

Package: TransPhylo (via r-universe)

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Title Inference of Transmission Tree from a Dated Phylogeny

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Description Inference of transmission tree from a dated phylogeny.

Includes methods to simulate and analyse outbreaks. The methodology is described in Didelot et al. (2014)

<doi:10.1093/molbev/msu121>, Didelot et al. (2017)

<doi:10.1093/molbev/msw275>.

License GPL (>=2)

Depends R (>= 3.0.0)

Imports Rcpp (>= 0.12.8), stats, graphics, ape

Suggests knitr, testthat, purrr, coda, grDevices, lattice, rmarkdown

LinkingTo Rcpp

Encoding UTF-8

RoxygenNote 7.2.3

SystemRequirements C++11

VignetteBuilder knitr

NeedsCompilation yes

Repository <https://xavierdidelot.r-universe.dev>

RemoteUrl <https://github.com/xavierdidelot/transphylo>

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TransPhylo-package *Inference of Transmission Tree from a Dated Phylogeny*

Description

Inference of transmission tree from a dated phylogeny. Includes methods to simulate and analyse outbreaks.

Author(s)

Xavier Didelot <xavier.didelot@gmail.com>

References

Didelot et al. (2014) <doi:10.1093/molbev/msu121> Didelot et al. (2017) <doi:10.1093/molbev/msw275>.

See Also

<https://github.com/xavierdidelot/TransPhylo>

as.mcmc.resTransPhylo *Convert to coda mcmc format*

Description

Convert to coda mcmc format

Usage

```
as.mcmc.resTransPhylo(x, burnin = 0.5)
```

Arguments

x	Output from inferTTree
burnin	Proportion of the MCMC output to be discarded as burnin

Value

mcmc object from coda package

computeMatTDist *Build a matrix indicating for each pairs of individuals how many intermediates there are in the transmission chain*

Description

Build a matrix indicating for each pairs of individuals how many intermediates there are in the transmission chain

Usage

```
computeMatTDist(record, burnin = 0.5)
```

Arguments

record	Output from inferTTree function
burnin	Proportion of the MCMC output to be discarded as burnin

Value

Matrix of intermediates in transmission chains between pairs of hosts

computeMatWIW	<i>Build a matrix of probability of who infected whom from a MCMC output</i>
---------------	--

Description

Build a matrix of probability of who infected whom from a MCMC output

Usage

```
computeMatWIW(record, burnin = 0.5)
```

Arguments

record	Output from inferTTree function
burnin	Proportion of the MCMC output to be discarded as burnin

Value

Matrix of probability of who infected whom

consTTree	<i>Build a consensus transmission tree from a MCMC output</i>
-----------	---

Description

Build a consensus transmission tree from a MCMC output

Usage

```
consTTree(record, burnin = 0.5, minimum = 0.2, debug = F)
```

Arguments

record	Output from inferTTree function
burnin	Proportion of the MCMC output to be discarded as burnin
minimum	Minimum probability for inclusion of a partition in the consensus
debug	Used for debugging

Value

The consensus transmission tree

convertToCoda	<i>Convert to coda mcmc format</i>
---------------	------------------------------------

Description

Convert to coda mcmc format

Usage

```
convertToCoda(record, burnin = 0.5)
```

Arguments

record	Output from inferTTree function
burnin	Proportion of the MCMC output to be discarded as burnin

Value

Object of class mcmc from coda package

dateLastSample	<i>Return the date of last sample from a ttree or ctree or ptree</i>
----------------	--

Description

Return the date of last sample from a ttree or ctree or ptree

Usage

```
dateLastSample(x)
```

Arguments

x	A transmission tree or colored tree or phylogenetic tree
---	--

Value

date of the last sample

extractCTree	<i>Return the combined tree corresponding to a given iteration of the TransPhylo results</i>
--------------	--

Description

Return the combined tree corresponding to a given iteration of the TransPhylo results

Usage

```
extractCTree(res, iteration)
```

Arguments

res	Output from inferTTree command
iteration	Number of the iteration to be extracted

