琉球大学研究基盤センター・共用計算サーバー
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Softwares

・「Path」は、サーバー上におけるソフトウェアまでの絶対パスを示します
・「Command name」に記入があるソフトウェアは、そのコマンドをパスの指定なしに実行できます

Software name	Purpose	Path	Command name	Last installation
NCBI Blast+	Blast search	/usr/local/bin/ncbi-blast-2.6.0+/bin	-	2017.07.12
Mafft	Multiple alignment	/usr/local/bin/mafft	mafft	2017.07.12
Samtools-1.5	SAM/BAM/SNP analysis	/usr/local/bin/samtools-1.5	samtools	2017.07.12
htslib / tabix	C library for high-throughput sequencing data format	/usr/local/bin/htslib-1.5/tabix	-	2017.07.12
Bcftools-1.5	SAM/BAM/SNP analysis	/usr/local/bin/bcftools-1.5	bcftools	2017.07.12
Cutadapt	Adapter/primer trimming	/usr/bin/cutadapt	-	2017.07.13
Stacks v. 2.2	Rad-seq data analysis	(default):/usr/local/bin/stacks-2.2/bin (latest):/usr/local/bin/stacks-2.53/bin	-	2018.10.25 2020.04.20
R v.3.4.0	Statistical anaysis	/usr/lib64/R/bin	R	2017.07.19
Trimmomatic-0.36	Adapter/primer trimming	/usr/local/bin/Trimmomatic-0.36/trimmomatic-0.36.jar	-	2017.08.07
BWA-0.7.16a	Mapping	/usr/local/bin/bwa-0.7.16a/bwa	-	2017.08.07
GATK-3.8.0	SAM/BAM/SNP analysis	/usr/local/bin/GenomeAnalysisTK-3.8-0-ge9d806836/GenomeAnalysisTK.jar	-	2017.08.07
Picard-2.10.10	manipulating HTS data and formats such as SAM/BAM/CRAM and VCF.	/usr/local/bin/picard-2.10.10/picard.jar	-	2017.08.23
Bowtie	memory-efficient short read aligner	/usr/local/bin/bowtie-1.2.1.1	bowtie	2017.10.18
Bowtie2	memory-efficient tool for aligning sequencing reads to long reference sequences	/usr/local/bin/bowtie2-2.3.3.1-linux-x86_64	bowtie2	2017.10.18
TopHat 2.1.1	a fast splice junction mapper for RNA-Seq read	/usr/local/bin/tophat-2.1.1.Linux_x86_64	tophat, tophat2	2017.10.17
cufflinks-2.2.1	assembles transcripts, estimates their abundances	/usr/local/bin/cufflinks-2.2.1/cufflinks-2.2.1.Linux_x86_64	-	2017.10.17
ROOT-6.08.06	A modular scientific software framework.	/usr/local/bin/root/root_v6.08.06/root/bin (source ./thisroot.shでパス設定可能)	-	2017.10.23
SpeedSeq-0.1.2	A flexible framework for rapid genome analysis and interpretation	/usr/local/bin/speedSeq/speedseq/bin	-	2017.10.23

Gemini	Built-in analysis tools for variant	/usr/local/gemini/bin	-	2017.10.25
Genepop version 4.7.0	Population genetic analysis (HWE, LD, etc.)	/usr/local/bin/genepop	-	2017.12.07
FastQC	quality control application for high throughput sequence data	/usr/local/bin/FastQC	-	2017.10.03
SolexaQA	SolexaQA calculates sequence quality statistics and creates visual representations of data quality	/usr/local/bin/SolexaQA_3.1.7.1	-	2018.01.11
FLASH	fast length adjustment of short reads to improve genome assemblies	/usr/local/bin/FLASH-1.2.11	-	2018.01.11
Tag cleaner	automatically remove the tag sequences	/usr/local/bin/tagcleaner-standalone-0.16	-	2018.01.11
Uchime 4.2	Chimera exclusion in metabarcoding analysis	/usr/local/bin/uchime4.2.40_i86linux32	-	2018.01.18
Usearch 7.0	Metabarcoding sequence analysis	/usr/local/bin/usearch7.0.1001_i86linux32	-	2018.01.18
Usearch 8.1	Metabarcoding sequence analysis	/usr/local/bin/usearch8.1.1756_i86linux32	-	2018.01.18
DynamicTrim	Fastq data tail quality trimming	/usr/local/bin/DynamicTrim.pl	-	2018.01.18
Molphy-2.3b3	Molecular phylogenetic analysis	/usr/local/bin/molphy-2.3b3/	-	2018.01.18
RAxML 8.2.11	A tool for Phylogenetic Analysis and Post-Analysis of Large Phylogenies	/usr/local/bin/raxml/8.2.11/raxmlHPC-PTHREADS-AVX2	-	2018.01.26
prottest3	High Performance Computing selection of empirical models of aminoacid replacement	/usr/local/bin/prottest3/prottest-3.0/prottest-3.0.jar	-	2018.01.31
beagle 4.1	performs genotype calling, genotype phasing, imputation of ungenotyped markers, and identity-by-descent segment detection	/usr/local/bin/beagle/beagle_4.1	-	2018.02.01
Trinity-v2.6.5	RNA-Seq De novo Assembly Using Trinity	/usr/local/bin/trinityrnaseq-Trinity-v2.6.5	Trinity	2018.02.26
HISAT2	a fast and sensitive alignment program for mapping next-generation sequencing reads (both DNA and RNA)	/usr/local/bin/HISAT2/hisat2-2.1.0	-	2018.02.26

