GenSAS v6.0

Available Tools

The below table lists the tools that have been integrated into GenSAS. Click on the tool name to be redirected to the tool website and documentation. We are working on updating many of the tools to the most current version. Click here for file with GenSAS tool and database references.

Category	Tool Name	Version	Description
Repeat Masking	RepeatMasker	4.1.1	Masks repeated sequences
	RepeatModeler	2.0.1	*de novo* repeat masker
Gene Prediction	Augustus	3.4.0	Eukaryotic gene predictor
	BRAKER2	2.1.5	Eukaryotic gene predictor
	GeneMarkES	4.48	Eukaryotic gene predictor
	GeneMarkS	4.32	Prokaryotic gene predictor
	Genscan	1.0	Eukaryotic gene predictor
	Glimmer3	3.0.2	Prokaryotic gene predictor
	GlimmerM	2.5.1	Eukaryotic gene predictor
	SNAP	11/29/2013	Semi-HMM-based Nucleic Acid Parser, gene predictor
Alignments	BLAST+	2.12.0	Alignment tool for transcripts and proteins
	pBLAT	2.5	Alignment tool for transcripts
	DIAMOND	2.0.6	Alignment tool for protein evidence
	HISAT2	2.2.1	Aligns RNA-seq reads to genome
	PASA	2.4.1	Aligns EST or transcript evidence
	TopHat	2.1.1	Aligns RNA-seq reads to genome
Genomic Features	Getorf	EMBOSS-6.6.0	Open reading frame finder
	RNAmmer	1.2	Finds rRNA sequences
	SSR Finder	N/A	Finds user defined simple sequence repeats
	tRNAScan-SE	2.0.7	Identifies tRNA sequences
Consensus Gene Models	EVidenceModeler	1.1.1	Creates consensus gene structures for eukaryotes
Functional Annotation	BLAST+	2.12.0	Alignment tool for proteins
	DIAMOND	2.0.6	Alignment tool for proteins
	InterProScan	5.53-87.0	Classifies proteins by families and identifies functional domains
	Pfam	1.6	Uses Pfam database to identify functional domains and families in proteins
	SignalP	5.0	Predicts signal peptide cleavage sites in protein sequences
	TargetP	2.0	Predicts the subcellular location of eukaryotic proteins based on signal peptide sequences
Genome Browser	Apollo	2.0.7	Annotation editor
	JBrowse	1.12.1	Genome browser
Assembly/annotation metrics	BUSCO	5.2.2	Determines genome assembly and annotation completeness based on orthologs
	One code to find them all	1.0	Reports repeat types from RepeatMasker
	PRINSEQ-lite	0.20.4	Used to analyze assembly file for sequence number and size