The bioinfomatics software on *sanger.uang* consists of the packages below, located in **/data1/bioprogs**

Package	Description	Remarks
abyss	de novo, parallel, sequence assembler for short reads	
arb	Graphically oriented package comprising various tools for sequence database handling and data analysis	
archaeopteryx	A phylogenetic tree viewer and editor	
artemis	Free genome viewer and annotation tool	
beam2	SNP-SNP interaction association mapping based on SNP-block models	
bedtools	suite of utilities for comparing genomic features	
big-blast	The big-blast script for annotation of long sequences	
biocode	Biocode plugin for Geneious workbench	
bioperl	Perl tools for computational molecular biology	
bioperl-run	BioPerl wrappers : scripts	
biosquid	utilities for biological sequence analysis	
bitseq	Bayesian Inference of Transcripts from Sequencing Data	
blast2	Basic Local Alignment Search Tool	
blimps-utils	blocks database improved searcher	
blixem	Interactive browser for viewing pairwise Blast results.	
bowtie	ultrafast memory-efficient short read aligner	
bowtie2	ultrafast memory-efficient short read aligner	
bowtie2-debug	ultrafast memory-efficient short read aligner	In bowtie2
bwa	Burrows-Wheeler Aligner	
cap3	A base calling system	Bio Perl
catchall	Analyze data about microbial species abundance	
cd-hit	a suite of programs designed to quickly group sequences	
cdbfasta	Constant DataBase indexing and retrieval tools for multi-FASTA files	
chimeraslayer	detects likely chimeras in PCR amplified DNA	
clcsequenceviewer	CLC Free Sequence Viewer	installed as rpm
clearcut	Relaxed Neighbor Joining	
clustalw	General purpose multiple sequence alignment program for DNA or proteins	
clustalx	General purpose multiple sequence alignment program for DNA or proteins	
cortex-con	efficient and low-memory software for consensus genome assembly	Installed Cortex
cufflinks	Transcript assembly, differential expression, and differential regulation for RNA-Seq	
cytoscape	Platform for visualizing complex-networks and integrating these with attribute data	
dendroscope	Interactive viewer for large phylogenetic trees.	
dialign	Segment-based multiple sequence alignment	
dotter	Graphical dotplot program for detailed comparison of two sequences	
embassy-domainatrix	Extra EMBOSS commands to handle domain classification file	
embassy-domalign	Extra EMBOSS commands for protein domain alignment	
embassy-domsearch	Extra EMBOSS commands to search for protein domains	
embassy-phylip	Extra EMBOSS commands to search for phylogeny	phylipnew
emboss	european molecular biology open software suite	6.6.0
estscan2	detects coding regions of DNA sequences	
exchanger	lets you store, annotate and share files via an omixed server	
fasta	Collection of programs for searching DNA and protein databases.	
fastdnaml	Tool for construction of phylogenetic trees of DNA sequences	
fastqc	A quality control application for high throughput sequence data	
fasttree	phylogenetic trees from alignments of nucleotide or protein sequences	
fastx-toolkit	FASTQ/A short nucleotide reads pre-processing tools	
galaxy-server	Web-based analysis environment for bioinformatics	
galaxy-server-apache-proxy	Activates Apache2 proxy for Galaxy server, and PAM authentication	To be configured
galaxy-server-pg-database	Activates PostgreSQL database back-end for Galaxy	To be configured
galaxy-tools-bl	Standard set of tool wrappers for Galaxy server	
geneious	Geneious Basic workbench from Biomatters	
geneious-genbanksubmit	GenBank submission for Geneious workbench	Copied to geneious dir
genquery	GenQuery is a set of Perl libraries for managing SQL query templates and making web-based query forms.	
glam2	gapped protein motifs from unaligned sequences	Part of MEME
glimmer3	Gene detection in archea and bacteria	
gnx-tools	Basic genome assembly statistic tool to calculate Nx values e.g. N50,N10,NG50	
handlebar	Handlebar is a database for storing data about barcodes and acessing the data via a web front-end.	
happy	Multipoint QTL Mapping in Genetically Heterogeneous Animals	
hmmer	profile hidden Markov models for protein sequence analysis	
hyphy	analysis of genetic sequences using multiple techniques	
infernal	inference of RNA secondary structural alignments	
isacreator	GUI to import and edit ISA dataset descriptions.	
jalview	multiple alignment editor	Installed and launch but it complained about errors during installation.
