

Package ‘TransPhylo’

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Type Package

Title Inference of Transmission Tree under a Within-Host Evolution Model

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Depends

Suggests ape, knitr

Description Inference of transmission tree under a within-host evolution model.

VignetteBuilder knitr

License GPL (>=2)

RoxygenNote 5.0.1

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TransPhylo-package *Inference of transmission tree under a within-host evolution model* ~~
TransPhylo ~~

Description

More about what it does (maybe more than one line) ~~ A concise (1-5 lines) description of the package ~~

Details

Package: TransPhylo
 Type: Package
 Version: 1.0
 Date: 2014-02-18
 License: GPL (>=2)

~~ An overview of how to use the package, including the most important functions ~~

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References

~~ Literature or other references for background information ~~

consTTree *Build a consensus transmission tree from a MCMC output*

Description

Build a consensus transmission tree from a MCMC output

Usage

```
consTTree(record, burnin = 0.5, minimum = 0.1)
```

Arguments

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

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

Extracts phylogenetic tree from a combined phylogenetic/transmission tree

Usage

```
extractPTree(ctree)
```

Arguments

ctree	Combined tree
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Value

phylogenetic tree

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

Extracts transmission tree from a combined phylogenetic/transmission tree

Usage

```
extractTTree(ctree)
```

Arguments

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

Value

transmission tree

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 = w.shape,
  ws.scale = w.scale, mcmcIterations = 1000, thinning = 1,
  startNeg = 100/365, startOff.r = 1, startOff.p = 0.5, startPi = 0.5,
  updateNeg = T, updateOff.r = T, updateOff.p = F, updatePi = T,
  startCTree = NA, updateTTree = TRUE, optiStart = T, dateT = Inf,
  allowTransPostSamp = T)
```

Arguments

ptree	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
updateNeg	Whether or not to update the parameter $Ne \cdot g$
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
startCTree	Optional combined tree to start from
updateTTree	Whether or not to update the transmission tree
optiStart	Whether or not to optimise the MCMC start point
dateT	Date when process stops (this can be Inf for fully simulated outbreaks)
allowTransPostSamp	Whether or not to allow transmission after sampling of a host

Value

posterior sample set of transmission trees

makeCtreeFromPtree	<i>Create a transmission tree compatible with the provided phylogenetic tree</i>
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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,
  allowTransPostSamp = NA)
```

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)
allowTransPostSamp	Whether or not to allow transmission after sampling of a host

Value

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

makeTTree *Simulate a transmission tree*

Description

Simulate a transmission tree

Usage

```
makeTTree(off.r, off.p, pi, w.shape, w.scale, ws.shape, ws.scale, maxTime,
          nSampled)
```

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

phyloFromPTree *Converts a phylogenetic tree into an ape phylo object*

Description

Converts a phylogenetic tree into an ape phylo object

Usage

```
phyloFromPTree(ptree)
```

Arguments

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

Value

phylo object

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

Plot both phylogenetic and transmission trees using colors on the phylogeny

Usage

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

Arguments

tree	Combined phylogenetic/transmission tree
showLabels	Whether or not to show the labels
cols	Colors to use for hosts
maxTime	Maximum time to show on the x axis

Examples

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

plotTTree	<i>Plot a transmission tree</i>
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Description

Plot a transmission tree

Usage

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

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

plotTTree2	<i>Plot a transmission tree in an economic format</i>
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Description

Plot a transmission tree in an economic format

Usage

```
plotTTree2(ttree, showLabels = TRUE, showMissingLinks = 0)
```

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

probPTreeGivenTTree	<i>Calculate the probability of a phylogenetic tree given a transmission tree</i>
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Description

Calculate the probability of a phylogenetic tree given a transmission tree

Usage

```
probPTreeGivenTTree(ctree, neg)
```

Arguments

ctree	Combined phylogenetic/transmission tree
neg	Within-host coalescent rate

Value

Probability of phylogeny given transmission tree

probTTree	<i>Calculates the log-probability of a transmission tree</i>
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Description

Calculates the log-probability of a transmission tree

Usage

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

Arguments

ttree	Transmission 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
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
dateT	Date when process stops (this can be Inf for fully simulated outbreaks)
allowTransPostSamp	Whether or not to allow transmission after sampling of a host

Value

Probability of the transmission tree

ptreeFromPhylo	<i>Converts an ape phylo object into a phylogenetic tree</i>
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Description

Converts an ape phylo object into a phylogenetic tree

Usage

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

Arguments

tr phylo object
 dateLastSample date of the last sample

Value

phylogenetic 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 = w.shape,
  ws.scale = w.scale, 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
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

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

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