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	amber
amber	autodock	bazel
amos	autodock_vina	beagle_lib
beast		beast
blast	**bio-align-gen:**	bioperl
blat	BWA	blast
bowtie	MUMMER	bowtie
bowtie2	Nucmer	bowtie2
bwa	ProgressiveMauve	bwa
cufflinks	T-Coffe	canu
gromacs	Vmatch	cufflinks
hmmer		fastx_toolkit
idba	**bio-align-rna:**	garli
lammps	Bowtie	gromacs
mauve	Bowtie2	hmmer
mira	RUM	idba
mummer	Tophat	ima2p
muscle	Cufflinks	lammps
namd		libgtextutils
oases	**bio-assembly-gen:**	mafft
r	ABySS	mauve
ray	AMOS	mira
remora	CAP3	mothur
rnnotator	IDBA-UD	mrbayes
rum	Minimus2	mummer
samtools	MIRA	muscle
soapdenovo	SOAPdenovo	namd
soapdenovo_trans	SSPACE	novoplasty
sparsehash	Velvet	oases
tophat		openbabel
velvet	**bio-assembly-trans:**	poretools
vmatch	Oases	qiime
	SOAPdenovo-Trans	r
	TransABySS	racon
	Trinity	raxml
		rum
	bio-gpu:	samtools
	CUSHAW	soapdenovo
	CUDASW++	soapdenovo_trans

	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	spades sparsehash stacks stampy structure tophat trinity velvet vmatch vmd

| | dendropy
exabayes
gromacs
lammps
mrbayes
namd
ncbiblast
r
tapir | |