

XIII. Appendix

Table: Third Party tools list and reference

Tools	Source/Reference	License	Citation
Parallel-ForkManager-1.03	http://search.cpan.org/~szabgab/Parallel-ForkManager-1.06/lib/Parallel/ForkManager.pm	Artistic License/GPL v1	
String-Approx-3.27	http://search.cpan.org/~jhi/String-Approx-3.27/Approx.pm	Artistic License/GPL v1	
PDF-API2-2.020	http://search.cpan.org/~ssimms/PDF-API2-2.020/lib/PDF/API2.pm	Artistic License/GPL v1	
Excel-Writer-XLSX-0.71	http://search.cpan.org/~jmcnamara/Excel-Writer-XLSX-0.76/lib/Excel/Writer/XLSX.pm	Artistic License/GPL v1	
bowtie2-2.1.0.	http://bowtie-bio.sourceforge.net/bowtie2/index.shtml	GPLv3	Langmead, B. and Salzberg, S.L. (2012) Fast gapped-read alignment with Bowtie 2, <i>Nature methods</i> , 9 , 357-359.
bwa-0.7.9	http://bio-bwa.sourceforge.net/	GPLv3	Li, H. and Durbin, R. (2009) Fast and accurate short read alignment with Burrows-Wheeler transform, <i>Bioinformatics</i> , 25 , 1754-1760.
idba-1.1.1	http://i.cs.hku.hk/~alse/hkubrg/projects/idba_ud/	GPLv2	Peng, Y., <i>et al.</i> (2012) IDBA-UD: a de novo assembler for single-cell and metagenomic sequencing data with highly uneven depth, <i>Bioinformatics</i> , 28 , 1420-1428.
MUMmer3.23	http://mummer.sourceforge.net/	GPLv3	Kurtz, S., <i>et al.</i> (2004) Versatile and open software for comparing large

R-2.15.3	http://www.r-project.org/	GPLv2	genomes, <i>Genome biology</i> , 5 , R12. R Core Team (2013). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL http://www.R-project.org/ .
samtools-0.1.19	http://samtools.sourceforge.net/	MIT	Li, H., <i>et al.</i> (2009) The Sequence Alignment/Map format and SAMtools, <i>Bioinformatics</i> , 25 , 2078-2079.
glimmer302b	http://ccb.jhu.edu/software/glimmer/index.shtml	Artistic License	Delcher, A.L., <i>et al.</i> (2007) Identifying bacterial genes and endosymbiont DNA with Glimmer, <i>Bioinformatics</i> , 23 , 673-679.
primer3-2.3.5	http://primer3.sourceforge.net/	GPLv2	Untergasser, A., <i>et al.</i> (2012) Primer3--new capabilities and interfaces, <i>Nucleic acids research</i> , 40 , e115.
KronaTools-2.4	http://sourceforge.net/projects/krona/	BSD	Ondov, B.D., Bergman, N.H. and Phillippy, A.M. (2011) Interactive metagenomic visualization in a Web browser, <i>BMC bioinformatics</i> , 12 , 385.
parallel-20130822	http://www.gnu.org/software/parallel/	GPLv3	O. Tange (2011): GNU Parallel - The Command-Line Power Tool, ;login: The USENIX Magazine, February 2011:42-47
metaphlan-1.7.7	http://huttenhower.sph.harvard.edu/metaphlan	Artistic License	Segata, N., <i>et al.</i> (2012) Metagenomic microbial community profiling using unique clade-specific marker genes, <i>Nature methods</i> , 9 , 811-814.
MetaPhylerSRV0.115	http://metaphyler.cbcb.umd.edu/	N.A	Liu, B., <i>et al.</i> (2011) Accurate and fast estimation of taxonomic profiles from metagenomic shotgun sequences, <i>BMC genomics</i> , 12 Suppl 2 , S4.
RATT	http://ratt.sourceforge.net/	N.A	Otto, T.D., <i>et al.</i> (2011) RATT: Rapid

