**Software List for biology, bioinformatics and biostatistics**

* **CCT - Delta**

|  |  |  |
| --- | --- | --- |
| **Software** | **Version** | **Application** |
| ALLPATHS-LG | 52488 | short read assembler and it works on both small and large (mammalian size) genomes |
| BAMtools | 2.4.0 | provides a fast, flexible C++ API & toolkit for reading, writing, and manipulating BAM files |
| Barracuda | 0.7.107b | a high level of alignment fidelity and is comparable to other mainstream alignment programs |
| bedtools | 2.25.0 | allows one to intersect, merge, count, complement, and shuffle genomic intervals from multiple files |
| Bfast | 0.7.0a | universal DNA sequence aligner tool |
| Bioconductor | 3.2 | analysis and comprehension of high-throughput genomic data using the R statistical programming |
| BioPython | 1.66 | tools for biological computation written in Python |
| Boost | 1.54.0 | a fast approach to detecting gene-gene interactions in genome-wide case-control studies |
| Bowtie | 1.1.2 | short read aligner geared toward quickly aligning large sets of short DNA sequences to large genomes |
| Bowtie2 | 2.2.6 | Bowtie + fully supports gapped alignment with affine gap penalties |
| BWA | 0.7.12 | mapping low-divergent sequences against a large reference genome |
| ClustalW | 2.1 | multiple sequence alignment program to align DNA and protein sequences |
| Cufflinks | 2.2.1 | assembles transcripts, estimates their abundances for differential expression and regulation in RNA-Seq samples |
| EBSEQ (R) | 1.10.0 | identifying genes and isoforms differentially expressed |
| EMBOSS | 6.5.7 | a comprehensive set of sequence analysis programs |
| FASTA | 36.3.8b | a DNA and protein sequence alignment software package |
| FastQC | 0.11.4 | provide a simple way to do some quality control checks on raw sequence data |
| gnuplot | 5.0.0 | command-driven, interactive, function plotting program |
| Graphviz | 2.38.0 | graph visualization software package of open-source tools |
| HMMER | 3.1b2 | searching sequence databases for sequence homologs, and for making sequence alignments |
| HTSeq | 0.6.1 | analysing high-throughput sequencing data with Python |
| htslib | 1.2.1 | a unified C library for accessing common file formats |
| IGV | 2.3.65 | a high-performance visualization tool for interactive exploration of large, integrated genomic datasets |
| iSAAC | 15.04.01 | a DNA sequence aligner that takes advantage of high memory hardware (>48GB) |
| Matplotlib | 1.5.0 | a plotting library for the Python programming language and its numerical mathematics extension NumPy |
| Mothur | 1.36.1 | the package is frequently used in the analysis of DNA from unculutured microbes |
| NCBI BLAST+ | 2.2.31 | a suite of command-line tools to run BLAST |
| Numpy | 1.9.2 | the fundamental package for scientific computing with Python |
| Oases | 0.2.8 | a de novo transcriptome assembler across the dynamic range of expression levels |
| Picard | 1.14 | a set of command line tools for manipulating high-throughput sequencing (HTS) data |
| PLINK | 1.07 | whole genome association analysis toolset |
| Pysam | 0.8.3 | a python module for reading, manipulating and writing genomic data sets |
| Python | 2.7.10 | a widely used high-level, general-purpose, interpreted, dynamic programming language |
| R | 3.2.2 | a software environment for statistical computing and graphics |
| RSEM | 1.2.25 | accurate transcript quantification from RNA-Seq data with or without a reference genome |
| Samtools | 1.2.0 | a set of utilities for interacting with and post-processing short DNA seq read alignments in the SAM, BAM formats |
| SHRiMP | 2.2.3 | a software package for aligning genomic reads against a target genome |
| SOAP3-DP | r177 | a GPU-based software for aligning short reads with a reference sequence |
| SOAPaligner | 2.2 | a program for faster and efficient alignment for short oligonucleotide onto reference sequences |
| SOAPbuilder | 2.2 | a solutions for interoperability of famous Vendors like Microsoft with Java |
| SOAPdenovo2 | 2.4.240 | a short read de novo assembly tool, is a package for assembling short oligonucleotide into contigs and scaffolds |
| SQLite | 3.8.4.1 | a relational database management system contained in a C programming library |
| STAR | 2.4.2a | ultrafast universal RNA-seq aligner |
| tabix | 1.2.1 | the first generic tool that indexes position sorted files in TAB- delimited formats |
| TMAP | 3.4.0 | predict and plot transmembrane segments in protein sequences |
| TopHat | 2.1.0 | sequence analysis tool for fast and high throughput alignment of shotgun transcriptomic cDNA sequencing reads |
| Trinity | 2.1.1 | assembler program for RNA-Seq de novo transcriptome assembly |
| variant\_tools | 2.6.3 | a software tool for the manipulation, annotation, selection, simulation, and analysis of variants |
| Velvet | 1.2.10 | an algorithm package that has been designed to deal with de novo genome assembly and short reads |

Delta also supports end-to-end solution through web-based customized pipeline interface, user can able to use pre-developed pipelines (ex, RNA-Seq pipeline) or Delta team can build it for users.

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

* **LSU HPC / LONI HPC**

|  |  |  |
| --- | --- | --- |
| **LSU HPC** | | **LONI** |
| **SuperMIC** | **Super Mike2** | **QB2** |
| abyss amber amos beast blast blat bowtie bowtie2 bwa cufflinks gromacs hmmer idba lammps mauve mira mummer muscle namd oases r ray remora rnnotator rum samtools soapdenovo soapdenovo\_trans sparsehash tophat velvet vmatch | amber autodock autodock\_vina  **bio-align-gen:**  BWA  MUMMER Nucmer ProgressiveMauve T-Coffe Vmatch  **bio-align-rna:**  Bowtie Bowtie2 RUM Tophat Cufflinks  **bio-assembly-gen:**  ABySS AMOS CAP3 IDBA-UD Minimus2 MIRA SOAPdenovo SSPACE Velvet  **bio-assembly-trans:**  Oases SOAPdenovo-Trans TransABySS Trinity  **bio-gpu:**  CUSHAW CUDASW++ MrBayes ghostm  **bio-misc:**  bcftools CD-HIT fastx\_toolkit Jellyfish Lucy migrate ProtTest Quake RepeatMasker Repet2 Samtools  **bio-phylo:**  BEAST DendroPy FastTree2 Garli MrBayes PhyloBayes-MPI RAxML PAUP tapir  **bio-pipeline:**  A5 Microbial Genome Assemply HAL Qiime  **bio-recomb-eval:**  ClonalFrame ClonalOrigin  **bio-seq-compare:**  BLAST HMMER3 LAST MUSCLE SINA  dendropy  exabayes gromacs lammps mrbayes namd ncbiblast r tapir | amber bazel beagle\_lib beast bioperl blast bowtie bowtie2 bwa canu cufflinks fastx\_toolkit garli gromacs hmmer idba ima2p lammps libgtextutils mafft mauve mira mothur mrbayes mummer muscle namd novoplasty oases openbabel poretools qiime r racon raxml rum samtools soapdenovo soapdenovo\_trans spades sparsehash stacks stampy structure tophat trinity velvet vmatch vmd |