# PhyML – Manual

Version 3.0
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http://www.atgc-montpellier.fr/phyml

# Contents

# 1 Citation

- PhyML: "A simple, fast and accurate algorithm to estimate large phylogenies by maximum likelihood" Guindon S., Gascuel O. 2003, *Systematic Biology*, **52**(5):696-704
- PhyTime: "Bayesian estimation of divergence times from large sequence alignments" Guindon S. 2010, *Molecular Biology and Evolution*, **27**(8):1768-81

# 2 Availability

- Binaries: http://www.atgc-montpellier.fr/phyml
- Sources: http://code.google.com/p/phyml
- Discussion forum: http://groups.google.com/group/phyml-forum

# 3 Authors

- Stéphane Guindon and Olivier Gascuel conceived the original PhyML algorithm.
- Stéphane Guindon conceived the PhyTime method.
- Stéphane Guindon, Wim Hordjik and Olivier Gascuel conceived the SPR-based tree search algorithm.
- Maria Anisimova and Olivier Gascuel conceived the aLRT method for branch support.
- Stéphane Guindon, Franck Lethiec, Jean-Francois Dufayard and Vincent Lefort implemented PhyML.
- Jean-Francois Dufayard created the benchmark and implemented the tools that are used to check PhyML accuracy and performances.
- Vincent Lefort, Stéphane Guindon, Patrice Duroux and Olivier Gascuel conceived and implemented PhyML web server.
- Stéphane Guindon wrote this document.

# 4 Overview

PhyML [1] is a software package which primary task that is to estimate maximum likelihood phylogenies from alignments of nucleotide or amino acid sequences. It provides a wide range of options that were designed to facilitate standard phylogenetic analyses. The main strengths of PhyML lies in the large number of substitution models coupled to various options to search the space of phylogenetic tree topologies, going from very fast and efficient methods to slower but generally more accurate approaches. It also implements two methods to evaluate branch supports in a sound statistical framework (the non-parametric bootstrap and the approximate likelihood ratio test,)

PhyML was designed to process moderate to large data sets. In theory, alignments with up to 4,000 sequences 2,000,000 character-long can analyzed. In practice however, the amount of memory required to process a data set is proportional of the product of the number of sequences by their length. Hence, a large number of sequences can only be processed provided that they are short. Also, PhyML can handle long sequences provided that they are not numerous. With most standard personal computers, the "comfort zone" for PhyML generally lies around 100-200 sequences less than 2,000 character long. For larger data sets, we recommend using other software's such as RAxML [2] or GARLI [3] or Treefinder (http://www.treefinder.de).

# 5 Installing PhyML

## 5.1 Sources and compilation

The sources of the program are available free of charge by sending an e-mail to Stéphane Guindon at guindon@lirmm.fr or guindon@stat.auckland.ac.nz.

The compilation on UNIX-like systems is fairly standard. It is described in the 'INSTALL' file that comes with the sources. In a command-line window, go to the directory that contains the sources and type:

```
./configure;
make clean;
make;
```

*Note* – when PhyML is going to be used mostly of exclusively in batch mode, it is preferable to turn on the batch mode option in the Makefile. In order to do so, the file `Makefile.am` needs to be modified: add `-DBATCH` to the line with `DEFS=-DUNIX -D$(PROG) -DDEBUG`.

## 5.2 Installing PhyML on UNIX-like systems (including Mac OS)

Copy PhyML binary file in the directory you like. For the operating system to be able to locate the program, this directory must be specified in the global variable `PATH`. In order to achieve this, you will have to add `export PATH="/your_path/:$PATH"` to the `.bashrc` or the `.bash_profile` located in your home directory (`your_path` is the path to the directory that contains PhyML binary).

## 5.3 Installing PhyML on Microsoft Windows

Copy the files `phyml.exe` and `phyml.bat` in the same directory. To launch PhyML, click on the icon corresponding to `phyml.bat`. Clicking on the icon for `phyml.exe` works too but the dimensions of the window will not fit PhyML interface.

## 5.4 Installing the parallel version of PhyML

Bootstrap analysis can run on multiple processors. Each processor analyses one bootstraped dataset. Therefore, the computing time needed to perform $R$ bootstrap replicates is divided by the number of processors available.

This feature of PhyML relies on the MPI (Message Passing Interface) library. To use it, your computer must have MPI installed on it. In case MPI is not installed, you can dowload it from http://www.mcs.anl.gov/research/projects/mpich2/. Once MPI is installed, a few modification of the file '`Makefile.am`' (in the `src/` directory) must be applied. The relevant section of this file and the instruction to add or remove the MPI option to PhyML are printed below:

```
# Uncomment (i.e. remove the '#' character at the begining of)
# the two lines below if you want to use MPI.
# Comment the two lines below if you don't want to use MPI.

# CC=mpicc
# DEFS=-DUNIX -D$(PROG) -DDEBUG -DMPI

# Comment the line below if you want to use MPI.
# Uncomment the line below if you don't want to use MPI.

DEFS=-DUNIX -D$(PROG) -DDEBUG
```

# 6 Program usage.

PhyML has two distinct user-interfaces. The first interface is probably the most popular. It corresponds to a PHYLIP-like text interface that makes the choice of the options self-explanatory (see Figure 1). The command-line interface is well-suited for people that are familiar with PhyML options or for running PhyML in batch mode.

## 6.1 PHYLIP-like interface

The default is to use the PHYLIP-like text interface (Figure 1) by simply typing '`phyml`' in a command-line window or by clicking on the PhyML icon (see Section 5.3). After entering the name of the input sequence file, a list of sub-menus helps the users to set up the analysis. There are currently four distinct sub-menus:

1. *Input Data*: specify whether the input file contains amino-acid or nucleotide sequences. What the sequence format is (see Section 7) and how many data sets should be analysed.

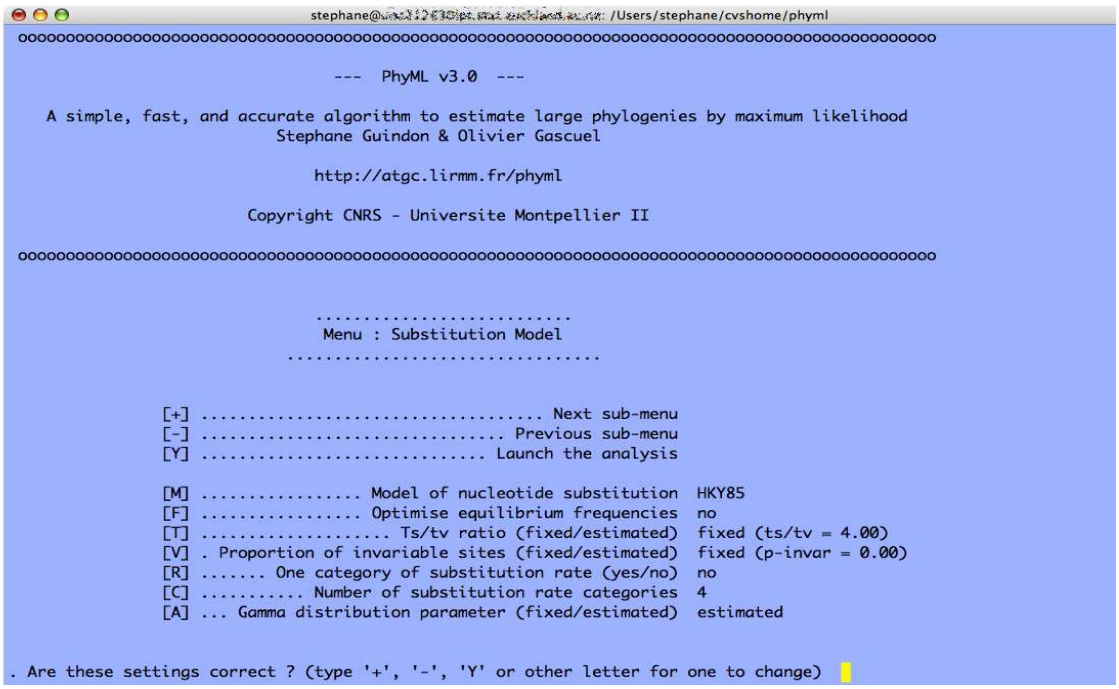


Figure 1. PHYLIP-like interface to PhyML.