Value

The colored tree at the specified iteeatino

extractPTree	<i>Extracts phylogenetic tree from a combined phylogenetic/transmission tree</i>
--------------	--

Description

Extracts phylogenetic tree from a combined phylogenetic/transmission tree

Usage

```
extractPTree(ctree)
```

Arguments

ctree	Combined tree
-------	---------------

Value

phylogenetic tree

Examples

```
extractPTree(simulateOutbreak())
```

extractTTree	<i>Extracts transmission tree from a combined phylogenetic/transmission tree</i>
--------------	--

Description

Extracts transmission tree from a combined phylogenetic/transmission tree

Usage

```
extractTTree(ctree)
```

Arguments

ctree	Combined tree
-------	---------------

Value

transmission tree

Examples

```
extractTTree(simulateOutbreak())
```

getGenerationTimeDist	<i>Extract and return realised generation time distribution</i>
-----------------------	---

Description

Extract and return realised generation time distribution

Usage

```
getGenerationTimeDist(  
  record,  
  burnin = 0.5,  
  maxi = 2,  
  numBins = 20,  
  show.plot = F  
)
```

Arguments

record	MCMC output produced by inferTTree
burnin	Proportion of the MCMC output to be discarded as burnin
maxi	Maximum generation time to consider
numBins	Number of time bins to compute and display distribution
show.plot	Show a barplot of the distribution

Value

Vector of times between becoming infected and infecting others (generation times) in the posterior

<code>getIncidentCases</code>	<i>Returns and/or plot numbers of sampled and unsampled cases over time</i>
-------------------------------	---

Description

Returns and/or plot numbers of sampled and unsampled cases over time

Usage

```
getIncidentCases(
  record,
  burnin = 0.5,
  numBins = 10,
  dateT = NA,
  show.plot = FALSE
)
```

Arguments

<code>record</code>	Output from <code>inferTTree</code> function
<code>burnin</code>	Proportion of the MCMC output to be discarded as burnin
<code>numBins</code>	Number of time bins to compute and display incident cases
<code>dateT</code>	Date when process stops (this can be <code>Inf</code> for fully resolved outbreaks)
<code>show.plot</code>	Show a plot of incident cases over time with stacked bars

Value

List with four entries. `Time` is a vector of the time points. `allCases` is the average number of cases at each time in the posterior. `sampledCases`: average number of sampled cases. `unsampCases`: average number of unsampled cases.

getInfectionTimeDist *Extract and return distribution of infection time of given sampled case(s)*

Description

Extract and return distribution of infection time of given sampled case(s)

Usage

```
getInfectionTimeDist(record, burnin = 0.5, k, numBins = 10, show.plot = F)
```

Arguments

record	MCMC output produced by inferTTree
burnin	Proportion of the MCMC output to be discarded as burnin
k	Case(s) whose posterior infection times are to be extracted. Either a string matching one of the case names in the data, or a vector of such strings
numBins	Number of bins to use for plot
show.plot	Show a barplot of the distribution

Value

Posterior infection times for the case(s) in k. If length(k)==1 then a vector is returned, otherwise a matrix

getOffspringDist *Extract and return offspring distribution of given sampled case(s)*

Description

Extract and return offspring distribution of given sampled case(s)

Usage

```
getOffspringDist(record, burnin = 0.5, k, show.plot = F)
```

Arguments

record	MCMC output produced by inferTTree
burnin	Proportion of the MCMC output to be discarded as burnin
k	Case(s) whose offspring distribution are to be extracted. Either a string matching one of the case names in the data, or a vector of such strings
show.plot	Show a barplot of the distribution

Value

Posterior offspring distribution for the case(s) in k. If length(k)==1 then a vector is returned, otherwise a matrix

getSamplingTimeDist *Extract and return realised sampling time distribution*

Description

Extract and return realised sampling time distribution

Usage

```
getSamplingTimeDist(
  record,
  burnin = 0.5,
  maxi = 2,
  numBins = 20,
  show.plot = F
)
```

