

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

Name of treefile in parenthesis format (if the parsimony method is chosen, a rooted tree must be used ! This requirement comes from the PHYLIP software)

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 substituti
ons 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 ?
0
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) ?
Y
Mutation rate at CpG sites (per site per MYA) ?
0.01
Indel rate per site per MYA ?
0.0001
Name of tree file (must use the same header as in the seq file and must be root
ed (since PHYLIP takes rooted trees)) ?
extreefile_rooted.txt
1 file(s) copied.
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 obs
erved indels) ?
extreefilelabels.txt
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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
Press any key to end !
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