2. *Substitution Model*: selection of the Markov model of substitution.
3. *Tree Searching*: selection of the tree topology searching algorithm.
4. *Branch Support*: selection of the method that is used to measure branch support.

'+' and '-' keys are used to move forward and backward in the sub-menu list. Once the model parameters have been defined, typing 'Y' (or 'y') launches the calculations. The meaning of some options may not be obvious to users that are not familiar with phylogenetics. In such situation, we strongly recommend to use the default options. As long as the format of the input sequence file is correctly specified (sub-menu *Input data*), the safest option for non-expert users is to use the default settings.

The different options provided within each sub-menu are described in what follows.

### 6.1.1 Input Data sub-menu

```
[D] ............................  Data type (DNA/AA)
```

Type of data in the input file. It can be either DNA or amino-acid sequences in PHYLIP format (see Section 7). Type D to change settings.

```
[I] ......  Input sequences interleaved (or sequential)
```

PHYLIP format comes in two flavours: interleaved or sequential (see Section 7). Type `I` to selected among the two formats.

```
[M] ....................  Analyze multiple data sets
```

If the input sequence file contains more than one data sets, PhyML can analyse each of them in a single run of the program. Type `M` to change settings.

```
[R] ........................................  Run ID
```

This option allows you to append a string that identifies the current PhyML run. Say for instance that you want to analyse the same data set with two models. You can then 'tag' the first PhyML run with the name of the first model while the second run is tagged with the name of the second model.

### 6.1.2 Substitution model sub-menu

```
[M] ................  Model of nucleotide substitution
```

```
[M] ................  Model of amino-acids substitution
```

PhyML implements a wide range of substitution models: JC69 [4], K80 [5], F81 [6], F84 [7], HKY85 [8], TN93 [9] GTR [10,11] and custom for nucleotides; LG [12], WAG [13], Dayhoff [14], JTT [15], Blosum62 [16], mtREV [17], rtREV [18], cpREV [19], DCMut [20], VT [21] and mtMAM [22] anf custom for amino acids. Cycle through the list of nucleotide or amino-acids substitution models by typing `M`. Both nucleotide and amino-acid lists include a 'custom' model. The custom option provides the most flexible way to specify the nucleotide substitution model. The model is defined by a string made of six digits. The default string is '`000000`', which means that the six relative rates of nucleotide changes: $A \leftrightarrow C$, $A \leftrightarrow G$, $A \leftrightarrow T$, $C \leftrightarrow G$, $C \leftrightarrow T$ and $G \leftrightarrow T$, are equal. The string '`010010`' indicates that the rates $A \leftrightarrow G$ and $C \leftrightarrow T$ are equal and distinct from $A \leftrightarrow C = A \leftrightarrow T = C \leftrightarrow G = G \leftrightarrow T$. This model corresponds to HKY85 (default) or K80 if the nucleotide frequencies are all set to 0.25. '`010020`' and '`012345`' correspond to TN93 and GTR models respectively. The digit string therefore defines groups of relative substitution rates. The initial rate within each group is set to 1.0, which corresponds to F81 (JC69 if the base frequencies are equal). Users also have the opportunity to define their own initial rate values. These rates are then optimised afterwards (option '`O`') or fixed to their initial values. The custom option can be used to implement all substitution models that are special cases of GTR.

The custom model also exists for protein sequences. It is useful when one wants to use an amino-acid substitution model that is not hard-coded in PhyML. The symmetric part of the rate matrix, as well as the equilibrium amino-acid frequencies, are given in a file which name is given as input of the program. The format of this file is described in the section 7.4.

```
[F] ................  Optimise equilibrium frequencies
```

```
[E] .........  Equilibrium frequencies (empirical/user)
```

```
[F] . Amino acid frequencies (empirical/model defined)
```

For nucleotide sequences, optimising nucleotide frequencies means that the values of these parameters are estimated in the maximum likelihood framework. When the custom model option is selected, it is also possible to give the program a user-defined nucleotide frequency distribution at equilibrium (option `E`). For protein sequences, the stationary amino-acid frequencies are either those defined by the substitution model or those estimated by counting the number of different amino-acids observed in the data. Hence, users should be well aware that the meaning of the `F` option depends on the type of the data to be processed.

```
[T] ....................  Ts/tv ratio (fixed/estimated)
```

Fix or estimate the transition/transversion ratio in the maximum likelihood framework. This option is only available when DNA sequences are to be analysed under K80, HKY85 or TN93 models. The definition given to this parameter by PhyML is the same as PAML's one. Therefore, the value of this parameter does *not* correspond to the ratio between the expected number of transitions and the expected number of transversions during a unit of time. This last definition is the one used in PHYLIP. PAML's manual gives more detail about the distinction between the two definitions.

```
[V] . Proportion of invariable sites (fixed/estimated)
```

The proportion of invariable sites, i.e., the expected frequency of sites that do not evolve, can be fixed or estimated. The default is to fix this proportion to 0.0. By doing so, we consider that each site in the sequence may accumulate substitutions at some point during its evolution, even if no differences across sequences are actually observed at that site. Users can also fix this parameter to any value in the $[0.0, 1.0]$ range or estimate it from the data in the maximum-likelihood framework.

```
[R] .......  One category of substitution rate (yes/no)
```

```
[C] ...........  Number of substitution rate categories
```

```
[A] ...  Gamma distribution parameter (fixed/estimated)
```

```
[G] .........'Middle' of each rate class (mean/median)
```

Rates of evolution often vary from site to site. This heterogeneity can be modelled using a discrete gamma distribution. Type `R` to switch this option on or off.

The different categories of this discrete distribution correspond to different (relative) rates of evolution. The number of categories of this distribution is set to 4 by default. It is probably not wise to go below this number. Larger values are generally preferred. However, the computational burden involved is proportional to the number of categories (i.e., an analysis with 8 categories will generally take twice the time of the same analysis with only 4 categories). Note that the likelihood will not necessarily increase as the number of categories increases. Hence, the number of categories should be kept below a "reasonable" number, say 20. The default number of categories can be changed by typing `C`.

The middle of each discretized substitution rate class can be determined using the mean or the median. PAML, MrBayes and RAxML use the mean. However, the median is generally associated with greater likelihoods than the mean. This conclusion is based on our analysis of several real-world data sets extracted from TreeBase. Despite this, the default option in PhyML is to use the mean in order to make PhyML likelihoods comparable to those of other phylogenetic software. One must bare in mind that likelihoods calculated with the mean approximation are not directly comparable to the likelihoods calculated using the median approximation.

The shape of the gamma distribution determines the range of rate variation across sites. Small values, typically in the $[0.1, 1.0]$ range, correspond to large variability. Larger values correspond to moderate to low heterogeneity. The gamma shape parameter can be fixed by the user or estimated via maximum-likelihood. Type `A` to select one or the other option.

### 6.1.3 Tree searching sub-menu

```
[O] ........................  Optimise tree topology
```

By default the tree topology is optimised in order to maximise the likelihood. However, it is also possible to avoid any topological alteration. This option is useful when one wants to compute the likelihood of a tree given as input (see below). Type `O` to select among these two options.

```
[S] ..................  Tree topology search operations
```

PhyML proposes three different methods to estimate tree topologies. The default approach is to use simultaneous NNI. This option corresponds to the original PhyML algorithm [1]. The second approach relies on subtree pruning and regrafting (SPR). It generally finds better tree topologies compared to NNI but is also significantly slower. The third approach, termed BEST, simply estimates the phylogeny using both methods and returns the best solution among the two. Type `S` to choose among these three choices.

```
[R] ........................  Use random starting tree
```

```
[N] ..................  Number of random starting trees
```

When the SPR or the BEST options are selected, is is possible to use random trees rather than BioNJ or a user-defined tree, as starting tree. If this option is turned on (type `R` to change), five trees, corresponding to five random starts, will be estimated. The output tree file will contain the best tree found among those five. The number of random starts can be modified by typing `N`.

```
[U] ........  Starting tree (BioNJ/parsimony/user tree)
```

When the tree topology optimisation option is turned on, PhyML proceeds by refining an input tree. By default, this input tree is estimated using BioNJ [23]. The alternative option is to use a parsimony tree. We found this option specially useful when analysing large data sets with NNI moves as it generally leads to greater likelihoods than those obtained when starting from a BioNJ trees. The user can also to input her/his own tree. This tree should be in Newick format (see Section 7). This option is useful when one wants to evaluate the likelihood of a given tree with a fixed topology, using PhyML. Type `U` to choose among these two options.