Arguments

record	MCMC output produced by inferTTree
burnin	Proportion of the MCMC output to be discarded as burnin
maxi	Maximum generation time to consider
numBins	Number of time bins to compute and display distribution
show.plot	Show a barplot of the distribution

Value

Vector of times between becoming infected and becoming sampled in the posterior

inferTTree *Infer transmission tree given a phylogenetic tree*

Description

Infer transmission tree given a phylogenetic tree

Usage

```
inferTTree(
  ptree,
  w.shape = 2,
  w.scale = 1,
  ws.shape = NA,
  ws.scale = NA,
  w.mean = NA,
  w.std = NA,
  ws.mean = NA,
  ws.std = NA,
  mcmcIterations = 1000,
  thinning = 1,
  startNeg = 100/365,
  startOff.r = 1,
  startOff.p = 0.5,
  startPi = 0.5,
  updateNeg = TRUE,
  updateOff.r = TRUE,
  updateOff.p = FALSE,
  updatePi = TRUE,
  qNeg = NA,
  qOff.r = NA,
  qOff.p = NA,
  qPi = NA,
  startCTree = NA,
  updateTTree = TRUE,
  optiStart = 2,
  dateT = Inf,
  delta_t = NA,
  verbose = F
)
```

Arguments

<code>ptree</code>	Phylogenetic tree
<code>w.shape</code>	Shape parameter of the Gamma distribution representing the generation time
<code>w.scale</code>	Scale parameter of the Gamma distribution representing the generation time
<code>ws.shape</code>	Shape parameter of the Gamma distribution representing the sampling time
<code>ws.scale</code>	Scale parameter of the Gamma distribution representing the sampling time
<code>w.mean</code>	Mean of the Gamma distribution representing the generation time
<code>w.std</code>	Std of the Gamma distribution representing the generation time
<code>ws.mean</code>	Mean of the Gamma distribution representing the sampling time
<code>ws.std</code>	Std of the Gamma distribution representing the sampling time
<code>mcmcIterations</code>	Number of MCMC iterations to run the algorithm for

thinning	MCMC thinning interval between two sampled iterations
startNeg	Starting value of within-host coalescent parameter $Ne * g$
startOff.r	Starting value of parameter off.r
startOff.p	Starting value of parameter off.p
startPi	Starting value of sampling proportion pi
updateNeg	Whether or not to update the parameter $Ne * g$
updateOff.r	Whether or not to update the parameter off.r
updateOff.p	Whether or not to update the parameter off.p
updatePi	Whether or not to update the parameter pi
qNeg	Proposal kernel range for parameter $Ne * g$
qOff.r	Proposal kernel range for parameter Off.r
qOff.p	Proposal kernel range for parameter Off.p
qPi	Proposal kernel range for parameter pi
startCTree	Optional combined tree to start from
updateTTree	Whether or not to update the transmission tree
optiStart	Type of optimisation to apply to MCMC start point (0=none, 1=slow, 2=fast)
dateT	Date when process stops (this can be Inf for fully simulated outbreaks)
delta_t	Grid precision (smaller is better but slower)
verbose	Whether or not to use verbose mode (default is false)

Value

posterior sample set of transmission trees

Examples

```
inferTTree(ptreeFromPhylo(ape::rtree(5),2020),mcmcIterations=100)
```

infer_multitree_share_param

Simultaneously infer transmission trees given phylogenetic trees User can specify any subset of parameters that will be shared by providing a character vector of parameter names to the argument "share".

Description

Simultaneously infer transmission trees given phylogenetic trees User can specify any subset of parameters that will be shared by providing a character vector of parameter names to the argument "share".