jellyfish	count k-mers in DNA sequences	Errors in autoconf
jemboss	graphical user interface to EMBOSS	According to the site it is incluced in the distribution of EMBOSS - to check
jmotu	Clusters barcode DNA sequence data into molecular operational taxonomic units	
jprofilegrid	Multiple sequence alignment tool that generates ProfileGrids	
last-align	genome-scale comparison of biological sequences	
lastz	Aligns two DNA sequences, inferring appropriate parameters automatically	
libbiojava-java	Java API to biological data and applications	Errors in compilation
libbiojava-java-demos	Example programs for BioJava	
lucy	Preparation of raw DNA sequence fragments for sequence assembly	

macs14	Model-based Analysis of ChIP-Seq on short reads sequencers	Installed in python
mafft	Multiple alignment program for amino acid or nucleotide sequences	rpm installed
maq	maps short fixed-length polymorphic DNA sequence reads to reference sequences	
maxd	maxd is a data warehouse and visualisation environment for genomic expression data.	
mdust	repetitive sequence masker	
meme	search for common motifs in DNA or protein sequences	
mesquite	Software for evolutionary biology.	
microbiomeutil	Microbiome Analysis Utilities	
mira-3rdparty	Additional useful tools to accomapany the MIRA assembler	
mira-assembler	Whole Genome Shotgun and EST Sequence Assembler	requires gcc >= 4.6.x + mpfr + mpc + gmp
mothur	sequence analysis suite for research on microbiota	compiled with mpi=yes
mothur-mpi	mpi-enabled binary for mothur	
mrbayes-mpi	Bayesian Inference of Phylogeny – mpi version	
msatfinder	Microsatellite Finder	
mspcrunch	a BLAST post-processing filter.	
mummer	Efficient sequence alignment of full genomes	
muscle	Multiple alignment program of protein sequences	
mview	Multiple alignment viewer for sequence database search results.	
natefoo-add-scores	small helper application used by Galaxy server	
natefoo-taxonomy	small taxonomy applications used by Galaxy server	
ncbi-blast+	next generation suite of BLAST sequence search tools	
ncbi-blast+-legacy	NCBI Blast legacy call script	
ncbi-seg	tool to mask segments of low compositional complexity in amino acid sequences	
ncbi-tools-bin	NCBI libraries for biology applications	
ncbi-tools-x11	NCBI libraries for biology applications	
njplot	phylogenetic tree drawing program	Requires vibrant
ocount	Oligonucleotide frequency counter	
oligoarray	Computes oligonucleotides for microarray construction	
oligoarrayaux	Free software that is required for the OligoArray2.1 software.	Provide program
omegamap	Detects natural selection and recombination in DNA or RNA sequences.	
paml	Phylogenetic Analysis by Maximum Likelihood	
parallel	shell tool for executing jobs in parallel	
parsinsert	Parsimonious Insertion of unclassified sequences into phylogenetic trees	only files
pass2	Peak calling in ChIP data based on Poisson de-clumping	requires gsl / gpfs
perm	Efficient mapping of short reads with periodic spaced seeds	
phylip	Package of programs for inferring phylogenies	
phyml	Phylogenetic estimation using Maximum Likelihood	phyml-mpi
picard-tools	Command line tools to manipulate SAM and BAM files	lot of packages
prank	Probabilistic Alignment Kit for DNA, codon and amino-acid sequences	
predictprotein	suite of protein sequence analysis tools	
priam	Generate enzyme-specific profiles for metabolic pathyway prediction	
primer3	Tool to design flanking oligo nucleotides for DNA amplification	
probcons	PROBabilistic CONSistency-based multiple sequence alignment	
pysam	python module for reading and manipulating Samfiles	
python-biopython	set of freely available tools for biological computation written in Python	
python-dev	Header files, a static library and development tools for building Python modules, extending the Python interpreter or embedding Python in applications	
python-h5py	Python interface to the HDF5 binary data format	
python-pip	A tool for installing and managing Python packages	
qiime	Quantitative Insights Into Microbial Ecology	Looks like a virtual machine
qtlcart	Map quantitative traits using a map of molecular markers.	
