**Some Phylogenetics Tools**

\*free = can be downloaded for free

\*online = online tool, no downloading necessary

**Websites that Compile Links to Tools**

<http://www.charite.de/bioinf/strap/links.html>

[http://evolution.genetics.washington.edu/phylip/software.pars.html](http://evolution.genetics.washington.edu/phylip/software.pars.html#PaupUp)

<http://en.wikipedia.org/wiki/List_of_phylogenetic_tree_visualization_software>

<http://www.expasy.org/genomics/sequence_alignment>

**Dealing with Raw Sequence Data**

**Lasergene**

<http://health.library.emory.edu/biomedical-resources/basic-sciences/analysis-tools/lasergene.html>

Within the Lasergene Package, **SeqMan Pro** allows you to assemble sanger sequences and export them as Fasta files for further analysis.

\* free through Emory Library

**Comprehensive Analysis Programs**

**Geneious**

<http://www.geneious.com/web/geneious/home>

Available for most platforms

The Pro version is absurdly expensive, particularly if you are not a student. It does allow you to use PAUP and also has many bioinformatics tools.

**Mesquite**

<http://mesquiteproject.org/mesquite/mesquite.html>

available for most platforms

Mesquite requires various packages and has a lot of tools to test hypotheses based on phylogenies.

The package for alignment is called **ALIGN.**

\*free

**MEGA**

<http://www.megasoftware.net/index.php>

available for most platforms

basic sequence manipulation, create draft neighbor joining tree, align in CLUSTAL/Muscle. The book *Phylogenetc Trees Made Easy* is a step by step guide to using MEGA.

\*free

**Computational Sequence Alignment**

**ClustalW**

<http://www.ebi.ac.uk/Tools/msa/clustalw2/>

Clustal is built into many software packages

\*free

\*online

**Clustal Omega**

<http://www.clustal.org/omega/>

Follow-up to ClustalW

\*free

\*online

**Muscle**

<http://www.ebi.ac.uk/Tools/msa/muscle/>

Muscle is built into many software packages

\*free

\*online

**T-Coffee**

<http://tcoffee.crg.cat/>

\*free

\*online

**TranslatorX**

<http://translatorx.co.uk/>

allows you to use amino acid information to align nucleotide sequences

\*free

\*online

**Manual Sequence Alignment**

*All computational tools for sequence alignment have limits. You should always look at your alignment carefully and make obvious adjustments manually. You will also may want to trim the ends of sequences if some are much longer than others, etc. There is no perfect solution to do this.*

**BioEdit**

<http://www.mbio.ncsu.edu/BioEdit/bioedit.html>

windows only

a great, easy to use program; unfortunately no longer being maintained

\*free

**Mesquite**

<http://mesquiteproject.org/mesquite/mesquite.html>

available for most platforms

The package for alignment is called **ALIGN.**

\*free

**SeaView**

<http://pbil.univ-lyon1.fr/software/seaview.html>

available for most platforms

basic sequence manipulation, create draft neighbor joining tree, align in CLUSTAL/Muscle

\*free

**Lasergene**

<http://health.library.emory.edu/biomedical-resources/basic-sciences/analysis-tools/lasergene.html>

Within the Lasergene Package, **MegAlign** allows you to do multiple alignments using Clustal and has some basic sequence editing features.

\*free through Emory Library

**Selection of Model of Evolution**

**jModelTest**

<http://code.google.com/p/jmodeltest2/>

This program is an independent tool used to carry out statistical selection of best-fit models of nucleotide substitution without the aid of PAUP\*. It implements five different model selection strategies: hierarchical and dynamical likelihood ratio tests (hLRT and dLRT), Akaike and Bayesian information criteria (AIC and BIC), and a decision theory method (DT). It also provides estimates of model selection uncertainty, parameter importances and model-averaged parameter estimates, including model-averaged phylogenies. Although jModelTest it is optimized for MacOS X Intel, executables are provided to run the program under MacOS X PPC, Windows XP and Linux.

\*free

**MrModelTest**

<http://www.abc.se/~nylander/mrmodeltest2/mrmodeltest2.html>

\*free though requires PAUP.

**Prottest 3**

<http://code.google.com/p/prottest3/>

For selecting best fit model of protein evolution

\*free

**Phylogeny Reconstruction – Likelihood**

**Garli**

<https://code.google.com/p/garli/>

Available for most platforms

Likelihood methods. Much faster at generating trees than likelihood methods implemented in PAUP and some other programs.

\*free

**PAUP\***

<http://paup.csit.fsu.edu/>

Still a gold standard for parsimony, distance and likelihood analyses

Unfortunately, you pay $85 to $100 for a command line version. There is a way to use PAUP through Geneious (see above)

**Phylip**

<http://evolution.genetics.washington.edu/phylip/general.html>

guide to using Phylip: <http://koti.mbnet.fi/tuimala/oppaat/phylip2.pdf>

\*free

**PhyML**

<http://www.atgc-montpellier.fr/phyml/>

\*free

\*online

**Phylogeny Reconstruction – Bayesian**

**BEAST**

<http://beast.bio.ed.ac.uk/>

BEAST is a cross-platform program for Bayesian MCMC analysis of molecular sequences. It is entirely orientated towards rooted, time-measured phylogenies inferred using strict or relaxed molecular clock models. It can be used as a method of reconstructing phylogenies but is also a framework for testing evolutionary hypotheses without conditioning on a single tree topology.

\*free

**MrBayes**

<http://mrbayes.sourceforge.net/>

Available for most platforms

Bayesian Methods.

\*free

**Tracer**

<http://tree.bio.ed.ac.uk/software/tracer/>

Tracer is a program that takes the output from a MrBayes run and allows you to confirm that your parameters have converged.

\*free

**Tree Viewing**

**FigTree**

<http://tree.bio.ed.ac.uk/software/figtree/>

\*free

**Dendroscope**

<http://ab.inf.uni-tuebingen.de/software/dendroscope/>

\*free

**Other Useful Tools**

**Sequence Alignment Converter**

<http://sequenceconversion.bugaco.com/converter/biology/sequences/index.php>

Why does every program require a different file format? Convert from one to the other here.

\*free

\*online

**Ribosomal RNAs**

Ribosomal RNA sequences, particularly 16s sequences of bacteria, are still the predominant sequence type used for constructing microbial phylogenies. Part of this is historical; once others have deposited rRNA sequences for organisms that you want to use as a comparison, then you too have to sequence the rRNA to facilitate comparison. One important point of consideration is that the evolution of ribosomal RNAs is tightly linked to how they fold. Several alignment methods have been developed to both fold and align RNA sequences. Links to many of these tools are available at: <http://molbiol-tools.ca/RNA_analysis.htm>

**Reference Books**

Baum, D. A. & S.D. Smith. 2013. *Tree Thinking: An Introduction to Phylogenetic Biology*. Roberts and Company.

Hall, B.C. 2011. *Phylogenetic Trees Made Easy, A How to Manual*. Sinauer Associates.

Lemey, P., Salemi, M. & A.M. Vandamme. 2009. *The Phylogenetic Handbook.* Cambridge University Press.