Usage

```
infer_multitree_share_param(
  ptree_lst,
  w.shape = 2,
  w.scale = 1,
  ws.shape = w.shape,
  ws.scale = w.scale,
  mcmcIterations = 1000,
  thinning = 1,
  startNeg = 100/365,
  startOff.r = 1,
  startOff.p = 0.5,
  startPi = 0.5,
  prior_pi_a = 1,
  prior_pi_b = 1,
  updateNeg = TRUE,
  updateOff.r = TRUE,
  updateOff.p = FALSE,
  updatePi = TRUE,
  share = NULL,
  startCTree_lst = rep(NA, length(ptree_lst)),
  updateTTree = TRUE,
  optiStart = 2,
  dateT = Inf,
  delta_t = 0.01,
  verbose = F
)
```

Arguments

ptree_lst	List of phylogenetic tree
w.shape	Shape parameter of the Gamma probability density function representing the generation time
w.scale	Scale parameter of the Gamma probability density function representing the generation time
ws.shape	Shape parameter of the Gamma probability density function representing the sampling time
ws.scale	Scale parameter of the Gamma probability density function representing the sampling time
mcmcIterations	Number of MCMC iterations to run the algorithm for
thinning	MCMC thinning interval between two sampled iterations
startNeg	Starting value of within-host coalescent parameter $Ne \cdot g$
startOff.r	Starting value of parameter off.r
startOff.p	Starting value of parameter off.p
startPi	Starting value of sampling proportion pi

prior_pi_a	First shape parameter of Beta prior for pi
prior_pi_b	Second shape parameter of Beta prior for pi
updateNeg	Whether or not to update the parameter Ne*g
updateOff.r	Whether or not to update the parameter off.r
updateOff.p	Whether or not to update the parameter off.p
updatePi	Whether or not to update the parameter pi
share	Character vector of parameters to be shared. For example, share = c("off.r", "off.p") would share the offspring distribution. Allowed parameter names are "neg", "off.r", "off.p" and "pi".
startCTree_lst	Optional combined list of trees to start from
updateTTree	Whether or not to update the transmission tree
optiStart	Type of optimisation to apply to MCMC start point (0=none, 1=slow, 2=fast)
dateT	Date when process stops (this can be Inf for fully simulated outbreaks)
delta_t	Grid precision (smaller is better but slower)
verbose	Whether or not to use verbose mode (default is false)

Value

list the same size as input, each element contains posterior transmission trees inferred from corresponding phylogenetic tree

Author(s)

Yuanwei Xu

makeCTreeFromPTree	<i>Create a transmission tree compatible with the provided phylogenetic tree</i>
--------------------	--

Description

Create a transmission tree compatible with the provided phylogenetic tree

Usage

```
makeCTreeFromPTree(
  ptree,
  off.r = NA,
  off.p = NA,
  neg = NA,
  pi = NA,
  w.shape = NA,
  w.scale = NA,
  ws.shape = NA,
```

```

    ws.scale = NA,
    T = NA,
    optiStart = 0
  )

```

Arguments

ptree	Phylogenetic tree
off.r	First parameter of the negative binomial distribution for offspring number
off.p	Second parameter of the negative binomial distribution for offspring number
neg	the within-host effective population size (N_e) times generation duration (g)
pi	probability of sampling an infected individual
w.shape	Shape parameter of the Gamma probability density function representing the generation time
w.scale	Scale parameter of the Gamma probability density function representing the generation time
ws.shape	Shape parameter of the Gamma probability density function representing the sampling time
ws.scale	Scale parameter of the Gamma probability density function representing the sampling time
T	Date when process stops (this can be Inf for fully simulated outbreaks)
optiStart	Method used to optimised colored tree (0=none, 1=slow, 2=fast)

Value

A minimal non-zero probability phylogenetic+transmission tree, or an optimised version if parameters are provided

makeTTree	<i>Simulate a transmission tree</i>
-----------	-------------------------------------

Description

Simulate a transmission tree

Usage

```

makeTTree(
  off.r,
  off.p,
  pi,
  w.shape,
  w.scale,
  ws.shape = w.shape,

```

```

ws.scale = w.scale,
maxTime = Inf,
nSampled = NA
)

```

Arguments

off.r	First parameter of the negative binomial distribution for offspring number
off.p	Second parameter of the negative binomial distribution for offspring number
pi	probability of sampling an infected individual
w.shape	Shape parameter of the Gamma probability density function representing the generation time
w.scale	Scale parameter of the Gamma probability density function representing the generation time
ws.shape	Shape parameter of the Gamma probability density function representing the sampling time
ws.scale	Scale parameter of the Gamma probability density function representing the sampling time
maxTime	Duration of simulation (can be Inf)
nSampled	Number of sampled individuals (can be NA for any)