edgeR '3.18.1'	Differential expression analysis of RNA-seq expression profiles with biological replication	(package in R)	-	2018.02.26
StringTie v1.3.4	Transcript assembly and quantification for RNA-Seq	/usr/local/bin/stringtie/stringtie-1.3.4d.Linux_x86_64	-	2018.03.20
Subread package 1.6.0	high-performance read alignment, quantification and mutation discovery	/usr/local/bin/subread/subread-1.6.0-Linux-x86_64/bin	-	2018.03.20
jellyfish 2.2.9	fast, memory-efficient counting of k-mers in DNA	/usr/local/bin/jellyfish	jellyfish	2018.04.23
salmon v0.9.1	quantifying the expression of transcripts using RNA-seq data	/usr/local/bin/salmon-0.9.1/bin	salmon	2018.04.23
Augusutus	program that predicts genes in eukaryotic genomic sequences	/opt/augustus-3.3/bin	augustus(etc)	2018.07.13
HMMER	biosequence analysis using profile hidden Markov models	/usr/local/bin/hmmer-3.2.1/bin	-	2018.07.13
BUSCO	Assessing genome assembly and annotation completeness	/usr/local/bin/busco-3.0.1/scripts	-	2018.07.13
TreeMix 1.12	Inferring the patterns of population splits and mixtures in the history of a set of populations	/usr/local/bin/treemix	treemix	2019.05.07
ADMIXTURE 1.3.0	a software tool for maximum likelihood estimation of individual ancestries from multilocus SNP genotype datasets	/usr/local/bin/admixture	admixture	2019.05.14
qualimap	Graphical User Inteface (GUI) and a command-line interface to facilitate the quality control of alignment sequencing data and its derivatives like feature counts	/usr/local/bin/qualimap_v2.2.1		2019.08.08
deeptools	deepTools is a suite of python tools particularly developed for the efficient analysis of high-throughput sequencing data, such		deeptools	2019.08.08

	as ChIP-seq, RNA-seq or MNase-seq			
vcftools 0.1.16	VCFtools is to provide easily accessible methods for working with complex genetic variation data in the form of VCF files		vcftools	2019.09.09
Nextgenmap 0.5.5	NextGenMap (NGM) is a flexible and fast read mapping program that is more than twice as fast as BWA	/usr/local/bin/ngm-0.5.5	ngm (etc)	2019.09.09
ALLPATHS-LG 52488	de novo assembler	/usr/local/bin	RunAllPathsLG etc	2019/12/20
Platanus 1.2.4	Platanus is a novel de novo sequence assembler that can reconstruct genomic sequences of highly heterozygous diploids	/usr/local/bin/platanus	-	2019/12/20
matemaker	matemaker will generate a pair of fastq files (left and right) that consist of artificial mate-pairs generated from one or more sequences sent in as input	/usr/local/bin/matemaker	matemaker	2019/12/20
SSPACE Standard 3.0	SSPACE is a script able to extend and scaffold pre-assembled contigs using one or more mate pairs or paired-end libraries, or even a combination.	/usr/local/bin/SSPACE/SSPACE-STANDARD-3.0_linux-x86_64	-	2019/12/20
SSPACE Longread v1.1	SSPACE-LongRead is a stand-alone program for scaffolding pre-assembled contigs using long reads (e.g. PacBio RS reads).	/usr/local/bin/SSPACE/SSPACE-LongRead_v1-1	-	2019/12/20
ABySS v2.2.4	de novo sequence assembler intended for short paired-end reads and large genomes.	/usr/local/bin	abyss-pe etc.	2020/07/30
AdmixTools 7.0	a software package that supports formal tests of whether admixture occurred, and makes it possible to infer admixture proportions	/usr/local/bin	convertf, qpDstat, etc	2020/12/10

PLINK 1.90	open-source whole genome association analysis toolset	/usr/local/bin	plink	2020/12/10
eigensoft 7.2.1	Population structure and stratification correction	/usr/local/bin/eigensoft/EIG/bin	smartpca, eigenstrat	2020/12/18
Vsearch	de novo and reference based chimera detection, clustering, full-length and prefix dereplication...	/usr/local/bin	vsearch	2020/12/22
Quast	QUAST stands for QUality ASsessment Tool	/usr/local/bin/	quast.py	2020/12/20
cutadapt ver.3.1	Adapter/primer trimming	/usr/local/bin/	cutadapt3.1	2020/12/20
SPAdes 3.14.1	experimental pipeline for hybrid metagenome assembly	/usr/local/bin	spades.py etc	2020.12.22
fastp 0.21.0	A tool designed to provide fast all-in-one preprocessing for FastQ files	/usr/local/bin	fastp	2021.06.21

Last Modified: Dec. 22, 2020 (Shingo, Fujimoto)