### 6.1.4 Branch support sub-menu

```
[B] ................  Non parametric bootstrap analysis
```

The support of the data for each internal branch of the phylogeny can be estimated using non-parametric bootstrap. By default, this option is switched off. Typing `B` switches on the bootstrap analysis. The user is then prompted for a number of bootstrap replicates. The largest this number the more precisely the bootstrap support are. However, for each bootstrap replicate a phylogeny is estimated. Hence, the time needed to analyse $N$ bootstrap replicates corresponds to $N$-times the time spent on the analysis of the original data set. $N = 100$ is generally considered as a reasonable number of replicates.

```
[A] ................  Approximate likelihood ratio test
```

When the bootstrap option is switched off (see above), approximate likelihood branch supports are estimated. This approach is considerably faster than the bootstrap one. However, both methods intend to estimate different quantities and conducting a fair comparison between both criteria is not straightforward. The estimation of approximate likelihood branch support comes in two flavours: the measured statistics is compared to a $\chi^2$ distribution or a non-parametric distribution estimated using a RELL approximation.

## 6.2 Command-line interface

The alternative to the PHYLIP-like interface is the command line. Users that do not need to modify the default parameters can launch the program with the '`phyml -i seq_file_name`' command. The list of all command line arguments and how to use them is given in the 'Help' section which is displayed after entering the '`phyml help`' command. The options are also described in what follows.

- `-i` (or `--input`) `seq_file_name`
  `seq_file_name` is the name of the nucleotide or amino-acid sequence file in PHYLIP format.

- `-d` (or `--datatype`) `data_type`
  `data_type` is `nt` for nucleotide (default) and `aa` for amino-acid sequences.

- `-q` (or `--sequential`)
  Changes interleaved format (default) to sequential format.

- `-n` (or `--multiple`) `nb_data_sets`
  `nb_data_sets` is an integer giving the number of data sets to analyse.

- `-p` (or `--pars`)
  Use a minimum parsimony starting tree. This option is taken into account when the '-u' option is absent and when tree topology modifications are to be done.

- `-b` (or `--bootstrap`) `int`

  - `int` $> 0$: `int` is the number of bootstrap replicates.
  - `int` $= 0$: neither approximate likelihood ratio test nor bootstrap values are computed.
  - `int` = -1: approximate likelihood ratio test returning aLRT statistics.
  - `int` = -2: approximate likelihood ratio test returning Chi2-based parametric branch supports.
  - `int` = -4: SH-like branch supports alone.

- `-m` (or `--model`) `model_name`
  `model_name` : substitution model name.

  - *Nucleotide-based models*: `HKY85` (default) `|` `JC69` `|` `K80` `|` `F81` `|` `F84` `|` `TN93` `|` `GTR` `|` `custom`
    The `custom` option can be used to define a new substitution model. A string of six digits identifies the model. For instance, 000000 corresponds to F81 (or JC69 provided the distribution of nucleotide frequencies is uniform). 012345 corresponds to GTR. This option can be used for encoding any model that is a nested within GTR. See Section 6.1.2. *NOTE:* the substitution parameters of the custom model will be optimised so as to

maximise the likelihood. It is possible to specify and fix (i.e., avoid optimisation) the values of the substitution rates only through the PHYLIP-like interface.

  - *Amino-acid based models*: `LG` (default) `WAG | JTT | MtREV | Dayhoff | DCMut | RtREV | CpREV | VT | Blosum62 | MtMam | MtArt | HIVw | HIVb | custom`
    The `custom` option is useful when one wants to use an amino-acid substitution model that is not available by default in PhyML. The symmetric part of the rate matrix, as well as the equilibrium amino-acid frequencies, are given in a file which name is asked for by the program. The format of this file is described in section 7.4.

- `--aa_rate_file file_name`
  This option is compulsory when analysing amino-acid sequences under a 'custom' model. `file_name` should provide a rate matrix and equilibrium amino acid in PAML format (see Section ).

- `-f e`, `m`, or "`fA,fC,fG,fT`"
  Nucleotide or amino-acid frequencies.

  - `e` : the character frequencies are determined as follows :
    * *Nucleotide sequences*: (Empirical) the equilibrium base frequencies are estimated by counting the occurence of the different bases in the alignment.
    * *Amino-acid sequences*: (Empirical) the equilibrium amino-acid frequencies are estimated by counting the occurence of the different amino-acids in the alignment.
  - `m` : the character frequencies are determined as follows :
    * *Nucleotide sequences*: (ML) the equilibrium base frequencies are estimated using maximum likelihood.
    * *Amino-acid sequences*: (Model) the equilibrium amino-acid frequencies are estimated using the frequencies defined by the substitution model.
  - "`fA,fC,fG,fT`" : only valid for nucleotide-based models. `fA`, `fC`, `fG` and `fT` are floating numbers that correspond to the frequencies of A, C, G and T respectively.

- `-t` (or `--ts/tv`) `ts/tv_ratio`
  `ts/tv_ratio`: transition/transversion ratio. DNA sequences only. Can be a fixed positive value (e.g., 4.0) or type `e` to get the maximum likelihood estimate.

- `-v` (or `--pinv`) `prop_invar`
  `prop_invar`: proportion of invariable sites. Can be a fixed value in the [0,1] range or type `e` to get the maximum likelihood estimate.

- `-c` (or `--nclasses`) `nb_subst_cat`
  `nb_subst_cat`: number of relative substitution rate categories. Default: `nb_subst_cat=4`. Must be a positive integer.

- `-a` (or `--alpha`) `gamma`
  `gamma`: value of the gamma shape parameter. Can be a fixed positive value or e to get the maximum likelihood estimate. The value of this parameter is estimated in the maximum likelihood framework by default.

- `--use_median`
  The middle of each substitution rate class in the discrete gamma distribution is taken as the median. The mean is used by default.

- `--free_rates`
  As an alternative to the discrete gamma model, it is possible to estimate the (relative) rate in each class of the (mixture) model and the corresponding frequencies. This model has more parameters than the discrete gamma one but usually provides a significantly better fit to the data.

- `--codpos 1,2 or 3`
  When analysing an alignment of coding sequences, use this option to consider only the first, second or third coding position for the estimation.

- `-s` (or `--search`) `move`
  Tree topology search operation option. Can be either `NNI` (default, fast) or `SPR` (a bit slower than `NNI`) or `BEST` (best of NNI and SPR search).

- `-u` (or `--inputtree`) `user_tree_file`
  `user_tree_file`: starting tree filename. The tree must be in Newick format.

- `-o params`
  This option focuses on specific parameter optimisation.
  - `params=tlr`: tree topology (`t`), branch length (`l`) and substitution rate parameters (`r`) are optimised.
  - `params=tl`: tree topology and branch lengths are optimised.
  - `params=lr`: branch lengths and substitution rate parameters are optimised.
  - `params=l`: branch lengths are optimised.
  - `params=r`: substitution rate parameters are optimised.
  - `params=n`: no parameter is optimised.

- `--rand_start`
  This option sets the initial tree to random. It is only valid if SPR searches are to be performed.

- `--n_rand_starts num`
  `num` is the number of initial random trees to be used. It is only valid if SPR searches are to be performed.

- `--r_seed num`
  `num` is the seed used to initiate the random number generator. Must be an integer.

- `--print_site_lnl`
  Print the likelihood for each site in file *_phyml_lk.txt.

- `--print_trace`
  Print each phylogeny explored during the tree search process in file *_phyml_trace.txt.

