

The toolbox

These are programs, servers, formats and the like which you may find helpful. Basically, you will use tools such as these to solve tasks given to you.

Software available as modules:

- For aligning sequences, we suggest KALIGN.
- For parsimony-based tree reconstruction, you can use dnapars or protpars from the PHYLIP package.
- For distance-based tree reconstruction, you can use belvu. Belvu can also generate a distance matrix for you, alternately, you can feed it an alignment and get a distance matrix out.
- For bootstrapped distance-based tree reconstruction, you can feed belvu an alignment and ask for a set of bootstrapped trees back. These can then be fed into PHYLIPs consense program to get a consensus tree.
- For sequence searches and finding homologs, use blast.
- For detecting Pfam domains, use HMMPFAM in the HMMER package.
- Dotter for dotplotting.

Online tools:

- [TreeView](#) for viewing trees.
- [GRIMM](#), a tool for gene order analysis
- [BioMart](#) (use MartView) is a nice site to get cross-references between databases, name schemata etc. Sometimes it is not complete, sometimes it is not updated, sometimes it is plain wrong, but for these purposes it suffices.