Value

A N*3 matrix in the following format with one row per infected host, first column is time of infection, second column is time of sampling, third column is infector

medTTree	<i>Return the medoid from a MCMC output</i>
----------	---

Description

Return the medoid from a MCMC output

Usage

```
medTTree(record, burnin = 0.5)
```

Arguments

record	Output from inferTTree function
burnin	Proportion of the MCMC output to be discarded as burnin

Value

The index of the medoid

phyloFromPTree	<i>Converts a phylogenetic tree into an ape phylo object</i>
----------------	--

Description

Converts a phylogenetic tree into an ape phylo object

Usage

```
phyloFromPTree(ptree)
```

Arguments

ptree	phylogenetic tree
-------	-------------------

Value

phylo object

Examples

```
phyloFromPTree(extractPTree(simulateOutbreak()))
```

plot.ctree	<i>Plotting for ctree</i>
------------	---------------------------

Description

Plotting for ctree

Usage

```
## S3 method for class 'ctree'  
plot(x, ...)
```

Arguments

x	Object of class ctree, ie a colored phylogenetic tree
...	Additional parameters are passed on

Value

Plot of ctree

Examples

```
plot(simulateOutbreak())
```

plot.ptree *Plotting for ptree*

Description

Plotting for ptree

Usage

```
## S3 method for class 'ptree'  
plot(x, ...)
```

Arguments

x Object of class ptree, ie a phylogenetic tree
... Additional parameters are passed on to ape::plot.phylo

Value

Plot of ptree

Examples

```
plot(ptreeFromPhylo(ape::rtree(5),2020))
```

plot.resTransPhylo *Plotting for resTransPhylo*

Description

Plotting for resTransPhylo

Usage

```
## S3 method for class 'resTransPhylo'  
plot(x, ...)
```

Arguments

x Output from inferTTree
... Additional parameters are passed on

Value

Plot of TransPhylo results

plot.ttree	<i>Plotting for ttree</i>
------------	---------------------------

Description

Plotting for ttree

Usage

```
## S3 method for class 'ttree'
plot(x, type = "summarised", w.shape = NA, w.scale = NA, ...)
```

Arguments

x	Object of class ttree, ie a transmission tree
type	Type of plot to display, can be 'detailed' or 'summarised' (default)
w.shape	Shape parameter of the generation time, needed for detailed plot only
w.scale	Scale parameter of the generation time, needed for detailed plot only
...	Additional parameters are passed on

Value

Plot of ttree

Examples

```
plot(extractTTree(simulateOutbreak()))
```

plotCTree	<i>Plot both phylogenetic and transmission trees using colors on the phylogeny</i>
-----------	--

Description

Plot both phylogenetic and transmission trees using colors on the phylogeny

Usage

```
plotCTree(
  tree,
  showLabels = TRUE,
  showStars = TRUE,
  cols = NA,
  maxTime = NA,
  cex = 1
)
```

Arguments

tree	Combined phylogenetic/transmission tree
showLabels	Whether or not to show the labels
showStars	Whether or not to show stars representing transmission events
cols	Colors to use for hosts
maxTime	Maximum time to show on the x axis
cex	Expansion factor

Value

Returns invisibly the first parameter

Examples

```
plotCTree(simulateOutbreak())
```

plotTraces

Plot MCMC traces

Description

Plot MCMC traces

Usage

```
plotTraces(record, burnin = 0, extend = F)
```

Arguments

record	Output from inferTTree function
burnin	Proportion of the MCMC output to be discarded as burnin
extend	Whether to also show traces of off.r and off.p

Value

Returns invisibly the first parameter

plotTTree *Plot a transmission tree in a detailed format*

Description

Plot a transmission tree in a detailed format

Usage

```
plotTTree(ttree, w.shape, w.scale, showLabels = TRUE, maxTime = NA, cex = 1)
```

