

S9 Text: Practical sessions for Phylogeny analyses (pdf).

Bioinformatics and Genome Analyses

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<https://webext.pasteur.fr/tekaia/BCGAIPT2017.html>

Consider SPO11.1.pep and SPO11.1.dna files including yeast and one fungi orthologs to construct phylogenetic trees.

We will consider the following tree construction methods in the Phylip package:

- 1- Neighbor joining method,
- 2- Parsimony method.
- 3- ML (Maximum likelihood) method

In all *Phylip* programs the input file is “infile” and the output file is “outfile”;
(in many circumstances the *outfile* of one program is the *infile* for the next program!)

Simple procedure:

- 0) mutiple alignment output : SPO11.1.phy
- 1) copy SPO11.1.phy into *infile*
- 2) *Protdist* (for dna: *dnadist*)
- 3) copy *outfile* into *infile*
- 4) *neighbor*
- 5) read the output file *outfile*

Procedure with bootstrapping:

- 1) align the sequences using the “clustalw” program;
- 2) use “seqboot” to construct a sample of 100 multiple alignments
- 3) use “protdist” to construct protein distances table;
- 4) “neighbor” program (using NJ method)
- 5) Copy “outtree” in “intree”
- 6) use “consense” program to construct consensus tree;

- 1) seqboot (100 samples, seed=113);
- 2) copy *outfile* into *infile*
- 3) Protdist (proteins) - dnadist (dna seq)
- 4) copy *outfile* into *infile*
- 5) neighbor
- 6) copy *outtree* into *intree*
- 7) consens

the obtained tree is the consensus tree

Parsimony method:

Run 1

Copy SPO11.1.pep.phy into infile
protpars

Run 2

seqboot

protpars
consense

Run 3

Copy SPO11.1.dna.phy into infile
dnapars

Run 4

seqboot
dnapars
consense

ML method:
SPO11.1.pep.phy
proml

SPO11.1.dna.phy
dnaml

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