PATHd8

users manual version 1.0 (2006-04-13)

Website:
www.math.su.se/PATHd8

Reference: Estimating divergence times in large phylogenetic trees: Tom Britton, Cajsa Lisa Anderson, David Jacquet, Samuel Lundqvist and Kåre Bremer (submitted to Systematic Biology)

Overview of the PATHd8 program

Input:

    Infile providing the program with the following information
    - Tree with branch lengths in Newick format
    - Time constraints

Output:

    Outfile containing the following information
    - PATHd8 chronogram (calibrated ultrametric tree)
    - Estimated ages for all nodes
    - PATH tree (ultrametric tree without calibration)
    - Clock test results for all nodes

Get and install PATHd8

Download PATHd8 (in OSX, UNIX, Windows or Linux version) from the website www.math.su.se/PATHd8

Run PATHd8

Open a terminal window (or the command window if you are running Microsoft Windows). Navigate to the folder in which you have saved PATHd8 and write:

PATHd8 infile outfile
or
./ PATHd8 infile outfile
(depending on your system)

Details of input data for PATHd8

The input file must be a pure text file. The input file must contain a Newick tree.

● Required input

1. Input tree
The tree must have branch lengths , and be in Newick format. This is the paren-thesis form that can be obtained from virtually any phylogeny reconstruction software.

2. Age constraints
You can use any number of time constraints.
OBS! The program requires one fixed age.
If you do not have any constraints, you can set the root to 1 and get the relative ages.

Constraints are given with the syntax
    mrca: taxa 1 , taxa2 , age=x;

taxa 1 , taxa2 , are two taxa defining the node of their most recent common
    ancestor, mrca (see example tree below)

age can be given as one of the following:
    minage   (the node has at least age x)
    maxage   (the node has at most age x)
    fixage   (the node has exactly age x)

● Optional input

3. Sequence length (if you provide branchlengths that are not integers) must be given by
    Sequence length=x;

4. Comments can be made in two ways:
    Within bracket: [this is a comment]
    After hash-symbol: #this is a comment

5. Name nodes (for easier reading of output in large trees)
    name of mrca: taxa1, taxa2, name=name_of_clade;

Example: Infile

Sequence length = 1823;

((((Rat:0.007148,Human:0.001808):0.024345,Platypus:0.016588):0.012920,(Ostrich:0.018119,Alligator:0.006232):0.004708):0.028037,Frog:0);

mrca: Rat, Ostrich, minage=260;
mrca: Human, Platypus, fixage=125;
mrca: Alligator, Ostrich, minage=150;

name of mrca: Platypus, Rat, name=crown_mammals;
name of mrca: Human, Rat, name=crown_placentals;
name of mrca: Ostrich, Alligator, name=crown_Archosaurs;

my own notes, not executed by PATHd8
fossil Archosaurus minage=260
fossil Archaeopteryx minage=150
fossil Eomaia minage=125

