

Name of file containing the sequences of the putative gene and an outgroup sequence

Choice of the method to reconstruct ancestral sequences

Number of simulations to perform

Choice of mutations/indels rate

Choice of likelihood models to reconstruct ancestral sequences using the maximum likelihood approach (the use of the models chosen here is advised)

Name of treefile in parenthesis format

Codonml from PAML runs to reconstruct the ancestral sequences !

Name of treefile in parenthesis format with a label for each branch

The program runs fine !

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D:\Softwares\reevolver_soft_windows\Reevolver1.0_windows.exe
This program performs simulations for genes present in several species - calls f
or PHYLIP (parsimony) or PAML (likelihood) software to reconstruct ancestral seq
uences - Estimates the distribution of synonymous and non synonymous substitutio
ns on a neutral tree (given the branch length and a neutral substitution rate) -
Estimates the distribution of the number of disablements (stop codons and indel
s) on a neutral tree (given the branch length and a neutral substitution rate) -
Estimates the likelihood of observing a tree structure as the one observed give
n the neutral hypothesis of evolution of the gene !
Uses only capital letters in sequences !
Assumes that 1st nucleotide of sequences corresponds to the 1st position of the
codon !
Name of file which contain the sequences ?
exseq.txt
Use parsimony (0) or likelihood (1) to reconstruct ancestral sequence ?
1
How many simulations for each dataset ?
1000
Mutation rate per site per MYA ?
0.001
Use a different mutation rate for CpG sites (Y/N) ?
N
Indel rate per site per MYA ?
0.0001
Model for the estimation of ka, ks in the different lineages (0/1/2) ?
0
Model for the estimation of ka, ks in the different sites (0/1/2) ?
0
Name of tree file (must use the same header as in the seq file) ?
extreefile.txt
1 file(s) copied.
CODONML in paml 3.14b, May 2005

168 bytes for distance
0 bytes for conP0
185440 bytes for conP1
0 bytes for fhK
800000 bytes for space

TREE # 1
<<<<(1, 2), 3), 4), 5), 6, 7); MP score: 188
463600 bytes for conP1, adjusted

nTime & nrate & np: 11 2 13
Out..
lnL = -3241.684630
105 lfun, 105 eigenQc, 1335 P(t)
end of tree file.

Time used: 0:03
Name of tree file with labels (must use the same header as in the seq file and g
ive for each branch in this order: time, number of observed stopcodons and obser
ved indels) ?
extreefilelabels.txt

Counting the observed substitutions and deleterious mutations

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Simulating substitutions and deleterious mutations
Simulation 0 done !
Simulation 100 done !
Simulation 200 done !
Simulation 300 done !
Simulation 400 done !
Simulation 500 done !
Simulation 600 done !
Simulation 700 done !
Simulation 800 done !
Simulation 900 done !

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Simulating substitutions between ancestral sequences
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