Package ‘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.
as.mcmc.resTransPhylo

Author(s)
Xavier Didelot <xavier.didelot@gmail.com>

References

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

**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**  
*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 = 0.2, 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**

Convert to coda mcmc format

**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**

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

**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

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 iteration

extractPTree

Extracts phylogenetic tree from a combined phylogenetic/transmission tree

Description

Extracts phylogenetic tree from a combined phylogenetic/transmission tree

Usage

extractPTree(ctree)

Arguments

ctree Combined tree

Value

phylogenetic tree

Examples

extractPTree(simulateOutbreak())
extractTTree

---

**extractTTree**

*Extracts transmission tree from a combined phylogenetic/transmission tree*

---

**Description**

Extracts transmission tree from a combined phylogenetic/transmission tree

**Usage**

```r
extractTTree(ctree)
```

**Arguments**

- `ctree`: Combined tree

**Value**

transmission tree

**Examples**

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

---

**getGenerationTimeDist**

*Extract and return realised generation time distribution*

---

**Description**

Extract and return realised generation time distribution

**Usage**

```r
generateTimeDist(
  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
getIncidentCases

Value

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

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

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

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

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,
  startCTree = NA,
  updateTTree = TRUE,
  optiStart = 2,
  dateT = Inf,
  verbose = F
)

Arguments

ptree  Phylogenetic tree
w.shape  Shape parameter of the Gamma distribution representing the generation time
w.scale  Scale parameter of the Gamma distribution representing the generation time
ws.shape  Shape parameter of the Gamma distribution representing the sampling time
ws.scale  Scale parameter of the Gamma distribution 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
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 * g
startOff.r  Starting value of parameter off.r
startOff.p  Starting value of parameter off.p
infer_multittree_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_multittree_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,
)

Value

posterior sample set of transmission trees

Examples

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

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`makeCTreeFromPTree` *Create a transmission tree compatible with the provided phylogenetic tree*

**Description**

Create a transmission tree compatible with the provided phylogenetic tree

**Usage**

```r
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 (Ne) 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
**makeTTree**

- `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

---

**Description**

Simulate a transmission tree

**Usage**

```r
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)
phyloFromPTree

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
Return the medoid from a MCMC output

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
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

Examples
phyloFromPTree(extractPTree(simulateOutbreak()))
### plot.ctree

**Plotting for ctree**

**Description**
Plotting for ctree

**Usage**
```r
defun(plot, x, ...) # 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**
```r
plot(simulateOutbreak())
```

### plot.ptree

**Plotting for ptree**

**Description**
Plotting for ptree

**Usage**
```r
defun(plot, x, ...) # 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::rmtree(5), 2020))

Description

Plotting for resTransPhylo

Usage

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

Arguments

x Output from inferTTree
...

Value

Plot of TransPhylo results

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
plotCTree

Value

Plot of ttree

Examples

plot(extractTTree(simulateOutbreak()))

plotCTree

Plot both phylogenetic and transmission trees using colors on the phylogeny

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**

```r
plotTTree2(extractTTree(simulateOutbreak()), 2, 1)
```

---

**Description**

Plot a transmission tree in an economic format

**Usage**

```r
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**

```r
plotTTree2(extractTTree(simulateOutbreak()))
```
**print.ctree**  
*Print function for ctree objects*

**Description**
Print function for ctree objects

**Usage**
```r
## 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**
```r
print(simulateOutbreak())
```

---

**print.ptree**  
*Print function for ptree objects*

**Description**
Print function for ptree objects

**Usage**
```r
## 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
print.resTransPhylo

Examples
print(extractPTree(simulateOutbreak()))

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

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

probPTreeGivenTTreeR(ctree, neg, w = NULL)

Arguments

cTree
Combined phylogenetic/transmission tree

e
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
probTTtreeR  
Calculates the log-probability of a transmission tree

Description
Calculates the log-probability of a transmission tree

Usage
probTTtreeR(
ttree, 
off.r, 
off.p, 
pi, 
w.shape, 
w.scale, 
ws.shape, 
ws.scale, 
dateT
)

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)

Value
Probability of the transmission tree
ptreeFromPhylo

| 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**

- `tr` phylo object
- `dateLastSample` date of the last sample

**Value**

phylogenetic tree

**Examples**

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

---

selectTTree

| selectTTree | Select the most representative transmission tree from a MCMC output |

**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  

*Simulate an outbreak*

**Description**

Simulate an outbreak

**Usage**

```r
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 (Ne) 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
Summary function for resTransPhylo objects

Description
Summary function for resTransPhylo objects

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