

已安装软件列表

Function	Name	Version	Webpage
Basic tools	BioPerl	1.6.0	www.bioperl.org
	picard	1.87	picard.sourceforge.net
	fastx_toolkit	0.13	hannonlab.cshl.edu/fastx_toolkit
	samtools	0.1.18	samtools.sourceforge.net
	R	2.11.1	www.r-project.org
	tabix	0.2.6	samtools.sourceforge.net/tabix.shtml
	BEDTools	v2.17	code.google.com/p/bedtools
	Python-2.7	2.7	www.python.org
	blast		blast.ncbi.nlm.nih.gov
Mapping	bwa	0.6.1	bio-bwa.sourceforge.net
	bowtie	2.0.2	bowtie-bio.sourceforge.net/bowtie2
Resequencing	GATK	2.4-7	www.broadinstitute.org/gatk/
	samtools	0.1.18	samtools.sourceforge.net
	vcftools	0.1.10	vcftools.sourceforge.net
RNA-seq	tophat	2.0.6	tophat.cbcb.umd.edu
	cufflinks	2.0.2	cufflinks.cbcb.umd.edu
	AStalavista	v2.2	genome.crg.es/astalavista
miRNA-seq	mireap	0.2	mireap.sourceforge.net
	miRDeep		www.mdc-berlin.de/rajewsky/miRDeep
	randfold	2.0	bioinformatics.psb.ugent.be/software/details/Randfold
	ViennaRNA	2.0.7h	www.tbi.univie.ac.at/RNA/
Other	cluster	1.50	http://rana.lbl.gov/EisenSoftwareSource.htm
	EVER-seq	1.0.7	code.google.com/p/ever-seq
	hmmSplicer	0.9.5	http://derisilab.ucsf.edu/index.php?software=105
	libpng	1.2.7	www.libpng.org/pub/png/libpng.html
	libsequence	1.7.5	molpopgen.org/software/libsequence.html
	meme	4.9.0	meme.nbcr.net
	nawk		gnuwin32.sourceforge.net/packages/nawk.htm
	numpy	1.7.0b2	www.numpy.org
	passion	1.2.1	https://trac.nbic.nl/passion/
	promoter	2.0	www.cbs.dtu.dk/services/Promoter
	RetroSeq	master	www.sanger.ac.uk/resources/software/retroseq
	RSeQC	2.3.3	code.google.com/p/rseqc
	smalt	0.5.7	www.sanger.ac.uk/resources/software/smalt
	snappy	1.0.3	code.google.com/p/snappy
	fastqc	0.10.0	www.bioinformatics.babraham.ac.uk/projects/fastqc/

注：1. 以上软件均安装在共享目录/home/share/bin/，详细功能请参照各自主页

2. 生物信息学软件开发市场一片繁荣，推陈出新速度惊人，在此所列软件必不能满足用户的所有需求，绝大多数情况下仍需要自行安装。

3. 软件更新信息将在植物细胞与染色体工程国家重点实验室网站/平台建设/数据分析平台(<http://pcce.genetics.cas.cn/ptjs/sjfx/>)上实时发布。