- `--run_id ID_string`
  Append the string ID_string at the end of each PhyML output file. This option may be useful when running simulations involving PhyML. It can also be used to 'tag' multiple analysis of the same data set with various program settings.

- `--no_memory_check`
  By default, when processing a large data set, PhyML will pause and ask the user to confirm that she/he wants to continue with the execution of the analysis despite the large amount of memory required. The `--no_memory_check` skips this question. It is especially useful when running PhyML in batch mode.

- `--no_jcolalias`
  By default, PhyML preprocesses each alignment by putting together (or aliasing) the columns that are identical. Use this option to skip this step but be aware that the analysis might then take more time to complete.

- `--contrained_lens`
  When an input tree with branch lengths is provided, this option will find the branch multiplier that maximises the likelihood (i.e., the relative branch lengths remain constant)

## 6.3 Parallel bootstrap

Bootstrapping is a highly parallelizable task. Indeed, bootstrap replicates are independent from each other. Hence, each bootstrap sample can be analysed separately. Modern computers often have more than one CPU. Each CPU can therefore be used to process a bootstrap sample. Using this parallel strategy, performing $R$ bootstrap replicates on $C$ CPUs 'costs' the same amount of computation time as processing $R \times C$ bootstrap replicates on a single CPU. In other words, for a given number of replicates, the computation time is divided by $R$ compared to the non-parallel approach.

PhyML sources must be compiled with specific options to turn on the parallel option (see Section 5.4). Once the binary file (`phyml`) has been generated, running a bootstrap analysis with, say 100 replicates on 2 CPUs, can be done by typing the following command-line:

```
mpd &;
mpirun -np 2 ./phyml -i seqfile -b 100;
```

PHYLIP interleaved

```
5 80
seq1  CCATCTCACGGTCGGTACGATACACCKGCTTTTGGCAGGAAATGGTCAATATTACAAGGT
seq2  CCATCTCACGGTCAG---GATACACCKGCTTTTGGCGGGAAATGGTCAACATTAAAAGAT
seq3  RCATCTCCCGCTCAG---GATACCCCKGCTGTTG??????????????ATTAAAAGGT
seq4  RCATCTCATGGTCAA---GATACTCCTGCTTTTGGCGGGAAATGGTCAATCTTAAAAGGT
seq5  RCATCTCACGGTCGGTAAGATACACCTGCTTTTGGCGGGAAATGGTCAAT????????GT

ATCKGCTTTTGGCAGGAAAT
ATCKGCTTTTGGCGGGAAAT
AGCKGCTGTTG??????????
ATCTGCTTTTGGCGGGAAAT
ATCTGCTTTTGGCGGGAAAT
```

PHYLIP sequential

```
5 40
seq1  CCATCTCANNNNNNNNACGATACACCKGCTTTTGGCAGG
seq2  CCATCTCANNNNNNNNNGGGATACACCKGCTTTTGGCGGG
seq3  RCATCTCCCGCTCAGTGAGATACCCCKGCTGTTGXXXXX
seq4  RCATCTCATGGTCAATG-AATACTCCTGCTTTTGXXXXX
seq5  RCATCTCACGGTCGGTAAGATACACCTGCTTTTGxxxxx
```

Figure 2. **PHYLIP interleaved and sequential formats.**

The first command launches the mpi daemon while the second launches the analysis. Note that launching the daemon needs to be done only once. The output files are similar to the ones generated using the standard, non-parallel, analysis (see Section 7). Note that running the program in batch mode, i.e.:

```
mpirun -np 2 ./phyml -i seqfile -b 100 &
```

will probably NOT work. I do not know how to run a mpi process in batch mode yet. Suggestions welcome... Also, at the moment, the number of bootstrap replicates must be a multiple of the number of CPUs required in the mpirun command.

# 7 Inputs / outputs

PhyML reads data from standard text files, without the need for any particular file name extension.

## 7.1 Sequence formats

Alignments of DNA or protein sequences must be in PHYLIP or NEXUS [24] sequential or interleaved format (Figures 7.1 and 3). For PHYLIP formated sequence alignments, the first line of the input file contains the number of species and the number of characters, in free format, separated by blank characters. One slight difference with PHYLIP format deals with sequence name lengths. While PHYLIP format limits this length to ten characters, PhyML can read up to hundred character long sequence names. Blanks and the symbols "(),:" are not allowed within sequence names because the Newick tree format makes special use of these symbols. Another slight difference with PHYLIP format is that actual sequences must be separated from their names by at least one blank character.

A PHYLIP input sequence file may also display more than a single data set. Each of these data sets must be in PHYLIP format and two successive alignments must be

Nexus nucleotides

```
[ This is a comment ]
#NEXUS
BEGIN DATA;
DIMENSIONS NTAX=10 NCHAR=20;
FORMAT DATATYPE=DNA;
MATRIX
tax1        ?ATGATTTCCTTAGTAGCGG
tax2        CAGGATTTCCTTAGTAGCGG
tax3        ?AGGATTTCCTTAGTAGCGG
tax4        ????????????GTAGCGG
tax5        CAGGATTTCCTTAGTAGCGG
tax6        CAGGATTTCCTTAGTAGCGG
tax7        ???GATTTCCTTAGTAGCGG
tax8        ????????????????????
tax9        ???GGATTTCTTCGTAGCGG
tax10       ????????????????AGCGG;
END;
```

Nexus digits

```
[ This is a comment ]
#NEXUS
BEGIN DATA;
DIMENSIONS NTAX=10 NCHAR=20;
FORMAT DATATYPE=STANDARD SYMBOLS="0 1 2 3";
MATRIX
tax1        ?0320333113302302122
tax2        10220333113302302122
tax3        ?0220333113302302122
tax4        ????????????2302122
tax5        10220333113302302122
tax6        10220333113302302122
tax7        ???20333113302302122
tax8        ????????????????????
tax9        ???220333133123021 22
tax10       ????????????????02122;
END;
```

Nexus digits

```
[ This is a comment ]
#NEXUS
BEGIN DATA;
DIMENSIONS NTAX=10 NCHAR=20;
FORMAT DATATYPE=STANDARD SYMBOLS="00 01 02 03";
MATRIX
tax1        ??000302000303030101030300020300020102 02
tax2        010002020003030301010303000203000201020 2
tax3        ??000202000303030101030300020300020102 02
tax4        ????????????????????????????0203000201020 2
tax5        010002020003030301010303000203000201020 2
tax6        010002020003030301010303000203000201020 2
tax7        ??????020003030301010303000203000201020 2
tax8        ????????????????????????????????????????
tax9        ??????020200030303010303010203000201020 2
tax10       ????????????????????????????????0002010202;
END;
```

Figure 3. **NEXUS formats.**

separated by an empty line. Processing multiple data sets requires to toggle the '`M`' option in the *Input Data* sub-menu or use the '`-n`' command line option and enter the number of data sets to analyse. The multiple data set option can be used to process re-sampled data that were generated using a non-parametric procedure such as cross-validation or jackknife (a bootstrap option is already included in PhyML). This option is also useful in multiple gene studies, even if fitting the same substitution model to all data sets may not be suitable.

PhyML can also process alignments in NEXUS format. Although not all the options provided by this format are supported by PhyML, a few specific features are exploited. Of course, this format can handle nucleotide and protein sequence alignments in sequential or interleaved format. It is also possible to use custom alphabets, replacing the standard 4-state and 20-state alphabets for nucleotides and amino-acids respectively. Examples of a 4-state custom alphabet are given in Figure 3. Each state must here correspond to one digit or more. The set of states must be a list of consecutive digits starting from 0. For instance, the list "0, 1, 3, 4" is not a valid alphabet. Each state in the symbol list must be separated from the next one by a space. Hence, alphabets with up to 100 states can be easily defined by using two-digit number, starting with 00, up to 99. Most importantly, this feature gives the opportunity to analyse data sets made of presence/absence character states (use the `symbols=''0 1''` option for such data). Alignments made of custom-defined states will be processed using the Jukes and Cantor model. Other options of the program (e.g., number of rate classes, tree topology search algorithm) are freely configurable.

