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Readme

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What you can do so far...

1 Required packages

You need to install the R package `ape` and `phangorn`

```
library(ape)
library(phangorn)
```

The files containing the scripts can be found github at the following address
GITHUB ADDRESS

2 Simulate genealogies

We have successfully implemented the simulation of genealogies. We can simulate genealogies with constant population size, with expanding population size and with one constant population with one expanding subpopulation (just one of each).

2.1 Constant population size

Required files :coalNonExp2.R

Command: `tree<-MakeTreeNon(timesNon=timesNon)`

Input: *timesNon*, a vector with the times at which the new leaves are to appear. (For an ultrametric tree they have to be all the same time...). In the end there will be as many leaves as the length of the vector

Examples: Example1

```
source("progs/coalNonExp2.R")
times0<-rep(0,10)+0.3*c(1:10)
tree<-MakeTreeNon(timesNon=times0)
plot.phylo(tree)
```

Example2: ultrametric tree

```
source("progs/coalNonExp2.R")
times0<-rep(0,10)
tree<-MakeTreeNon(timesNon=times0)
plot.phylo(tree)
```

2.2 Expanding population size

Required files: coalExp.R coalNonExp2.R coalBoth.R

Command: `tree<-MakeTreeExp(alphaExp=alphaExp,timesExp=timesExp)`

Input: *timesExp* the vector of times at which the new lineages are to appear. To get an ultrametric tree the vector should contain n times the same time. The number of leaves in the tree is the length of the *timesExp* vector.

alphaExp a number: the rate at which the population is expanding.

Example Example 1:

```
source("progs/coalExp.R")
timesExp<-rep(0,20)+0.00001*c(1:20)
alphaExp<-20
tree<-MakeTreeExp(alphaExp=alphaExp,timesExp=timesExp)
plot.phylo(tree)
```

Example 2: ultrametric tree

```
source("progs/coalExp.R")
timesExp<-rep(0,20)
alphaExp<-50
tree<-MakeTreeExp(alphaExp=alphaExp,timesExp=timesExp)
plot.phylo(tree)
```

2.3 Constant pupulation with expanding subpopulation

Required files: coalExp.R

Command: `tree<-MakeTreeBoth(timesExp,timesNon,alpha,Ts,Texp)`

Input: *timesExp* the vector of times at which the new lineages of the expanding subpopulation are to appear. To get an ultrametric tree the vector should contain n times the same time. The number of leaves in this subtree is the length of the *timesExp* vector.

timesNon, a vector with the times at which the new leaves of the non expanding subpopulation are to appear. (For an ultrametric tree they have to be all the same time...). In the end there will be as many leaves in the nonexpanding subpopulation as the length of the vector

alpha a number: the rate at which the population is expanding.

Ts the time at which the two subpopulations separate. For any $t > Ts$ (the zero of time is at the more recent leave) the two subpopulations will be merged and treated as one (any lineage can coalesce with any other).

Texp the time at which one of the expanding subpopulations starts to expand. If we set this time to 0 we just have two identical subpopulations that expand at the same rate $Texp \leq Ts$.

Example Example 1:

```
source("progs/coalNonExp2.R")
source("progs/coalExp.R")
source("progs/coalBoth.R")
timesExp<-c(seq(0.5,0.51,0.001))
timesNon<-c(seq(0.1,0.2,0.01))
alpha<-25
Ts<-2
Texp<-2
tree<-MakeTreeBoth(timesExp,timesNon,alpha,Ts,Texp)
plot.phylo(tree)
```

Example 2: ultrametric tree

```
source("progs/coalNonExp2.R")
source("progs/coalExp.R")
source("progs/coalBoth.R")
timesExp<-rep(0,20)
timesNon<-rep(0,20)
alphaExp<-50
Ts<-20
Texp<-10
tree<-MakeTreeBoth(timesExp,timesNon,alpha,Ts,Texp)
plot.phylo(tree)
```

Example 3: two subpopulations, none expanding

```
source("progs/coalNonExp2.R")
source("progs/coalExp.R")
source("progs/coalBoth.R")
timesExp<-rep(0,20)
timesNon<-rep(0,20)
alphaExp<-50
Ts<-20
Texp<-0
tree<-MakeTreeBoth(timesExp,timesNon,alpha,Ts,Texp)
plot.phylo(tree)
```

3 Compute Likelihood of a genealogy

We compute the likelihood of the genealogy using the Likelihood derived in Drummond et al []

3.1 Constant population size

Required files :like0.2.R

Command: `l<-LikeliHood(tree,theta)`

Input: *tree*, the tree that we want to compute the likelihood of

theta, theta is the factor converting "coalescent time" into calendar time. In our simulated trees is 1 because time is already in units of "coalescent time".

