Package ‘phylosamp’

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Type Package

Title The Probability of Transmission Given Phylogenetic Linkage

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Description
Implements novel tools that estimate the probability of true transmission between two cases given phylogenetic linkage and the expected number of true transmission links in a sample. Methods described in
Wohl, Giles, and Lessler (2021) <doi:10.1371/journal.pcbi.1009182>.

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URL `https://github.com/HopkinsIDD/phylosamp`

BugReports `https://github.com/HopkinsIDD/phylosamp/issues`

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Depends R (>= 2.10), stats

Imports reshape2, ggplot2, cowplot, RColorBrewer

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

NeedsCompilation no

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R topics documented:

`exp_links` *Calculate expected number of links in a sample*

Description

This function calculates the expected number of observed pairs in the sample that are linked by the linkage criteria. The function requires the sensitivity η and specificity χ of the linkage criteria, and sample size M. Assumptions about transmission and linkage (single or multiple) can be specified.

Usage

```
exp_links(eta, chi, rho, M, R = NULL, assumption = "mtml")
```

Arguments

`eta`	scalar or vector giving the sensitivity of the linkage criteria
`chi`	scalar or vector giving the specificity of the linkage criteria
`rho`	scalar or vector giving the proportion of the final outbreak size that is sampled
`M`	scalar or vector giving the number of cases sampled
`R`	scalar or vector giving the effective reproductive number of the pathogen (default=NULL)
`assumption`	a character vector indicating which assumptions about transmission and linkage criteria. Default = `'mtml'`. Accepted arguments are:

1. `'stsl'` for the single-transmission single-linkage assumption (`prob_trans_stsl`).
2. `'mtsl'` for the multiple-transmission single-linkage assumption (`prob_trans_mtsl`).
3. `'mtml'` for the multiple-transmission multiple-linkage assumption (`prob_trans_mtml`).

Value

scalar or vector giving the expected number of observed links in the sample

Author(s)

John Giles, Shirlee Wohl, and Justin Lessler

See Also

Other obs_pairs: `obs_pairs_mtml()`, `obs_pairs_mtsl()`, `obs_pairs_stsl()`

Examples

```
# The simplest case: single-transmission, single-linkage, and perfect sensitivity
exp_links(eta=1, chi=0.9, rho=0.5, M=100, assumption='stsl')

# Multiple-transmission and imperfect sensitivity
exp_links(eta=0.99, chi=0.9, rho=1, M=50, R=1, assumption='mtsl')

# Small outbreak, larger sampling proportion
exp_links(eta=0.99, chi=0.95, rho=1, M=50, R=1, assumption='mtml')

# Large outbreak, small sampling proportion
exp_links(eta=0.99, chi=0.95, rho=0.05, M=1000, R=1, assumption='mtml')
```

`falsediscoveryrate` *Calculate false discovery rate of a sample*

Description

This function calculates the false discovery rate (proportion of linked pairs that are false positives) in a sample given the sensitivity η and specificity χ of the linkage criteria, and sample size M. Assumptions about transmission and linkage (single or multiple) can be specified.

Usage

```
falsediscoveryrate(eta, chi, rho, M, R = NULL, assumption = "mtml")
```

Arguments

`eta`	scalar or vector giving the sensitivity of the linkage criteria
`chi`	scalar or vector giving the specificity of the linkage criteria
`rho`	scalar or vector giving the proportion of the final outbreak size that is sampled
`M`	scalar or vector giving the number of cases sampled
`R`	scalar or vector giving the effective reproductive number of the pathogen (default=NULL)
`assumption`	a character vector indicating which assumptions about transmission and linkage criteria. Default = `'mtml'`. Accepted arguments are: 1. `'stsl'` for the single-transmission single-linkage assumption (`prob_trans_stsl`). 2. `'mtsl'` for the multiple-transmission single-linkage assumption (`prob_trans_mtsl`). 3. `'mtml'` for the multiple-transmission multiple-linkage assumption (`prob_trans_mtml`).