Arguments

ttree	Transmission tree
w.shape	Shape parameter of the Gamma probability density function representing the generation time
w.scale	Scale parameter of the Gamma probability density function representing the generation time
showLabels	Whether or not to show the labels
maxTime	Maximum value of time to show on x axis
cex	Expansion factor

Value

Returns invisibly the first parameter

Examples

```
plotTTree(extractTTree(simulateOutbreak()),2,1)
```

plotTTree2 *Plot a transmission tree in an economic format*

Description

Plot a transmission tree in an economic format

Usage

```
plotTTree2(  
  ttree,  
  showLabels = TRUE,  
  showMissingLinks = 0,  
  maxTime = NA,  
  cex = 1  
)
```

Arguments

ttree	Transmission tree
showLabels	Boolean for whether or not to show the labels
showMissingLinks	Option for how to show missing links: (0) as dots, (1) as several gray levels, (2) as a single gray level
maxTime	Maximum value of time to show on x axis
cex	Expansion factor

Value

Returns invisibly the first parameter

Examples

```
plotTTree2(extractTTree(simulateOutbreak()))
```

print.ctree *Print function for ctree objects*

Description

Print function for ctree objects

Usage

```
## S3 method for class 'ctree'
print(x, ...)
```

Arguments

x	Object of class ctree, ie a colored phylogenetic tree
...	Additional parameters are passed on

Value

Print out details of the ctree

Examples

```
print(simulateOutbreak())
```

print.ptree	<i>Print function for ptree objects</i>
-------------	---

Description

Print function for ptree objects

Usage

```
## S3 method for class 'ptree'  
print(x, ...)
```

Arguments

x	Object of class ptree, ie a phylogenetic tree
...	Additional parameters are passed on

Value

Print out details of the ptree

Examples

```
print(extractPTree(simulateOutbreak()))
```

print.resTransPhylo	<i>Print function for resTransPhylo objects</i>
---------------------	---

Description

Print function for resTransPhylo objects

Usage

```
## S3 method for class 'resTransPhylo'  
print(x, ...)
```

Arguments

x	output from inferTTree
...	Additional parameters are passed on

Value

Print out details of TransPhylo results

```
print.ttree          Print function for tree objects
```

Description

Print function for ttree objects

Usage

```
## S3 method for class 'ttree'
print(x, ...)
```

Arguments

```
x          Object of class ttree, ie a transmission tree
...        Additional parameters are passed on
```

Value

Print out details of the ttree

Examples

```
print(extractTTree(simulateOutbreak()))
```

```
probPTreeGivenTTree  Calculate the probability of a phylogenetic tree given a transmission tree
```

Description

Calculate the probability of a phylogenetic tree given a transmission tree

Usage

```
probPTreeGivenTTree(ctree, neg, w = integer(0))
```

Arguments

```
ctree      Combined phylogenetic/transmission tree
neg        Within-host coalescent rate
w          Vector of hosts for which to calculate the probability, or nothing for all
```

Value

Probability of phylogeny given transmission tree

probPTreeGivenTTreeR *Calculate the probability of a phylogenetic tree given a transmission tree*

Description

Calculate the probability of a phylogenetic tree given a transmission tree

Usage

```
probPTreeGivenTTreeR(ctree, neg, w = NULL)
```

Arguments

ctree	Combined phylogenetic/transmission tree
neg	Within-host coalescent rate
w	Vector of hosts for which to calculate the probability, or NULL for all

Value

Probability of phylogeny given transmission tree

probTTree *Calculates the log-probability of a transmission tree*

Description

Calculates the log-probability of a transmission tree

Usage

```
probTTree(
  ttree,
  rOff,
  pOff,
  pi,
  shGen,
  scGen,
  shSam,
  scSam,
  dateT,
  delta_t = 0.01
)
```

Arguments

ttree	Transmission tree
rOff	First parameter of the negative binomial distribution for offspring number
pOff	Second parameter of the negative binomial distribution for offspring number
pi	probability of sampling an infected individual
shGen	Shape parameter of the Gamma probability density function representing the generation time
scGen	Scale parameter of the Gamma probability density function representing the generation time
shSam	Shape parameter of the Gamma probability density function representing the sampling time
scSam	Scale parameter of the Gamma probability density function representing the sampling time
dateT	Date when process stops (this can be Inf for fully simulated outbreaks)
delta_t	Grid precision