### 7.1.1 Gaps and ambiguous characters

Gaps correspond to the '`-`' symbol. They are systematically treated as unknown characters "on the grounds that we don't know what would be there if something were there" (J. Felsenstein, PHYLIP main documentation). The likelihood at these sites is summed over all the possible states (i.e., nucleotides or amino acids) that could actually be observed at these particular positions. Note however that columns of the alignment that display only gaps or unknown characters are simply discarded because they do not carry any phylogenetic information (they are equally well explained by any model). PhyML also handles ambiguous characters such as $R$ for $A$ or $G$ (purines) and $Y$ for $C$ or $T$ (pyrimidines). Tables 1 and 2 give the list of valid characters/symbols and the corresponding nucleotides or amino acids.

### 7.1.2 Specifying outgroup sequences

PhyML can return rooted trees provided outgroup taxa are identified from the sequence file. In order to do so, sequence names that display a '*' character will be automatically considered as belonging to the outgroup.

The topology of the rooted tree is exactly the same as the unrooted version of the same tree. In other words, PhyML first ignores the distinction between ingroup and outgroup sequences, builds a maximum likelihood unrooted tree and then tries to add the root. If the outgroup has more than one sequence, the position of the root might be ambiguous. In such situation, PhyML tries to identify the most

| Character | Nucleotide | Character | Nucleotide |
|---|---|---|---|
| $A$ | Adenosine | $Y$ | $C$ or $T$ |
| $G$ | Guanine | $K$ | $G$ or $T$ |
| $C$ | Cytosine | $B$ | $C$ or $G$ or $T$ |
| $T$ | Thymine | $D$ | $A$ or $G$ or $T$ |
| $U$ | Uracil ($=T$) | $H$ | $A$ or $C$ or $T$ |
| $M$ | $A$ or $C$ | $V$ | $A$ or $C$ or $G$ |
| $R$ | $A$ or $G$ | $-$ or $N$ or $X$ or ? | unknown |
| $W$ | $A$ or $T$ | | ($=A$ or $C$ or $G$ or $T$) |
| $S$ | $C$ or $G$ | | |

Table 1. **List of valid characters in DNA sequences and the corresponding nucleotides.**

| Character | Amino-Acid | Character | Amino-Acid |
|---|---|---|---|
| $A$ | Alanine | $L$ | Leucine |
| $R$ | Arginine | $K$ | Lysine |
| $N$ or $B$ | Asparagine | $M$ | Methionine |
| $D$ | Aspartic acid | $F$ | Phenylalanine |
| $C$ | Cysteine | $P$ | Proline |
| $Q$ or $Z$ | Glutamine | $S$ | Serine |
| $E$ | Glutamic acid | $T$ | Threonine |
| $G$ | Glycine | $W$ | Tryptophan |
| $H$ | Histidine | $Y$ | Tyrosine |
| $I$ | Isoleucine | $V$ | Valine |
| $L$ | Leucine | $-$ or $X$ or ? | unknown |
| $K$ | Lysine | | (can be any amino acid) |

Table 2. **List of valid characters in protein sequences and the corresponding amino acids.**

relevant position of the root by considering which edge provides the best separation between ingroup and outgroup taxa (i.e., we are trying to make the outgroup "as monophyletic as possible").

## 7.2 Tree format

PhyML can read one or several phylogenetic trees from an input file. This option is accessible through the *Tree Searching* sub menu or the '`-u`' argument from the command line. Input trees are generally used as initial maximum likelihood estimates to be subsequently adjusted by the tree searching algorithm. Trees can be either rooted or unrooted and multifurcations are allowed. Taxa names must, of course, match the corresponding sequence names.

```
((seq1:0.03,seq2:0.01):0.04,(seq3:0.01,(seq4:0.2,seq5:0.05):0.2):0.01);
((seq3,seq2),seq1,(seq4,seq5));
```

Figure 4. **Input trees**. The first tree (top) is rooted and has branch lengths. The second tree (bottom) is unrooted and does not have branch lengths.

## 7.3 Multiple alignments and trees

Single or multiple sequence data sets may be used in combination with single or multiple input trees. When the number of data sets is one ($n_D = 1$) and there is only one input tree ($n_T = 1$), then this tree is simply used as input for the single data set analysis. When $n_D = 1$ and $n_T > 1$, each input tree is used successively for the analysis of the single alignment. PhyML then outputs the tree with the highest likelihood. If $n_D > 1$ and $n_T = 1$, the same input tree is used for the analysis of each data set. The last combination is $n_D > 1$ and $n_T > 1$. In this situation, the $i$-th tree in the input tree file is used to analyse the $i$-th data set. Hence, $n_D$ and $n_T$ must be equal here.

## 7.4 Custom amino-acid rate model

The custom amino-acid model of substitutions can be used to implement a model that is not hard-coded in PhyML. This model must be time-reversible. Hence, the matrix of substitution rates is symmetrical. The format of the rate matrix with the associated stationary frequencies is identical to the one used in PAML. An example is given below:

Sequence file name : 'seq'

| Output file name | Content |
|---|---|
| `seq_phyml_tree.txt` | ML tree |
| `seq_phyml_stats.txt` | ML model parameters |
| `seq_phyml_boot_trees.txt` | ML trees – bootstrap replicates |
| `seq_phyml_boot_stats.txt` | ML model parameters – bootstrap replicates |
| `seq_phyml_rand_trees.txt` | ML trees – multiple random starts |

Table 3. **Standard output files**

```
0.55
0.51 0.64
0.74 0.15 5.43
1.03 0.53 0.27 0.03
0.91 3.04 1.54 0.62 0.10
1.58 0.44 0.95 6.17 0.02 5.47
1.42 0.58 1.13 0.87 0.31 0.33 0.57
0.32 2.14 3.96 0.93 0.25 4.29 0.57 0.25
0.19 0.19 0.55 0.04 0.17 0.11 0.13 0.03 0.14
0.40 0.50 0.13 0.08 0.38 0.87 0.15 0.06 0.50 3.17
0.91 5.35 3.01 0.48 0.07 3.89 2.58 0.37 0.89 0.32 0.26
0.89 0.68 0.20 0.10 0.39 1.55 0.32 0.17 0.40 4.26 4.85 0.93
0.21 0.10 0.10 0.05 0.40 0.10 0.08 0.05 0.68 1.06 2.12 0.09 1.19
1.44 0.68 0.20 0.42 0.11 0.93 0.68 0.24 0.70 0.10 0.42 0.56 0.17 0.16
3.37 1.22 3.97 1.07 1.41 1.03 0.70 1.34 0.74 0.32 0.34 0.97 0.49 0.55 1.61
2.12 0.55 2.03 0.37 0.51 0.86 0.82 0.23 0.47 1.46 0.33 1.39 1.52 0.17 0.80 4.38
0.11 1.16 0.07 0.13 0.72 0.22 0.16 0.34 0.26 0.21 0.67 0.14 0.52 1.53 0.14 0.52 0.11
0.24 0.38 1.09 0.33 0.54 0.23 0.20 0.10 3.87 0.42 0.40 0.13 0.43 6.45 0.22 0.79 0.29 2.49
2.01 0.25 0.20 0.15 1.00 0.30 0.59 0.19 0.12 7.82 1.80 0.31 2.06 0.65 0.31 0.23 1.39 0.37 0.31

8.66 4.40 3.91 5.70 1.93 3.67 5.81 8.33 2.44 4.85 8.62 6.20 1.95 3.84 4.58 6.95 6.10 1.44 3.53 7.09
```

The entry on the $i$-th row and $j$-th column of this matrix corresponds to the rate of substitutions between amino-acids $i$ and $j$. The last line in the file gives the stationary frequencies and must be separated from the rate matrix by one line. The ordering of the amino-acids is alphabetical, i.e, Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr and Val.