r-base	GNU R statistical computation and graphics system	
r-base-core	GNU R core of statistical computation and graphics system	
r-base-dev	GNU R installation of auxiliary GNU R packages	
r-bioc-affy	GNU R package “Methods for Affymetrix Oligonucleotide	
r-bioc-affyio	GNU R package “Tools for parsing Affymetrix data files”	
r-bioc-annotate	GNU R package “Annotation for microarrays”	
r-bioc-annotationdbi	GNU R package “Annotation Database Interface”	
r-bioc-biobase	GNU R package “Biobase: Base functions for Bioconductor”	
r-bioc-biocgenerics	GNU R package “Generic functions for Bioconductor”	
r-bioc-biocinstaller	GNU R package “Install/Update Bioconductor and CRAN	
r-bioc-biomart	GNU R Interface to BioMart databases	
r-bioc-biostrings	GNU R package “String objects representing biological	
r-bioc-bitseq	Bioconductor package “Transcript expression inference and differential	
r-bioc-deseq	Differential gene expression analysis based on the -ve binomial distribn.	
r-bioc-edger	GNU R package “Empirical analysis of digital gene	
r-bioc-genefilter	GNU R package “genefilter: methods for filtering genes	
r-bioc-geneplotter	Graphics related functions for Bioconductor	
r-bioc-genomeinfodb	GNU R package “Utilities for manipulating chromosome and other	
r-bioc-genomicranges	GNU R package “Representation and manipulation of genomic	
r-bioc-hilbertvis	GNU R package to visualise long vector data	
r-bioc-impute	GNU R package “impute: Imputation for microarray data”	
r-bioc-iranges	GNU R package “Infrastructure for manipulating intervals	
r-bioc-limma	GNU R package “Linear Models for Microarray Data”	
r-bioc-multtest	GNU R package “Resampling-based multiple hypothesis	
r-bioc-pcamethods	Bioconductor “pcaMethods: A collection of PCA methods.”	
r-bioc-preprocesscore	GNU R package “A collection of pre-processing functions”	
r-bioc-qvalue	Bioconductor package “Q-value estimation for false discovery rate control”	
r-bioc-rsamtools	GNU R package “Binary alignment	
r-bioc-xvector	GNU R package “Representation and manpulation of external	

r-bioc-zlibbioc	GNU R package “An R packaged zlib-1.2.5?	
r-cran-abind	GNU R package “Combine multi-dimensional arrays”	
r-cran-ade4	GNU R package “Analysis of Ecological Data : Exploratory	
r-cran-ape	GNU R package “Analyses of Phylogenetics and Evolution”	
r-cran-aplpack	GNU R package “Another Plot PACKage: stem.leaf, bagplot,	
r-cran-bitops	GNU R package implementing bitwise operations	
r-cran-catools	GNU R package “Tools: moving window statistics, GIF,	
r-cran-cluster	GNU R package for cluster analysis by Rousseeuw et al	
r-cran-dichromat	Color schemes for dichromats	
r-cran-digest	GNU R package “Create cryptographic hash digests of R	
r-cran-evaluate	GNU R package “Parsing and evaluation tools that provide	
r-cran-gdata	GNU R package with data manipulation tools by Greg Warnes et al	
r-cran-gee	GNU R package “Generalized Estimation Equation solver”	
r-cran-getopt	GNU R package “C-like getopt behavior.”	
r-cran-ggplot2	GNU R package “An implementation of the Grammar of	
r-cran-gplots	GNU R package with tools for plotting data by Greg Warnes et al	
r-cran-gtable	GNU R package “Arrange grobs in tables.”	
r-cran-gtools	GNU R package with R programming tools by Greg Warnes et al	
r-cran-labeling	GNU R package “Axis Labeling”	
r-cran-lattice	GNU R package “Lattice Graphics”	
r-cran-leaps	GNU R package “regression subset selection”	
r-cran-lme4	GNU R package “Linear mixed-effects models using Eigen and	
r-cran-locfit	Local Regression, Likelihood and Density Estimation.	
r-cran-matrix	GNU R package of classes for dense and sparse matrices	
r-cran-matrixstats	R package “Methods that apply to rows and columns of a matrix”	
r-cran-munsell	GNU R package “Munsell colour system”	
r-cran-nlme	GNU R package for	
r-cran-optparse	GNU R package “Command line option parser.”	
r-cran-permute	GNU R package “Functions for generating restricted	
r-cran-plotrix	GNU R package “Various plotting functions”	
r-cran-plyr	GNU R package “Tools for splitting, applying and combining	
r-cran-prettyr	GNU R package “Pretty descriptive stats.”	