Examples: Example1

```
source("progs/coalNonExp2.R")
source("progs/like0.2.R")
times0<-rep(0,10)+0.3*c(1:10)
tree<-MakeTreeNon(timesNon=times0)
plot.phylo(tree)
 l<-LikeliHood(tree,1)
```

   Example2: ultrametric tree

```
source("progs/coalNonExp2.R")
source("progs/like0.2.R")
times0<-rep(0,10)
tree<-MakeTreeNon(timesNon=times0)
plot.phylo(tree)
 l<-LikeliHood(tree,1)
```

3.2   Expanding population size

Required files   :like0.2.R

Command: `l<-LikeliHoodExp(tree,theta, alpha)`

Input: *tree*, the tree that we want to compute the likelihood of
   theta, theta is the factor converting "coalescent time" into calendar time. In our simulated trees is 1 because time is already in units of "coalescent time".
   alpha, the rate at which the population is expanding

Examples:

```
source("progs/coalExp.R")
source("progs/like0.2.R")
timesExp<-rep(0,20)+0.00001*c(1:20)
alphaExp<-20
tree<-MakeTreeExp(alphaExp=alphaExp,timesExp=timesExp)
plot.phylo(tree)
l<-LikeliHoodExp(tree,1,10)
```

   Example 2: ultrametric tree

```
source("progs/coalExp.R")
source("progs/like0.2.R")
timesExp<-rep(0,20)
alphaExp<-50
tree<-MakeTreeExp(alphaExp=alphaExp,timesExp=timesExp)
plot.phylo(tree)
l<-LikeliHoodExp(tree,1,10)
```

3.3 Constant pupulation with expanding subpopulation

Required files :like0.2.R

Command: `l<-LikeliHoodBoth(tree, branch, alpha,theta)`

Input: *tree*, the tree that we want to compute the likelihood of
    branch, the branch where the two subpopulations split
    theta, theta is the factor converting "coalescent time" into calendar time. In our simulated trees is 1 because time is already in units of "coalescent time".
    alpha, the rate at which the population is expanding

Problem: there's a problem somehow in the way I generate the tree so that extract.clade does not work in my tree. Anyway if you write and reread the same tree, the format gets fixed and extract.clade works perfectly. This is something that needs to be fixed...

Example Example 1:

```
source("progs/coalNonExp2.R")
source("progs/coalExp.R")
source("progs/coalBoth.R")
source("progs/like0.2.R")
timesExp<-c(seq(0.5,0.51,0.001))
timesNon<-c(seq(0.1,0.2,0.01))
alpha<-25
Ts<-2
Texp<-2
tree<-MakeTreeBoth(timesExp,timesNon,alpha,Ts,Texp)
plot.phylo(tree)
write.tree(tree, file="treetemp.tre")
tree<-read.tree("treetemp.tre")

l<-LikelihoodBoth(tree,40,10,1)
```

    Example 2: ultrametric tree

```
source("progs/coalNonExp2.R")
source("progs/coalExp.R")
source("progs/coalBoth.R")
source("progs/like0.2.R")
timesExp<-rep(0,20)
timesNon<-rep(0,20)
alphaExp<-50
Ts<-20
Texp<-10
tree<-MakeTreeBoth(timesExp,timesNon,alpha,Ts,Texp)
plot.phylo(tree)
write.tree(tree, file="treetemp.tre")
tree<-read.tree("treetemp.tre")

l<-LikelihoodBoth(tree,20,10,1)
```

Example 3: two subpopulations, none expanding

```
source("progs/coalNonExp2.R")
source("progs/coalExp.R")
source("progs/coalBoth.R")
source("progs/like0.2.R")
timesExp<-rep(0,20)
timesNon<-rep(0,20)
alphaExp<-50
Ts<-20
Texp<-0
tree<-MakeTreeBoth(timesExp,timesNon,alpha,Ts,Texp)
write.tree(tree, file="treetemp.tre")
tree<-read.tree("treetemp.tre")

plot.phylo(tree)
l<-LikelihoodBoth(tree,20,10,1)
```