Value

Probability of the transmission tree

probTTreeR

Calculates the log-probability of a transmission tree

Description

Calculates the log-probability of a transmission tree

Usage

```
probTTreeR(
  ttree,
  off.r,
  off.p,
  pi,
  w.shape,
  w.scale,
  ws.shape,
  ws.scale,
  dateT
)
```

Arguments

<code>ttree</code>	Transmission tree
<code>off.r</code>	First parameter of the negative binomial distribution for offspring number
<code>off.p</code>	Second parameter of the negative binomial distribution for offspring number
<code>pi</code>	probability of sampling an infected individual
<code>w.shape</code>	Shape parameter of the Gamma probability density function representing the generation time
<code>w.scale</code>	Scale parameter of the Gamma probability density function representing the generation time
<code>ws.shape</code>	Shape parameter of the Gamma probability density function representing the sampling time
<code>ws.scale</code>	Scale parameter of the Gamma probability density function representing the sampling time
<code>dateT</code>	Date when process stops (this can be Inf for fully simulated outbreaks)

Value

Probability of the transmission tree

`ptreeFromPhylo` *Converts an ape phylo object into a phylogenetic tree*

Description

Converts an ape phylo object into a phylogenetic tree

Usage

```
ptreeFromPhylo(tr, dateLastSample)
```

Arguments

<code>tr</code>	phylo object
<code>dateLastSample</code>	date of the last sample

Value

phylogenetic tree

Examples

```
ptreeFromPhylo(ape::rtree(5), 2020)
```

selectTTree	<i>Select the most representative transmission tree from a MCMC output</i>
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Description

Select the most representative transmission tree from a MCMC output

Usage

```
selectTTree(record, burnin = 0.5)
```

Arguments

record	Output from inferTTree function
burnin	Proportion of the MCMC output to be discarded as burnin

Value

The index of the selected transmission tree

simulateOutbreak	<i>Simulate an outbreak</i>
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Description

Simulate an outbreak

Usage

```
simulateOutbreak(
  off.r = 1,
  off.p = 0.5,
  neg = 0.25,
  nSampled = NA,
  pi = 0.5,
  w.shape = 2,
  w.scale = 1,
  ws.shape = NA,
  ws.scale = NA,
  w.mean = NA,
  w.std = NA,
  ws.mean = NA,
  ws.std = NA,
  dateStartOutbreak = 2000,
  dateT = Inf
)
```

Arguments

off.r	First parameter of the negative binomial distribution for offspring number
off.p	Second parameter of the negative binomial distribution for offspring number
neg	the within-host effective population size (N_e) times generation duration (g)
nSampled	number of sampled infected individuals, or NA for any
pi	probability of sampling an infected individual
w.shape	Shape parameter of the Gamma probability density function representing the generation time
w.scale	Scale parameter of the Gamma probability density function representing the generation time
ws.shape	Shape parameter of the Gamma probability density function representing the sampling time
ws.scale	Scale parameter of the Gamma probability density function representing the sampling time
w.mean	Mean of the Gamma distribution representing the generation time
w.std	Std of the Gamma distribution representing the generation time
ws.mean	Mean of the Gamma distribution representing the sampling time
ws.std	Std of the Gamma distribution representing the sampling time
dateStartOutbreak	Date when index case becomes infected
dateT	Date when process stops (this can be Inf for fully simulated outbreaks)

Value

Combined phylogenetic and transmission tree

Examples

```
simulateOutbreak()
simulateOutbreak(off.r=2,dateStartOutbreak=2010,dateT=2015)
```

summary.resTransPhylo *Summary function for resTransPhylo objects*

Description

Summary function for resTransPhylo objects

Usage

```
## S3 method for class 'resTransPhylo'
summary(object, ...)
```

Arguments

object	output from inferTTree
...	Passed on to print.phylo

Value

Print out details of TransPhylo results

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