

# 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)