r-cran-proto	GNU R package “Prototype object-based programming”	
r-cran-r.methodss3	GNU R package “Utility function for defining S3 methods”	
r-cran-rcolorbrewer	GNU R package providing suitable color palettes	
r-cran-rcpp	GNU R package for Seamless R and C++ Integration	
r-cran-rcurl	GNU R package “General network	
r-cran-relimp	GNU R package for inference on relative importance of regressors	
r-cran-reshape2	GNU R package “Flexibly reshape data: a reboot of the	
r-cran-rggobi	GNU R package for the GGobi data visualization system	
r-cran-rgl	GNU R package for three-dimensional visualisation using OpenGL	
r-cran-rgtk2	GNU R binding for Gtk2	
r-cran-rmpi	GNU R package interfacing MPI libraries for distributed computing	
r-cran-rsqlite	GNU R package “SQLite interface for R”	
r-cran-rwave	GNU R package “Time-Frequency analysis of 1-D signals”	
r-cran-samr	GNU R package “SAM: Significance Analysis of Microarrays”	
r-cran-scales	GNU R package “Scale functions for graphics.”	
r-cran-scatterplot3d	GNU R package “3D Scatter Plot”	
r-cran-snowfall	GNU R package “Easier cluster computing	
r-cran-sp	GNU R package “classes and methods for spatial data”	
r-cran-stringr	GNU R package “Make it easier to work with strings.”	
r-cran-tcltk2	GNU R package “Tcl/Tk Additions”	
r-cran-testthat	GNU R package “Testthat code. Tools to make testing fun	
r-cran-vegan	GNU R package “Community Ecology Package”	
r-cran-waveslim	GNU R package “Basic wavelet routines for one-, two- and	
r-cran-wavethresh	GNU R package “Wavelets statistics and transforms.”	
r-cran-xml	GNU R package “Tools for parsing and generating XML within	
r-cran-xtable	GNU R coerce data to LaTeX and HTML tables	
r-mathlib	GNU R standalone mathematics library	
r-recommended	GNU R collection of recommended packages [metapackage]	
raxml	Randomized Axelerated Maximum Likelihood of phylogenetic trees	
ray	parallel de novo genome assemblies of next-gen sequencing data	
ray-extra	Scripts and XSL sheets for post-processing for ray de novo assembler	
rbs-finder	A program to find Ribosomal binding sites.	
rdp-classifier	taxonomic assignment from next generation sequencing	ant/maven problems
readseq	Conversion between sequence formats	ant/maven problems
sampledata	Sample data for Bio-Linux packages	
samtools	processing sequence alignments in SAM and BAM formats	
savant	genome browser for high-throughput sequencing data	rpm
scythe	Bayesian adapter trimmer for nextgen sequence reads	
seaview	Graphical user interface for multiple sequence alignment and molecular phylogeny	
sickle	windowed adaptive trimming tool for FASTQ files using quality	
sift	predicts if a substitution in a protein has a phenotypic effect	
splitstree	Analysis and visualisation tool for distance data from biological sequences	
sputnik-mononucleotide	Searches DNA sequence files in FASTA format for microsatellite repeats	
squint	Java-based multiple alignment program and editor	
ssake	genomics application for assembling millions of very short DNA sequences	
staden	DNA sequence assembly	v. 2.0.0b8
staden-common	Architecture independent files for Staden	
stars	STARS is an alternative interface to Staden.	
t-coffee	Multiple Sequence Alignment	

tablet	Graphical viewer for next gen sequence assemblies and alignments	
taxinspector	Browser for entries in the NCBI taxonomy database	
tetra	tetranucleotide frequency calculator with GUI	
tophat	fast splice junction mapper for RNA-Seq reads	
trace2dbest	Processes trace files into dbEST submissions	
transterm-hp	Transterm finds rho-independent transcription terminators in bacterial genomes.	
transtermhp	find rho-independent transcription terminators in bacterial genomes	
tree-puzzle	Reconstruction of phylogenetic trees by maximum likelihood	
tree-puzzle-doc	Reconstruction of phylogenetic trees by maximum likelihood	
trnascan	tRNAscan-SE searches for tRNA genes in genomic sequences.	
trnascan-se	search for tRNA genes in genomic sequences	
ugene	integrated bioinformatics toolkit	
velvet	Nucleic acid sequence assembler for very short reads	
velvet-example	Example data for the Velvet sequence assembler	
velvet-long	Nucleic acid sequence assembler for very short reads, long version	A compiler
velvetoptimiser	Automatically optimise Velvet do novo assembly parameters	
weblogo	create sequence logos from biological sequence alignments	
wise	comparison of biopolymers, commonly DNA and protein sequences	
xcut	A re-write of the GNU cut command with many new features.	