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| **Allpaths-lg (v44837)** | <ftp://ftp.broadinstitute.org/pub/crd/ALLPATHS/Release-LG/AllPaths-LG_Manual.pdf>  Our version is the pre-gcc4.7 requirement.  PATH: /share/apps/Installs/allpaths-44837/bin |
| **Augustus** | version: 2.7  Description: Augustus is a gene prediction software package. It is one of the gene predictors used by Maker. Augustus can be customized for use on a specific organism.  Path: /share/apps/Installs/Sickler/maker/exe/augustus/bin  <http://augustus.gobics.de/> |
| **BLAST** | 2 versions: 2.2.25 and 2.28  Description: The Basic Local Alignment Search Tool (BLAST) is probably the most widely used bioinformatics software suite. Version 2.2.25 is an older version of BLAST that is used by inparanoid. Version 2.28 is the current version of BLAST.  Path: version 2.2.25: /share/apps/Installs/Sickler/LegacyBlast/blast-2.2.25/bin  version 2.28: /share/apps/Installs/Sickler/maker/exe/blast/bin  Module for 2.28:  $ module load BLAST  <http://blast.ncbi.nlm.nih.gov/> |
| Bowtie2 | PATH: /share/apps/Installs/walls/bowtie2-2.1.0 |
| BWA | BWA is a software package for mapping low-divergent sequences against a large reference genome, such as the human genome.  PATH: /share/apps/Installs/walls/bwa-0.7.5a  <http://bio-bwa.sourceforge.net/bwa.shtml> |
| **ClustalW** | version: 2.1  Description: A command-line multiple sequence alignment program that can align both nucleotides and amino acids.  Path: /share/apps/Installs/Sickler/clustalw-2.1/bin  <http://www.clustal.org/> |
| **Crass**  **Crass cont’d** | V0.3.12 Description: CRisprASSembler<https://github.com/ctSkennerton/crass> module= crass  Path: /usr/local/bin/crass-0.3.12 |
| **Exonerate** | version: 2.2.0  Description: Exonerate improves the alignments of BLASTn and BLASTx by improving the ends of alignments where BLAST is often faulty.  Path: /share/apps/Installs/Sickler/maker/exe/exonerate/bin  <http://www.ebi.ac.uk/~guy/exonerate/> |
| fastStructure | PATH=$PATH:/share/apps/Installs/walls/fastStructure/fastStructure  export LD\_LIBRARY\_PATH=$LD\_LIBRARY\_PATH:/usr/local/lib64 |
| Galaxy (not supporting development at this time) | 10.39.6.10:8080 on campus  192.112.102.21:8080 off campus  http://galaxyproject.org/ |
| GCC and G++ | gcc version 4.4.7 20120313 (Red Hat 4.4.7-11)  /usr/bin/gcc  /usr/bin/g++ |
| GSL | GNU scientific libraries  PATH=$PATH:/share/apps/Installs/walls/gsl-1.16 |
| **Inparanoid** | version: 4.1  Description: Inparanoid will identify orthologs and paralogs between protein sequence sets. Inparanoid must be copied from its directory and unpacked into your working directory before it can be used.  Path: /share/apps/Installs/Sickler/inparanoid\_4.1.tar.gz  <http://inparanoid.sbc.su.se/cgi-bin/index.cgi> |
| **Jellyfish** | version: 1.1.10  Description: Jellyfish is a k-mer counting program designed to be fast and efficient.  Path: /share/apps/Installs/Sickler/jellyfish-1.1.10/bin  <http://www.cbcb.umd.edu/software/jellyfish/> |
| **Maker2.28** | NOT WORKING 4/4/2015  version: 2.28  Description: Maker is a gene annotation pipeline that combines the output of several programs to generate high quality gene annotations.  Path: /share/apps/Installs/Sickler/maker/bin  <http://www.yandell-lab.org/software/maker.html> |
| **Maker2.31** | Module Maker2.31  Path = /share/apps/Installs/Sickler/maker2.31/maker/bin |
| MaSuRCA | **MaSuRCA 2.3.2.** Tar is located at /share/apps/Installs/walls/MaSuRCA-2.3.2.tar.gz. Best option is to copy to home, tar xvzf the file and edit configuration file following instructions and run from home.  PATH = /share/apps/Installs/walls/MaSuRCA/MaSuRCA-2.1.0  ftp://ftp.genome.umd.edu/pub/MaSuRCA/MaSuRCA\_QuickStartGuide.pdf |