ncbi-blast-2.2.28+-x64-linux	ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/2.2.28/	Public domain	Annotation Transfer Tool, <i>Nucleic acids research</i> , 39 , e57.
blast-2.2.26-x64-linux	ftp://ftp.ncbi.nlm.nih.gov/blast/executables/release/2.2.6/	Public domain	Camacho, C., <i>et al.</i> (2009) BLAST+: architecture and applications, <i>BMC bioinformatics</i> , 10 , 421.
infernai-1.1rc4 linux64.tbl2asn	http://infernai.janelia.org/ http://www.ncbi.nlm.nih.gov/genbank/tbl2asn2/	GPLv3 N.A	Altschul, S.F., <i>et al.</i> (1990) Basic local alignment search tool, <i>Journal of molecular biology</i> , 215 , 403-410.
prodigal.v2_60	http://prodigal.ornl.gov/	GPLv3	Nawrocki, E.P. and Eddy, S.R. (2013) Infernal 1.1: 100-fold faster RNA homology searches, <i>Bioinformatics</i> , 29 , 2933-2935.
aragorn1.2.36	http://mbio-serv2.mbioekol.lu.se/ARAGORN/	N.A	Hyatt, D., <i>et al.</i> (2010) Prodigal: prokaryotic gene recognition and translation initiation site identification, <i>BMC bioinformatics</i> , 11 , 119.
hmmer-3.1b1	http://hmmer.janelia.org/	GPLv3	Laslett, D. and Canback, B. (2004) ARAGORN, a program to detect tRNA genes and tmRNA genes in nucleotide sequences, <i>Nucleic acids research</i> , 32 , 11-16.
prokka-1.9	http://www.vicbioinformatics.com/software.prokka.shtml	GPLv2	Eddy, S.R. (2011) Accelerated Profile HMM Searches, <i>PLoS computational biology</i> , 7 , e1002195
barrnap-0.4.2.tar.gz	http://www.vicbioinformatics.com/software.barrnap.shtml	GPLv3	Seemann, T. (2014) Prokka: rapid prokaryotic genome annotation, <i>Bioinformatics</i> .
tRNAscan-SE.1.3.1	http://lowelab.ucsc.edu/tRNAscan-SE/	GPLv2	Lowe, T.M. and Eddy, S.R. (1997)

			tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence, <i>Nucleic acids research</i> , 25 , 955-964.
phage_finder_v2.1	http://phage-finder.sourceforge.net/	GPLv3	Fouts, D.E. (2006) Phage_Finder: automated identification and classification of prophage regions in complete bacterial genome sequences, <i>Nucleic acids research</i> , 34 , 5839-5851.
kraken-0.10.4-beta	http://ccb.jhu.edu/software/kraken/	GPLv3	Wood, D.E. and Salzberg, S.L. (2014) Kraken: ultrafast metagenomic sequence classification using exact alignments, <i>Genome biology</i> , 15 , R46.
JBrowse-1.11.3	http://jbrowse.org	Artistic License 2.0/LGPLv.1	Skinner, M.E., <i>et al.</i> (2009) JBrowse: a next-generation genome browser, <i>Genome research</i> , 19 , 1630-1638.
bedtools-2.19.1	https://github.com/arq5x/bedtools2	GPLv2	Quinlan, A.R. and Hall, I.M. (2010) BEDTools: a flexible suite of utilities for comparing genomic features, <i>Bioinformatics</i> , 26 , 841-842.
HTML-Template-2.6	http://search.cpan.org/~wonko/HTML-Template-2.95/lib/HTML/Template.pm	Artistic License/GPL v1	
Archive-Zip-1.37	http://search.cpan.org/~phred/Archive-Zip-1.37/lib/Archive/Zip.pm	Artistic License/GPL v1	
gridExtra_0.9.1	http://cran.r-project.org/web/packages/gridExtra/index.html	GPLv2	
wigToBigWig	https://genome.ucsc.edu/goldenPath/help/bigWig.html#Ex3	Open source	Kent, W.J., <i>et al.</i> (2010) BigWig and BigBed: enabling browsing of large distributed datasets, <i>Bioinformatics</i> , 26 , 2204-2207.

tabix	http://sourceforge.net/projects/samtools/files/tabix/	N.A	
RAxML-8.0.26	http://sco.hits.org/exelixis/web/software/raxml/index.html	GPLv2	Stamatakis,A. 2014. RAxML version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics
FastTree2.1.7	http://www.microbesonline.org/fasttree/	GPLv2	Morgan N. Price, Paramvir S. Dehal, and Adam P. Arkin. 2009. FastTree: Computing Large Minimum Evolution Trees with Profiles instead of a Distance Matrix. Mol Biol Evol (2009) 26 (7): 1641-1650
HTML-Parser-3.71	http://search.cpan.org/dist/HTML-Parser/lib/HTML/Entities.pm	Artistic License/GPL v1	
JSON-2.90	http://search.cpan.org/~makamaka/JSON-2.90/lib/JSON.pm	Artistic License/GPL v1	