## 7.5 Output files

Table 3 presents the list of files resulting from an analysis. Basically, each output file name can be divided into three parts. The first part is the sequence file name, the second part corresponds to the extension '`_phyml_`' and the third part is related to the file content. When launched with the default options, PhyML only generates two files: the tree file and the model parameter file. The estimated maximum likelihood tree is in standard Newick format (see Figure 4). The model parameters file, or statistics file, displays the maximum likelihood estimates of the substitution model parameters, the likelihood of the maximum likelihood phylogenetic model, and other important information concerning the settings of the analysis (e.g., type of data, name of the substitution model, starting tree, etc.). Two additional output files are created if bootstrap supports were evaluated. These files simply contain the maximum likelihood trees and the substitution model parameters estimated from each bootstrap replicate. Such information can be used to estimate sampling errors around each parameter of the phylogenetic model. When the random tree option is

turned on, the maximum likelihood trees estimated from each random starting trees are printed in a separate tree file (see last row of Table 3).

### 7.6 Treatment of invariable sites with fixed branch lengths

PhyML allows users to give an input tree with fixed topology and branch lengths and find the proportion of invariable sites that maximise the likelihood (option `-o r`). These two options can be considered as conflicting since branch lengths depend on the proportion of invariants. Hence, changing the proportion of invariants implies that branch lengths are changing too. More formally, let $l$ denote the length of a branch, i.e., the expected number of substitutions per site, and $p$ be the proportion of invariants. We have $l = (1-p)l'$, where $l'$ is the expected number of substitutions per _variable_ sites. When asked to optimize $p$ but leave $l$ unchanged, PhyML does the following:

1. Calculate $l' = l/(1-p)$ and leave $l'$ unchanged throughout the optimization.
2. Find the value of $p$ that maximises the likelihood. Let $p^*$ denote this value.
3. Set $l^* = (1-p^*)l'$ and print out the tree with $l^*$ (instead of $l$).

PhyML therefore assumes that the users wants to fix the branch lengths measured at _variable_ sites only (i.e., $l^*$ is fixed). This is the reason why the branch lengths in the input and output trees do differ despite the use of the the `-o r` option. While we believe that this approach relies on a sound rationale, it is not perfect. In particular, the original transformation of branch lengths ($l' = l/(1-p)$) relies on a default value for $p$ with is set to 0.2 in practice. It is difficult to justify the use of this value rather than another one. One suggestion proposed by Bart Hazes is to avoid fixing the branch lengths altogether and rather estimate the value of a scaling factor applied to each branch length in the input tree (option `--contrained_lens`). We agree that this solution probably matches very well most users expectation, i.e., "find the best value of $p$ while constraining the ratio of branch lengths to be that given in the input tree". Please feel free to send us your suggestions regarding this problem by posting on forum (http://groups.google.com/group/phyml-forum).

## 8 Other programs in the PhyML package

PhyML is software package that provides tools to tackle problems other than estimating maximum likelihood phylogenies. Installing these tools and processing data sets is explained is the following sections.

### 8.1 PhyTime (Guindon, *Mol. Biol. Evol.* 2010)

PhyTime is a program that estimates node ages and substitution rates using a fast Bayesian approach. It relies on a Gibbs sampler which outperforms the "standard" Metropolis-Hastings algorithm implemented in a number of phylogenetic softwares. The details and performance of this approach are described in the following article:

Guindon S. "Bayesian estimation of divergence times from large data sets", *Mol. Biol. Evol.*, 2010, 27(8):1768:81.

### 8.1.1 Installing PhyTime

Compiling PhyTime is straightforward on Unix-like machines (i.e., linux and MacOS systems). PhyTime is not readily available for Windows machines but compilation should be easy on this system too. In the 'phyml' directory, where the 'src/' and 'doc/' directories stand, enter the following commands:

```
./configure --enable-phytime;
make clean;
make;
```

This set of commands generates a binary file called `phytime` which can be found in the 'src/' directory.

### 8.1.2 Running PhyTime

Passing options and running PhyTime on your data set is quite similar to running PhyML in commmand-line mode. The main differences between the two programs are explained below:

- PhyTime takes as mandatory input a *rooted* phylogenetic tree. Hence, the '`-u`' option must be used. Also, unlike PhyML, PhyTime does not modify the tree topology. Hence, the options that go with the '`-s`' command do not alter the input tree topology.

- PhyTime needs an input file giving information about calibration nodes. The command '`--calibration=`' followed by the name of the file containing the calibration node information is mandatory. The content of that file should look as follows:

Calibration node file

```
Dugong_dugon Procavia_capensis Elephantidae | -65 -54
Equus_sp. Ceratomorpha | -58 -54
Cercopithecus_solatus Macaca_mulatta Hylobates_lar Homo_sapiens | -35 -25
Lepus_crawshayi Oryctolagus_cuniculus Ochotona_princeps | -90 -37
Marmota_monax Aplodontia_rufa | -120 -37
Dryomys_nitedula Glis_glis | -120 -28.5
@root@ | -100 -120
```

Every row in this file lists a set of taxa that belong to the same subtree (i.e., a clade). This list of taxa is followed by the character '`|`' and two real numbers corresponding to the lower and upper bounds of the calibration interval for the node at the root of the clade. In the example given here, the clade grouping the three taxa "Dugong_dugon", "Procavia_capensis" and "Elephantida" has -65 as lower bound and -54 as upper bound. Node ages (or node heights) are relative to the most recent tip node in the phylogeny, which age is set to 0.

Note that the node corresponding to the root of the whole tree has a specific label: '`@root@`'. It is important to specify upper and lower bounds for the

root node in order to ensure convergence of the Gibbs sampler. If the prior interval for the root height is not specified, the upper bound will be set to the upper bound of the oldest calibration node and the lower bound will be set to twice this age. As a consequence, leaving the prior on root height interval unspecified may produce inaccurate estimates of node ages, especially if there are only few otherwise calibration nodes available.

A notable exception to this rule comes from the analysis of serial sample data, i.e., alignments in which sequences were not sampled at the same time point. For such data, the estimated number of substitutions accumulated between successive time points is used to estimate the substitution rate averaged over lineages. Because the time of collection of the sequences is generally known without ambiguity, this extra piece of data is translated into very informative calibration intervals for the tip nodes (i.e., calibration interval of zero width), which in turn results in substitution rate estimates with descreased variances. Posterior distribution of substitution rates with small variances then allows one to get good estimates of the root age.

A typical PhyTime command-line should look like the following:

```
./phytime -i seqname -u treename --calibration=calibration_file -m GTR -c 8
```

Assuming the file '`seqname`' contains DNA sequences in PHYLIP or NEXUS format, '`treename`' is the rooted input tree in NEXUS format and '`calibration_file`' is a set of calibration nodes, PhyTime will estimate the posterior distribution of node times and substitution rates under the assumption that the substitution process follows a GTR model with 8 classes of rates in the Gamma distribution of rates across sites. The model parameter values are estimated by a Gibbs sampling technique. This algorithm tries diferent values of the model parameters and record the most probable ones. By default, $10^6$ values for each parameter are collected. These values are recorded every $10^3$ sample. These settings can be modified using the appropriate command-line options (see below).

### 8.1.3 Upper bounds of model parameters

The maximum expected number of substitutions per along a given branch is set to 1.0. Since calibration times provide prior information about the time scale considered, it is possible to use that information to define an upper bound for the substitution rate. This upper bound is equal to the ratio of the maximum value for a branch length (1.0) by the amount of time elapsed since the oldest calibration point (i.e., the minimum of the lower bounds taken over the whole set of calibration points)[1]. It is important to keep in mind that the upper bound of the average substitution rate depends on the time unit used in the calibration priors. The value of the upper bound is printed on screen at the start of the execution.

PhyTime implements two models that authorize rates to be autocorrelated. The strength of autocorrelation is governed by a parameter which value is estimated

[1]The actual formula involves an extra parameter which does not need to be introduced here

from the data. However, it is necessary to set an appropriate upper bound for this parameter prior running the analysis. The maximum value is set such that the correlation between the rate at the beginning and at the end of a branch of length 1.0 calendar time unit is not different from 0. Here again the upper bound for the model parameter depends on the time unit. It is important to choose this unit so that a branch of length 1.0 calendar unit can be considered as short. For this reason, we recommend to select a time unit so that the calibration times take values between -10 and -1000.