Value

scalar or vector giving the true discovery rate

Author(s)

John Giles, Shirlee Wohl, and Justin Lessler

See Also

Other discovery_rate: `truediscoveryrate()`

Examples

```
# The simplest case: single-transmission, single-linkage, and perfect sensitivity
falsediscoveryrate(eta=1, chi=0.9, rho=0.5, M=100, assumption='stsl')

# Multiple-transmission and imperfect sensitivity
falsediscoveryrate(eta=0.99, chi=0.9, rho=1, M=50, R=1, assumption='mtsl')

# Small outbreak, larger sampling proportion
falsediscoveryrate(eta=0.99, chi=0.95, rho=1, M=50, R=1, assumption='mtml')

# Large outbreak, small sampling proportion
falsediscoveryrate(eta=0.99, chi=0.95, rho=0.5, M=1000, R=1, assumption='mtml')
```

`gen_dists` *Calculate genetic distance distribution*

Description

Function calculates the distribution of genetic distances in a population of viruses with the given parameters

Usage

```
gen_dists(
  mut_rate,
  mean_gens_pdf,
  max_link_gens = 1,
  max_gens = NULL,
  max_dist = NULL
)
```

Arguments

`mut_rate`	mean number of mutations per generation, assumed to be poisson distributed
`mean_gens_pdf`	the density distribution of the mean number of generations between cases; the index of this vector is assumed to be the discrete distance between cases
`max_link_gens`	the maximium generations of separation for linked pairs
`max_gens`	the maximum number of generations to consider, if `NULL` (default) value is set to the highest number of generations in mean_gens_pdf with a non-zero probability
`max_dist`	the maximum distance to calculate, if `NULL` (default) value is set to max_gens * 99.9th percentile of mut_rate poisson distribution

Value

a data frame with distances and probabilities

Author(s)

Shirlee Wohl and Justin Lessler

See Also

Other mutrate_functions: `get_optim_roc()`, `sens_spec_calc()`, `sens_spec_roc()`

Examples

```
# ebola-like pathogen
R <- 1.5
mut_rate <- 1

# use simulated generation distributions from the provided 'gen_dist_sim' data object
data("gen_dist_sim")
mean_gens_pdf <- as.numeric(gen_dist_sim[gen_dist_sim$R == R, -(1:2)])

# get theoretical genetic distance dist based on mutation rate and generation parameters
gen_dists(mut_rate = mut_rate,
          mean_gens_pdf = mean_gens_pdf,
          max_link_gens = 1)
```

`gen_dist_sim` *Simulations of the genetic distance distribution*

Description

This data object contains the genetic distance distributions for 168 values of R between 1.3 and 18. The distributions represent the the average of 1000 simulations for each value, which can be used as a reasonable proxy for the generation distribution for large outbreaks.

Usage

```
gen_dist_sim
```

Format

dataframe

Author(s)

Shirlee Wohl, John Giles, and Justin Lessler

Examples

```
data(gen_dist_sim)
```

`get_optim_roc` *Find optimal ROC threshold*

Description

This function takes the dataframe output of the ‘sens_spec_roc()‘ function and finds the optimnal threshold of sensitivity and specificity by minimizing the distance to the top left corner of the Receiver Operating Characteriztic (ROC) curve

Usage

```
get_optim_roc(roc)
```

Arguments

`roc`	a dataframe produced by the ‘sens_spec_roc()‘ function containing the Receiver Operating Characteriztic (ROC) curve

Value

vector containg optimal thresholds ofsensitivity and specificity

Author(s)

Shirlee Wohl, John Giles, and Justin Lessler

See Also

Other mutrate_functions: `gen_dists()`, `sens_spec_calc()`, `sens_spec_roc()`

Examples

```
# ebola-like pathogen
R <- 1.5
mut_rate <- 1

# use simulated generation distributions
data("gen_dist_sim")
mean_gens_pdf <- as.numeric(gen_dist_sim[gen_dist_sim$R == R, -(1:2)])

# get theoretical genetic distance dist based on mutation rate and generation parameters
dists <- as.data.frame(gen_dists(mut_rate = mut_rate,
                                 mean_gens_pdf = mean_gens_pdf,
                                 max_link_gens = 1))

# reshape dataframe for plotting
dists <- reshape2::melt(dists,
                        id.vars = "dist",
                        variable.name = "status",
```

```
                        value.name = "prob")

# get sensitivity and specificity using the same paramters
roc_calc <- sens_spec_roc(cutoff = 1:(max(dists$dist)-1),
                          mut_rate = mut_rate,
                          mean_gens_pdf = mean_gens_pdf)

# get the optimal value for the ROC plot
optim_point <- get_optim_roc(roc_calc)
```

`obs_pairs_mtml` *Expected number of observed pairs assuming multiple-transmission and multiple-linkage*

Description

This function calculates the expected number of pairs observed in a sample of size `M`. The multiple-transmission and multiple-linkage method assumes the following:

1. Each case i is, on average, the infector of `R` cases in the population (N)
2. Each case i is allowed to be linked by the linkage criteria to multiple cases j in the sampled population (M).
3. Linkage events are independent of one another (i.e, linkage of case i to case j has no bearing on linkage of case i to any other sample).