Phylogram corresponding to
the example infile above.
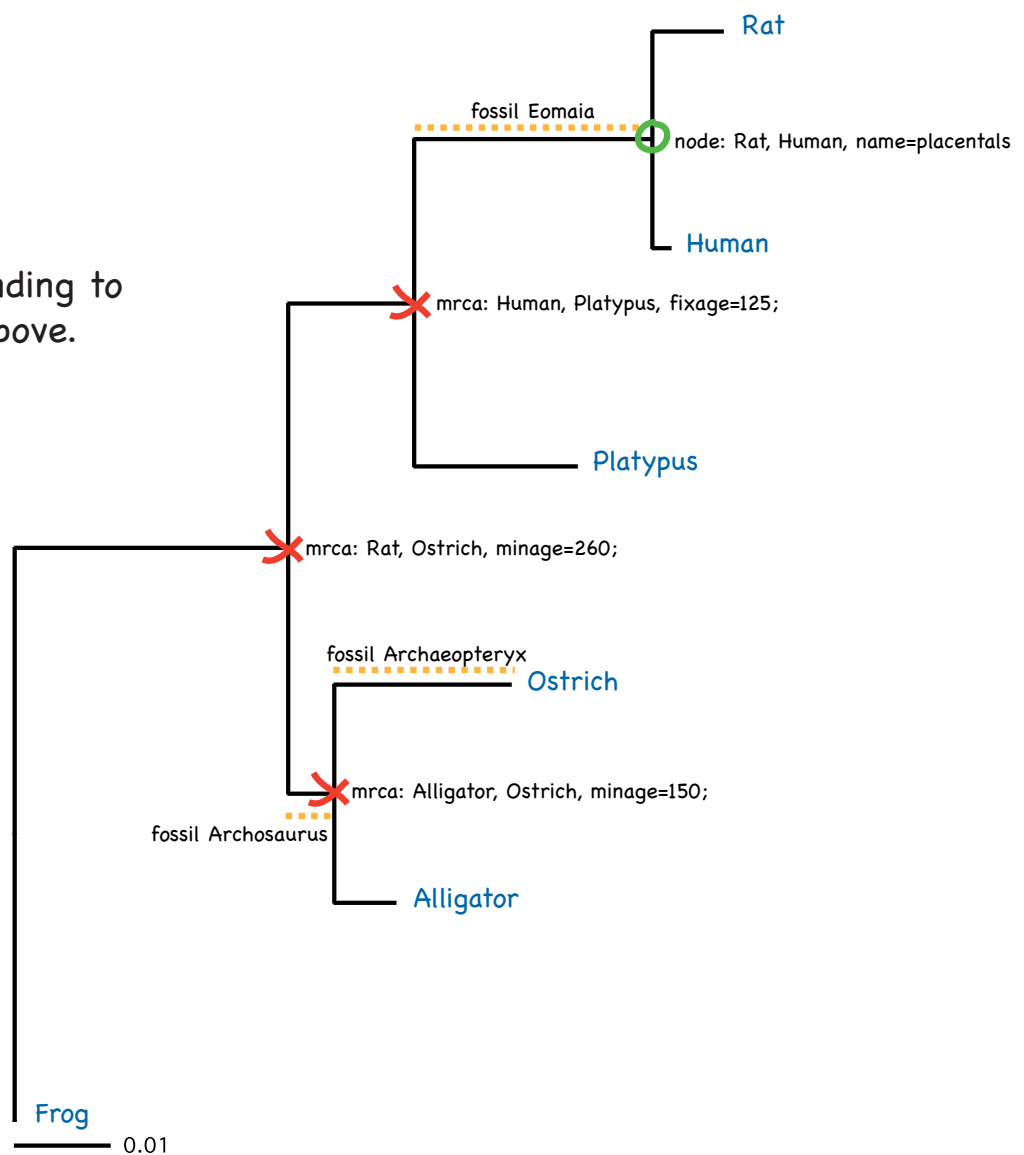
Example: Outfile

```
********************************************************************************
* d 8  C A L C U L A T I O N                                    *
********************************************************************************
```

Number of informative fixnodes: 1
Number of informative minnodes: 2
Number of informative maxnodes: 0

d8 tree   : ((((Rat:22.388060,Human:22.388060)crown_placentals:102.611940,Platypus:125.000000)crown_mammals:
135.000000,(Ostrich:150.000000,Alligator:150.000000)crown_Archosaurs:110.000000):166.742712,Frog:426.742712);

Ancestor of	Ancestor of	Name	Age	#Terminals	MPL	Rate *	minage	maxage
Rat	Frog	-	426.743	6	86.333	0.202308	-	-
Rat	Alligator	-	260.000	5	52.600	0.202308	260.0	-
Rat	Platypus	crown_mammals	125.000	3	44.667	0.357333	125.0	125.0
Rat	Human	crown_placentals	22.388	2	8.000	0.357333	-	-
Ostrich	Alligator	crown_Archosaurs	150.000	2	22.000	0.146667	150.0	-

*) Rate = MPL / Age

```
********************************************************************************
* M P L  C A L C U L A T I O N                                  *
********************************************************************************
```

Clock test confidence: 0.950000
Clock tests   : 5   (one for each node)
Accepted   : 1
Rejected   : 4

MPL tree   : ((((Rat:8.000000,Human:8.000000)crown_placentals:36.666667,Platypus:44.666667)crown_mammals:
7.933333,(Ostrich:22.000000,Alligator:22.000000)crown_Archosaurs:30.600000):33.733333,Frog:86.333333);

Ancestor of	Ancestor of	Name	MPL	#Terminals	Clock test: Acc/Rej
Rat	Frog	-	86.333 +/- 13.772	6	Acc
Rat	Alligator	-	52.600 +/- 8.803	5	Rej, prob=0.000004
Rat	Platypus	crown_mammals	44.667 +/- 9.727	3	Rej, prob=0.012738
Rat	Human	crown_placentals	8.000 +/- 3.917	2	Rej, prob=0.012419
Ostrich	Alligator	crown_Archosaurs	22.000 +/- 6.496	2	Rej, prob=0.000911

Chronogram corresponding to d8 tree from the example outfile above.