

***** END OF LIST*****