### 8.1.4 PhyTime specific options

Beside the `--calibration` option, there are other command line options that are specific to PhyTime:

- `--chain_len=num`
  `num` is the number of iterations required to estimate the joint posterior density of all the model parameters, i.e., the length of the MCMC chain. Its default is set to 1E+6.

- `--sample_freq=num`
  `num` is the number of generations between successive collection of the model parameter values throughout the MCMC algorithm. For instance, the `--sample_freq=1E+2` option will make PhyTime sample the model parameter every 100th iteration of the MCMC algorithm. Its default is set to 1E+3.

- `--fastlk=yes (no)` [Default: no]
  The option is used to turn on (off) the approximation of the likelihood function using a multivariate normal density. By default, the exact likelihood is used. Using the normal approximation considerably speeds up the calculation. However, it is necessary to ensure that this approximation is appropriate by looking at the correlation between the exact and approximated likelihood values that are sampled. Please read Section 9.2 for a description of the appropriate steps to take.

- `--no_data`
  Use this option to sample from the priors only (rather from the posterior joint density of the model parameters).

### 8.1.5 PhyTime output

The program PhyTime generates two output files. The file called '`phytime.XXXX`', where XXXX is a randomly generated integer, lists the node times and branch relative rates sampled during the estimation process. It also gives the sampled values for other parameters, such as the autocorrelation of rates (parameter 'Nu'), and the rate of evolution (parameter 'EvolRate') amongst others. This output file can be analysed with the program Tracer from the BEAST package (`http://beast.bio.ed.ac.uk/Main_Page`). The second file is called

'`phytime.XXXX.trees`'. It is the list of trees that were collected during the estimation process, i.e., phylogenies sampled from the posterior density of trees. This file can be processed using the software TreeAnnotator, also part of the BEAST package (see `http://beast.bio.ed.ac.uk/Main_Page`) in order to generate confidence sets for the node time estimates.

Important information is also displayed on the standard output of PhyTime (the standard output generally corresponds to the terminal window from which PhyTime was launched). The first column of this output gives the current generation, or run, of the chain. It starts at 1 and goes up to 1E+6 by default (use `--chain_len` to change this value, see above). The second column gives the time elapsed in seconds since the sampling began. The third column gives the log likelihood of the phylogenetic model (i.e., 'Felsenstein's likelihood'). The fourth column gives the current sampled value of the EvolRate parameter along with the corresponding Effective Sample Size (ESS) for this parameter. The fifth column gives the tree height and the corresponding ESS. The EvolRate and the tree height parameters are generally considered as important parameters of the model. They are also difficult to estimate independently if the signal conveyed by the calibration intervals is weak. The MCMC technique generates samples from a target distribution (in our case, the joint posterior density of parameters). Due to the Markovian nature of the method, these samples are not independent. The ESS is the estimated number of independent measurements obtained from a set of (usually dependent) measurements. It is calculated using the following formula:

$$\mathrm{ESS} = N\left(\frac{1-r}{1+r}\right),$$

where $N$ is the length of the chain (i.e., the 'raw' or 'correlated' sample size) and $r$ is the autocorrelation value, which is obtained using the following formula:

$$r = \frac{1}{(N-k)\sigma_x^2}\sum_{i=1}^{N-k}(X_i-\mu_x)(X_{i+k}-\mu_x),$$

where $\mu_x$ and $\sigma_x$ are the mean and standard deviation of the $X_i$ values respectively and $k$ is the lag. The value of $r$ that is used in PhyTime corresponds to the case where $k = 1$, which therefore gives a first order approximation of the 'average' autocorrelation value (i.e., the autocorrelation averaged over the set of possible values of the lag).

The last column of the standard output gives the minimum of the ESS values taken over the whole set of node height estimates. It provides useful information when one has to decide whether or not the sample size is large enough to draw valid conclusion, i.e., decide whether the chain was run for long enough (see Section 9.2 for more detail about adequate chain length).

### 8.1.6 ClockRate vs. EvolRate

The average rate of evolution along a branch is broken into two components. One is called ClockRate and is the same throughout the tree. The other is called EvolRate and corresponds to a weighted average of branch-specific rates. The model of

rate evolution implemented in PhyTime forces the branch-specific rate values to be greater than one. As a consequence, ClockRate is usually smaller EvolRate.

In more mathematical terms, let $\mu$ be the value of ClockRate, $r_i$ be the value of the relative rate along branch $i$ and $\Delta_i$ the time elapsed along branch $i$. The value of EvolRate is then given by:

$$\text{EvolRate} = \mu \frac{\sum_i^{2n-3} r_i \Delta_i}{\sum_i^{2n-3} \Delta_i}.$$

It is clear from this equation that multiplying each $r_i$ by a constant and dividing $\mu$ by the same constant does not change the value of EvolRate. The $r_i$s and $\mu$ are then confounded, or non-identifiable, and only the value of EvolRate can be estimated from the data. Please make sure that you use the value of EvolRate rather than that of ClockRate when referring to the estimate of the substitution rate.

# 9 Recommendations on program usage.

## 9.1 PhyML

The choice of the tree searching algorithm among those provided by PhyML is generally a tough one. The fastest option relies on local and simultaneous modifications of the phylogeny using NNI moves. More thorough explorations of the space of topologies are also available through the SPR options. As these two classes of tree topology moves involve different computational burdens, it is important to determine which option is the most suitable for the type of data set or analysis one wants to perform. Below is a list of recommendations for typical phylogenetic analyses.

1. *Single data set, unlimited computing time.* The best option here is probably to use a SPR search (i.e., straight SPR of best of SPR and NNI). If the focus is on estimating the relationships between species, it is a good idea to use more than one starting tree to decrease the chance of getting stuck in a local maximum of the likelihood function. Using NNIs is appropriate if the analysis does not mainly focus on estimating the evolutionary relationships between species (e.g. a tree is needed to estimate the parameters of codon-based models later on). Branch supports can be estimated using bootstrap and approximate likelihood ratios.

2. *Single data set, restricted computing time.* The three tree searching options can be used depending on the computing time available and the size of the data set. For small data sets (i.e., $< 50$ sequences), NNI will generally perform well provided that the phylogenetic signal is strong. It is relevant to estimate a first tree using NNI moves and examine the reconstructed phylogeny in order to have a rough idea of the strength of the phylogenetic signal (the presence of small internal branch lengths is generally considered as a sign of a weak phylogenetic signal, specially when sequences are short). For larger data sets ($> 50$ sequences), a SPR search is recommended if there are good evidence of a lack

of phylogenetic signal. Bootstrap analysis will generally involve large computational burdens. Estimating branch supports using approximate likelihood ratios therefore provides an interesting alternative here.

3. *Multiple data sets, unlimited computing time.* Comparative genomic analyses sometimes rely on building phylogenies from the analysis of a large number of gene families. Here again, the NNI option is the most relevant if the focus is not on recovering the most accurate picture of the evolutionary relationships between species. Slower SPR-based heuristics should be used when the topology of the tree is an important parameter of the analysis (e.g., identification of horizontally transferred genes using phylogenetic tree comparisons). Internal branch support is generally not a crucial parameter of the multiple data set analyses. Using approximate likelihood ratio is probably the best choice here.

4. *Multiple data sets, limited computing time.* The large amount of data to be processed in a limited time generally requires the use of the fastest tree searching and branch support estimation methods Hence, NNI and approximate likelihood ratios rather than SPR and non-parametric bootstrap are generally the most appropriate here.

Another important point is the choice of the substitution model. While default options generally provide acceptable results, it is often warranted to perform a pre-analysis in order to identify the best-fit substitution model. This pre-analysis can be done using popular software such as Modeltest [25] or ProtTest [26] for instance. These programs generally recommend the use of a discrete gamma distribution to model the substitution process as variability of rates among sites is a common feature of molecular evolution. The choice of the number of rate classes to use for this distribution is also an important one. While the default is set to four categories in PhyML, it is recommended to use larger number of classes if possible in order to best approximate the patterns of rate variation across sites [27]. Note however that run times are directly proportional to the number of classes of the discrete gamma distribution. Here again, a pre-analysis with the simplest model should help the user to determine the number of rate classes that represents the best trade-off between computing time and fit of the model to the data.