Usage

```
obs_pairs_mtml(chi, eta, rho, M, R)
```

Arguments

`chi`	scalar or vector giving the specificity of the linkage criteria
`eta`	scalar or vector giving the sensitivity of the linkage criteria
`rho`	scalar or vector giving the proportion of the final outbreak size that is sampled
`M`	scalar or vector giving the number of cases sampled
`R`	scalar or vector giving the effective reproductive number of the pathogen

Value

scalar or vector giving the expected number of linked pairs observed in the sample

Author(s)

John Giles, Shirlee Wohl and Justin Lessler

See Also

Other obs_pairs: `exp_links()`, `obs_pairs_mtsl()`, `obs_pairs_stsl()`

Examples

```
obs_pairs_mtml(eta=1, chi=1, rho=0.5, M=100, R=1) # Perfect sensitivity and specificity

obs_pairs_mtml(eta=0.99, chi=0.9, rho=1, M=50, R=1)

obs_pairs_mtml(eta=0.99, chi=0.9, rho=0.5, M=100, R=1)
```

`obs_pairs_mtsl` *Expected number of observed pairs assuming multiple-transmission and single-linkage*

Description

This function calculates the expected number of pairs observed in a sample of size `M`. The multiple-transmission and single-linkage method assumes the following:

1. Each case i is, on average, the infector of `R` cases in the population (N)
2. Each case i is allowed to be linked by the linkage criteria to only one other case j in the sampled population (M).

Usage

```
obs_pairs_mtsl(chi, eta, rho, M, R)
```

Arguments

`chi`	scalar or vector giving the specificity of the linkage criteria
`eta`	scalar or vector giving the sensitivity of the linkage criteria
`rho`	scalar or vector giving the proportion of the final outbreak size that is sampled
`M`	scalar or vector giving the number of cases sampled
`R`	scalar or vector giving the effective reproductive number of the pathogen

Value

scalar or vector giving the expected number of linked pairs observed in the sample

Author(s)

John Giles, Shirlee Wohl and Justin Lessler

See Also

Other obs_pairs: `exp_links()`, `obs_pairs_mtml()`, `obs_pairs_stsl()`

Examples

```
obs_pairs_mtsl(eta=1, chi=1, rho=0.5, M=100, R=1) # Perfect sensitivity and specificity

obs_pairs_mtsl(eta=0.99, chi=0.9, rho=1, M=50, R=1)

obs_pairs_mtsl(eta=0.99, chi=0.9, rho=0.5, M=100, R=1)
```

`obs_pairs_stsl` *Expected number of observed pairs assuming single-transmission and single-linkage*

Description

This function calculates the expected number of link pairs observed in a sample of size `M`. The single-transmission and single-linkage method assumes the following:

1. Each case i is linked by transmission to only one other case j in the population (N).
2. Each case i is linked by the linkage criteria to only one other case j in the sampled population (M).

Usage

```
obs_pairs_stsl(eta, chi, rho, M)
```

Arguments

`eta`	scalar or vector giving the sensitivity of the linkage criteria
`chi`	scalar or vector giving the specificity of the linkage criteria
`rho`	scalar or vector giving the proportion of the final outbreak size that is sampled
`M`	scalar or vector giving the number of cases sampled

Value

scalar or vector giving the expected number of linked pairs observed in the sample

Author(s)

John Giles, Shirlee Wohl, and Justin Lessler

See Also

Other obs_pairs: `exp_links()`, `obs_pairs_mtml()`, `obs_pairs_mtsl()`

Examples

```
obs_pairs_stsl(eta=1, chi=1, rho=0.5, M=100) # perfect sensitivity and specificity

obs_pairs_stsl(eta=0.99, chi=0.9, rho=1, M=50)

obs_pairs_stsl(eta=0.99, chi=0.9, rho=0.5, M=100)
```

`prob_trans_mtml` *Probability of transmission assuming multiple-transmission and multiple-linkage*

Description

This function calculates the probabilitiy that two cases are linked by direct transmission given that they have been linked by phylogenetic criteria. The multiple-transmission and multiple-linkage method assumes the following:

1. Each case i is, on average, the infector of `R` cases in the population (N)
2. Each case i is allowed to be linked by the linkage criteria to multiple cases j in the sampled population (M).
3. