インストール済みパッケージ一覧 (2018/1/22 現在)

下記以外のパッケージのセットアップもお気軽にご相談ください。

パッケージ名称	パッケージ内容
abacas	Algorithm Based Automatic Contiguation of Assembled Sequences
acedb-other	retrieval of DNA or protein sequences
acedb-other-belvu	multiple sequence alignment editor
acedb-other-dotter	visualisation of sequence similarity
adun.app	Molecular Simulator for GNUstep (GUI)
aegean	integrated genome analysis toolkit
aevol	digital genetics model to run Evolution Experiments in silico
alien-hunter	Interpolated Variable Order Motifs to identify horizontally acquired DNA
altree	program to perform phylogeny-based association and localization analysis
amap-align	Protein multiple alignment by sequence annealing
ampliconnoise	removal of noise from 454 sequenced PCR amplicons
anfo	Short Read Aligner/Mapper from MPG
aragorn	tRNA and tmRNA detection in nucleotide sequences
arden	specificity control for read alignments using an artificial reference
autodock	analysis of ligand binding to protein structure
autodock-vina	docking of small molecules to proteins
autogrid	pre-calculate binding of ligands to their receptor
bamtools	toolkit for manipulating BAM (genome alignment) files
barrnap	rapid ribosomal RNA prediction
bedtools	suite of utilities for comparing genomic features
blast2	Basic Local Alignment Search Tool
bowtie	Ultrafast memory-efficient short read aligner
bowtie2	ultrafast memory-efficient short read aligner
boxshade	Pretty-printing of multiple sequence alignments
bwa	Burrows-Wheeler Aligner
cassiopee	index and search tool in genomic sequences
cd-hit	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
circos	plotter for visualizing data
clearcut	extremely efficient phylogenetic tree reconstruction
clonalframe	inference of bacterial microevolution using multilocus sequence data
clustalo	General purpose multiple sequence alignment program for proteins
clustalw	global multiple nucleotide or peptide sequence alignment
concavity	predictor of protein ligand binding sites from structure and conservation
conservation-code	protein sequence conservation scoring tool
dialign	Segment-based multiple sequence alignment
dialign-tx	Segment-based multiple sequence alignment
discosnp	discovering Single Nucleotide Polymorphism from raw set(s) of reads
disulfinder	cysteines disulfide bonding state and connectivity predictor
dnaclust	tool for clustering millions of short DNA sequences
dssp	protein secondary structure assignment based on 3D structure
ecopcr	estimate PCR barcode primers quality
edtsurf	triangulated mesh surfaces for protein structures
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
emboss	European molecular biology open software suite
exonerate	generic tool for pairwise sequence comparison
fastaq	FASTA and FASTQ file manipulation tools
fastdnaml	Tool for construction of phylogenetic trees of DNA sequences
fastlink	faster version of pedigree programs of Linkage
fastqc	quality control 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
ffindex	simple index/database for huge amounts of small files
figtree	graphical phylogenetic tree viewer
filo	FILe and stream Operations
fitgcp	fitting genome coverage distributions with mixture models
flexbar	flexible barcode and adapter removal for sequencing platforms

freecontact	fast protein contact predictor
gamgi	General Atomistic Modelling Graphic Interface (GAMGI)
garlic	A visualization program for biomolecules
gasic	genome abundance similarity correction
gdpc	visualiser of molecular dynamic simulations
genometools	versatile genome analysis toolkit
gff2aplot	pair-wise alignment-plots for genomic sequences in PostScript
gff2ps	produces PostScript graphical output from GFF-files
ghemical	GNOME molecular modelling environment
giira	RNA-Seq driven gene finding incorporating ambiguous reads
glam2	gapped protein motifs from unaligned sequences
grinder	Versatile omics shotgun and amplicon sequencing read simulator
gromacs	Molecular dynamics simulator, with building and analysis tools
gwama	Genome-Wide Association Meta Analysis
hhsuite	sensitive protein sequence searching based on HMM-HMM alignment
hmmer	profile hidden Markov models for protein sequence analysis
hmmer2	profile hidden Markov models for protein sequence analysis
idba	iterative De Bruijn Graph De Novo short read assembler for transcriptome
infernal	inference of RNA secondary structural alignments
ipig	integrating PSMs into genome browser visualisations
jalview	multiple alignment editor
jellyfish	count k-mers in DNA sequences
jmol	Molecular Viewer
kalign	Global and progressive multiple sequence alignment
kissplice	Detection of various kinds of polymorphisms in RNA-seq data
kmer	suite of tools for DNA sequence analysis
last-align	genome-scale comparison of biological sequences
librg-utils-perl	parsers and format conversion utilities used by (e.g.) profphd
loki	MCMC linkage analysis on general pedigrees
ltrsift	postprocessing and classification of LTR retrotransposons
macs	Model-based Analysis of ChIP-Seq on short reads sequencers
macsyfinder	Detection of macromolecular systems in protein datasets.
mafft	Multiple alignment program for amino acid or nucleotide sequences
maq	maps short fixed-length polymorphic DNA sequence reads to reference sequences
maqview	graphical read alignment viewer for short gene sequences
massxpert	linear polymer mass spectrometry software
mauve-aligner	multiple genome alignment
melting	compute the melting temperature of nucleic acid duplex

metastudent	predictor of Gene Ontology terms from protein sequence
microbegps	explorative taxonomic profiling tool for metagenomic data
microbiomeutil	Microbiome Analysis Utilities
minia	short-read biological sequence assembler
mipe	Tools to store PCR-derived data
mira-assembler	Whole Genome Shotgun and EST Sequence Assembler
mlv-smile	Find statistically significant patterns in sequences
mothur	sequence analysis suite for research on microbiota
mrbayes	Bayesian Inference of Phylogeny
mummer	Efficient sequence alignment of full genomes
muscle	Multiple alignment program of protein sequences
mustang	multiple structural alignment of proteins
nast-ier	NAST-based DNA alignment tool
ncbi-blast+	next generation suite of BLAST sequence search tools
ncbi-epcr	Tool to test a DNA sequence for the presence of sequence tagged sites
ncbi-seg	tool to mask segments of low compositional complexity in amino acid sequences
ncbi-tools-bin	NCBI libraries for biology applications (text-based utilities)
ncbi-tools-x11	NCBI libraries for biology applications (X-based utilities)
ncoils	coiled coil secondary structure prediction
neobio	computes alignments of amino acid and nucleotide sequences
njplot	phylogenetic tree drawing program
norsnet	tool to identify unstructured loops in proteins
norsp	predictor of non-regular secondary structure
paraclu	Parametric clustering of genomic and transcriptomic features
parsinsert	Parsimonious Insertion of unclassified sequences into phylogenetic trees
pdb2pqr	Preparation of protein structures for electrostatics calculations
perlprimer	Graphical design of primers for PCR
perm	efficient mapping of short reads with periodic spaced seeds
phyml	Phylogenetic estimation using Maximum Likelihood
phyutility	simple analyses or modifications on both phylogenetic trees and data matrices
picard-tools	Command line tools to manipulate SAM and BAM files
plasmidomics	draw plasmids and vector maps with PostScript graphics export
plink	whole-genome association analysis toolset
poa	Partial Order Alignment for multiple sequence alignment
populations	population genetic software
prank	Probabilistic Alignment Kit for DNA, codon and amino-acid sequences
predictnls	prediction and analysis of protein nuclear localization signals
predictprotein	suite of protein sequence analysis tools

prime-phylo	bayesian estimation of gene trees taking the species tree into account
primer3	Tool to design flanking oligo nucleotides for DNA amplification
proalign	Probabilistic multiple alignment program
probabel	Toolset for Genome-Wide Association Analysis
probalign	multiple sequence alignment using partition function posterior probabilities
probcons	PROBabilistic CONSistency-based multiple sequence alignment
proda	multiple alignment of protein sequences
prodigal	Microbial (bacterial and archaeal) gene finding program
profbval	predictor of flexible/rigid protein residues from sequence
profisis	prediction of protein-protein interaction sites from sequence
profnet-bval	neural network architecture for profbval
profnet-chop	neural network architecture for profchop
profnet-con	neural network architecture for profcon
profnet-isis	neural network architecture for profisis
profnet-md	neural network architecture for metadisorder
profnet-norsnet	neural network architecture for norsnet
profnet-prof	neural network architecture for profacc
profnet-snapfun	neural network architecture for snapfun
profphd	secondary structure and solvent accessibility predictor
profphd-net	neural network architecture for profphd
profphd-utils	profphd helper utilities convert_seq and filter_hssp
proftmb	per-residue prediction of bacterial transmembrane beta barrels
progressivemauve	multiple genome alignment algorithms
pycorrfit	tool for fitting correlation curves on a logarithmic plot
pymol	Molecular Graphics System
pynast	alignment of short DNA sequences
pyscanfcs	scientific tool for perpendicular line scanning FCS
python-cogent	framework for genomic biology
qiime	Quantitative Insights Into Microbial Ecology
r-bioc-biostrings	GNU R string objects representing biological sequences
r-bioc-cummerbund	tool for analysis of Cufflinks RNA-Seq output
r-bioc-gviz	Plotting data and annotation information along genomic coordinates
r-bioc-hilbertvis	GNU R package to visualise long vector data
r-bioc-rtracklayer	GNU R interface to genome browsers and their annotation tracks
r-cran-ape	GNU R package for Analyses of Phylogenetics and Evolution
r-cran-genabel	GNU R package for genome-wide SNP association analysis
r-cran-phangorn	GNU R package for phylogenetic analysis
r-cran-qtl	GNU R package for genetic marker linkage analysis

r-cran-seqinr	GNU R biological sequences retrieval and analysis
r-cran-vegan	Community Ecology Package for R
r-other-bio3d	GNU R package for biological structure analysis
r-other-mott-happy.hbrem	GNU R package for fine-mapping complex diseases
rasmol	Visualize biological macromolecules
rate4site	detector of conserved amino-acid sites
raxml	Randomized Axelerated Maximum Likelihood of phylogenetic trees
ray	de novo genome assemblies of next-gen sequencing data
rdp-alignment	Ribosomal Database Project (RDP) alignment tools package
rdp-classifier	extensible sequence classifier for fungal lsu, bacterial and archaeal 16s
rdp-readseq	Ribosomal Database Project (RDP) sequence reading and writing
readseq	Conversion between sequence formats
relion-bin	toolkit for 3D reconstructions in cryo-electron microscopy
reprof	protein secondary structure and accessibility predictor
rna-star	ultrafast universal RNA-seq aligner
rnahybrid	Fast and effective prediction of microRNA/target duplexes
rtax	Classification of sequence reads of 16S ribosomal RNA gene
saint	Significance Analysis of INTeractome
samtools	processing sequence alignments in SAM and BAM formats
scythe	Bayesian adaptor trimmer for sequencing reads
seq-gen	simulate the evolution of nucleotide or amino acid sequences
seqan-apps	C++ library for the analysis of biological sequences
seqprep	stripping adaptors and/or merging paired reads of DNA sequences with overlap
seqtk	Fast and lightweight tool for processing sequences in the FASTA or FASTQ format
sibsim4	align expressed RNA sequences on a DNA template
sickle	windowed adaptive trimming tool for FASTQ files using quality
sigma-align	Simple greedy multiple alignment of non-coding DNA sequences
sim4	tool for aligning cDNA and genomic DNA
smalt	Sequence Mapping and Alignment Tool
snap	location of genes from DNA sequence with hidden markov model location of genes from DNA sequence with hidden markov model
snp-sites	Binary code for the package snp-sites
soapdenovo	short-read assembly method to build de novo draft assembly
soapdenovo2	short-read assembly method to build de novo draft assembly
squizz	Converter for genetic sequences and alignments
sra-toolkit	utilities for the NCBI Sequence Read Archive

ssake	genomics application for assembling millions of very short DNA sequences
stacks	pipeline for building loci from short-read DNA sequences
staden	DNA sequence assembly (Gap4/Gap5), editing and analysis tools
staden-io-lib-utils	programs for maniuplating DNA sequencing files
subread	toolkit for processing next-gen sequencing data
swarm	robust and fast clustering method for amplicon-based studies
t-coffee	Multiple Sequence Alignment
tabix	generic indexer for TAB-delimited genome position files
tensorflow	TensorFlow helps the tensors flow
theseus	superimpose macromolecules using maximum likelihood
tigr-glimmer	Gene detection in archea and bacteria
tm-align	structual alignment of proteins
tophat	fast splice junction mapper for RNA-Seq reads
toppred	transmembrane topology prediction
transdecoder	find coding regions within RNA transcript sequences
transtermhp	find rho-independent transcription terminators in bacterial genomes
tree-puzzle	Reconstruction of phylogenetic trees by maximum likelihood
treeviewx	Displays and prints phylogenetic trees
trimmomatic	flexible read trimming tool for Illumina NGS data
uc-echo	error correction algorithm designed for short-reads from NGS
ugene	integrated bioinformatics toolkit
vcftools	Collection of tools to work with VCF files
velvet	Nucleic acid sequence assembler for very short reads
velvetoptimiser	automatically optimise Velvet do novo assembly parameters
vsearch	tool for processing metagenomic sequences
wigeon	reimplementation of the Pintail 16S DNA anomaly detection utility
wise	comparison of biopolymers, like DNA and protein sequences
zalign	parallel local alignment of biological sequences