## 9.2 PhyTime

Analysing a data set using PhyTime should involve three steps based on the following questions: (1) do the priors seem to be adequate (2) can I use the fast approximation of the likelihood and (3) how long shall I run the program for? I explain below how to provide answers to these questions.

- *Are the priors adequate?* Bayesian analysis relies on specifiying the joint prior density of model parameters. In the case of node age estimation, these priors essentially describe how rates of substitution vary across lineages and the probabilistic distribution that node ages have when ignoring the information provided by the genetic sequences. These priors vary from tree to tree. It

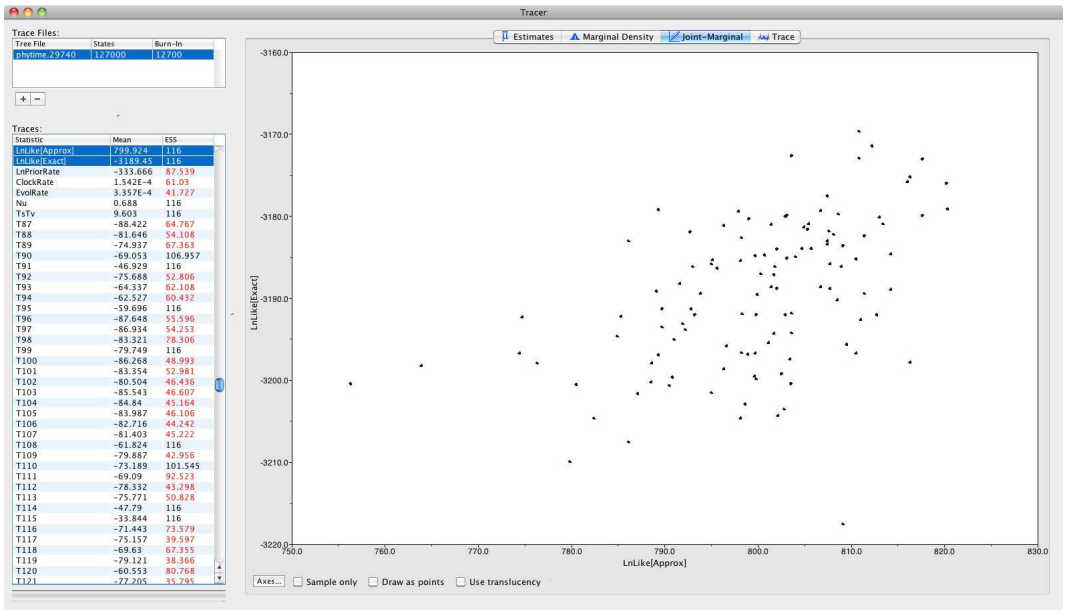


Figure 5. **Exact vs. approximate likelihoods.** The correlation between the normally approximated (Y-axis) and the exact (X-axis) likelihoods is weak here. The exact likelihood should be used (option `fastlk=no`).

is therefore essential to check the adequacy of priors for each user-defined input tree. In order to do so, PhyTime needs to be run with the `--no_data` option. When this option is required, the sequence data provided as input will be ignored and the rest of the analysis will proceed normally. The prior distribution of model parameters, essentially edge rates and node heights, can then be checked using the program Tracer as one would do for the standard 'posterior' analysis.

- *Can I use the fast approximation to the likelihood?* The suface of the log-likelihood function can be approximated using a multivariate normal density. This technique is saving very substantial amounts of computation time. However, like most approximations, there are situations where it does not provide a good fit to the actual function. This usually happens when the phylogeny displays a lot of short branches, i.e., the signal conveyed by the sequences is weak. It is therefore important to first check whether using the approximate likelihood is reasonable. In order to do so, it is recommended to first run the program without the approximation, i.e., using the default settings. Once the minimum value of the ESS of node ages (the last column on the right of the standard output) has reached 40-50, open the `phytime.XXXX` output file with Tracer and examine the correlation between the exact and approximate likelihood values. Figure 5 gives an example where the correlation is too weak and the approximation of the likelihood should be avoided. Figure 5 gives an example where the approximation is good enough. The current execution of PhyTime can be terminated and then re-launched using the `--fast_lk` option.

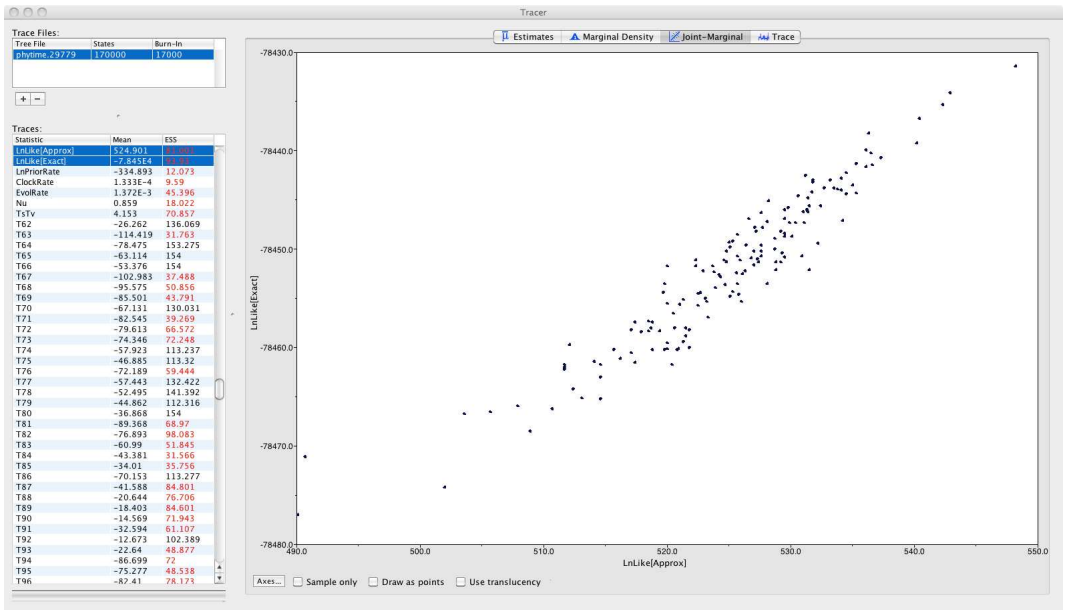


Figure 6. **Exact vs. approximate likelihoods.** The correlation between the normally approximated (Y-axis) and the exact (X-axis) likelihoods is good. The approximation of the likelihood can be used (option `fastlk=yes`).

- *How long shall I run the program for?* PhyTime should be run long enough such that the ESS of each parameter is 'large enough'. The last column on the right handside of the standard output gives the minimum ESS across all internal node heights. It is recommended to run the program so that this number reaches at least 100.

# 10 Frequently asked questions

1. *PhyML crashes before reading the sequences. What's wrong ?*

   - The format of your sequence file is not recognized by PhyML. See Section 7
   - The carriage return characters in your sequence files are not recognized by PhyML. You must make sure that your sequence file is a plain text file, with standard carriage return characters (i.e., corresponding to "`\n`", or "`\r`")

2. *The program crashes after reading the sequences. What's wrong ?*

   - You analyse protein sequences and did not enter the `-d aa` option in the command-line.
   - The format of your sequence file is not recognized by PhyML. See Section 7

3. *Does PhyML handle outgroup sequences ?*

   - Yes, it does. Outgroup taxa are identified by adding the '*' sign at the end of each corresponding sequence name (see Section 7.1.2)

4. *Does PhyML estimate clock-constrained trees ?*

   - No, the PhyML program does not estimate clock-contrained trees. One can however use the program PhyTime to perform such analysis but the tree topology will not be estimated.

5. *Can PhyML analyse partitioned data, such as multiple gene sequences ?*

   - We are currently working on this topic. Future releases of the program will provide options to estimate trees from phylogenomic data sets, with the opportunity to use different substitution models on the different data partitions (e.g., different genes). PhyML will also include specific algorithms to search the space of tree topologies for this type of data.

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