| **MUMmer** | version: 3.2.3  Description: MUMmer is a program that aligns entire genomes.  Path: /share/apps/Installs/Sickler/MUMmer3.2.3  <http://mummer.sourceforge.net/> |
| **Nseg** | Description: Nseg analyzes sequences for simple and tandem repeats.  Path: /share/apps/Installs/Sickler/nseg  <ftp://ftp.ncbi.nih.gov/pub/seg/nseg/> |
| **Perl** | version: 5.14  Description: Version 5.14 of the Perl programming language. The cluster uses 5.10 by default and the user must choose to use the new version.  Path: /opt/perl/bin  [www.perl.org](http://www.perl.org/) |
| **Python** | version: 2.7.3 and 3.2.1  Description: Like with perl, there exists by default an older version and the user must choose to use either of the new versions. Python is another programming language. Python right now has two versions (2 and 3) are similar but also incompatible with each other.  Path: /opt/python/bin  Commands: python2 – use python version 2.7.3  python3 – use python version 3.2.1.  [www.python.org](http://www.python.org/) |
| **QIIME** | Versions 1.7.0/1.8.0 and 1.9.0 installed |
| **Quake** | Description: Quake corrects errors in raw sequencing reads.  Path: /share/apps/Installs/Sickler/Quake/bin  <http://www.cbcb.umd.edu/software/quake/> |
| **R** | version: 3.0.1  Description: A pirate's favorite programming language. Can be used to efficiently calculate statistical and other mathematical algorithms.  Path: /share/apps/Installs/Sickler/R-3.0.1/bin  <http://www.r-project.org/> |
| **Ray** | Ray assembler: Ray is a parallel software that computes *de novo* genome assemblies with next-generation sequencing data.  Modulefile: Ray |
| **RepeatMasker** | version: 4.0.2  Description: RepeatMasker scans a genome and masks repetitive elements from the genome. RepeatMasker can also be used with a custom library of repeats from an organism.  Path: /share/apps/Installs/Sickler/maker/exe/RepeatMasker  <http://www.repeatmasker.org/> |
| **RepeatScout** | version: 1.0.5  Description: RepeatScout scans a genome to generate a custom library of repetitive elements for use in RepeatMasker.  Path: /share/apps/Installs/Sickler/RepeatScout-1 |
| **samtools** | Utilities for the Sequence Alignment/Map (SAM) format  http://samtools.sourceforge.net/samtools.shtml#1  Modulefile: samtools  PATH=$PATH://share/apps/Installs/walls/samtools-0.1.19 |
| **SNAP** | version: 2006-07-28  Description: SNAP is another gene predictor that is used by Maker. SNAP has its own additional programs that can be used to analyze an annotation set and train SNAP based on those results.  Path: /share/apps/Installs/Sickler/maker/exe/snap  <http://korflab.ucdavis.edu/software.html> |
| **SOAPdenovo2 and GapCloser** | version: SOAPDenovo2: 2.04 GapCloser: 1.12  Description: SOAPdenovo2 is a genome assembler suite. GapCloser improves the quality of an assembly.  Path: /share/apps/Installs/Sickler/SOAP/bin  <http://sourceforge.net/projects/soapdenovo2/>  Module: SOAPdenovo2 |
| **Spade** | Smart Python multi-Agent Development Environment  10.39.6.10:8008 if running  <http://pythonhosted.org/SPADE/spade.basic.html> |
| **SPAdes** | http://spades.bioinf.spbau.ru/release2.5.1/manual.html  PATH: /share/apps/Installs/walls/SPAdes/SPAdes-2.5.1-Linux/bin  Module: SPAdes-2.5.1 |
| **structure** | PATH=$PATH://share/apps/Installs/walls/console |
| **Trinity** | de novo reconstruction of transcriptomes from RNA-seq data. Trinity combines three independent software modules: Inchworm, Chrysalis, and Butterfly, applied sequentially to process large volumes of RNA-seq reads.  Modulefile: trinity  PATH=$PATH://share/apps/Installs/walls/ trinityrnaseq\_r20131110  trinity.py |
| **Velvet** | v1.2.10  Sequence assembler for very short reads  https://www.ebi.ac.uk/~zerbino/velvet/ |
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