

ACTION FLOW

Software, File Format

DNA or protein sequences, edited

Editing: BioEdit, Sequencher
(format: fasta)

Make alignment

(insert gaps, adjust ends)

= Data matrix of aligned sequences

(if wanted, code indels as additional characters)

Automatic: BioEdit, Clustal
MUSCLE, MAFFT, POY,
Se-AI

Manual: BioEdit, Sequencher
Format: Nexus, fasta, aln
Coding gaps: Seqstate

Run phylogenetic analyses

(settings, models, branch support)

3 basic methods for
tree building

**Estimate molecular
evolution model**

Software: jModeltest

**Maximum
parsimony (MP)**

Software: PAUP,
Winclada, NONA,
TNT, MEGA5,
PHYLIP, POY

**Maximum
likelihood (ML)**

Software: GARLI,
PAUP, PhyML,
RaxML, MEGA5,
PHYLIP

Bayesian

Software: PAUP,
MrBayes, BEAST,
BayesPhylogenies

3 basic methods for
branch support
analysis: bootstrap,
jackknife, Bayesian
posterior probability

Save tree and log files

(consensus trees, branch support values)

Consensus trees: strict or
majority rule
Format: .tre, at end of nexus
file

View tree files

(trace character evolution, compare trees,
phylograms with branch lengths)

Tree editing and manipulation:
TreeView, FigTree, Winclada,
Mesquite, MacClade,
PHYLIP, BayesTraits,
BayesTrees,

Figure for publication

Use Treeviewing software,
save as: emf, png, jpg
Edit in Illustrator (import emf
file).
Powerpoint (only presentation,
insert emf file)

Software links

BayesTraits etc.	http://www.evolution.reading.ac.uk/SoftwareMain.html
BEAST	http://beast.bio.ed.ac.uk/Main_Page
BioEdit	http://www.mbio.ncsu.edu/bioedit/bioedit.html
Clustal *	http://www.clustal.org/
FigTree	http://tree.bio.ed.ac.uk/software/figtree/
GARLI *	https://www.nescent.org/wg_garli/Main_Page
Geneious \$	http://www.geneious.com
MAFFT *	http://mafft.cbrc.jp/alignment/software/
MEGA 5	http://www.megasoftware.net/
Modeltest	http://darwin.uvigo.es/software/jmodeltest.html
MrBayes *	http://mrbayes.csit.fsu.edu/
MUSCLE *	http://www.drive5.com/muscle/
NONA	http://www.cladistics.com/
PAUP \$*	http://paup.csit.fsu.edu/
PaupUp	http://www.agro-montpellier.fr/sppe/Recherche/JFM/PaupUp/main.htm
PHYLIP	http://evolution.genetics.washington.edu/phylip.html
PhyML #	http://www.atgc-montpellier.fr/phyml/
POY *	http://research.amnh.org/scicomp/scripts/download.php
RaxML *	http://mac.softpedia.com/get/Math-Scientific/RAXML.shtml
SeqBoot *	http://evolution.genetics.washington.edu/phylip/doc/seqboot.html
SeqState	http://bioinfweb.info/Software/SeqState
Sequencher \$	http://www.genecodes.com/
TNT	http://www.cladistics.com/
TreeView	http://taxonomy.zoology.gla.ac.uk/rod/treeview.html
Winclada	http://www.cladistics.com/

\$ = not free

* = available for free at CIPRES for online analysis: <http://www.phylo.org/>

= available for free at ACTG-Montpelier for online analysis: <http://www.atgc-montpellier.fr/>

(more links and descriptions here: <http://softlinks.amnh.org/phylogeny.html>)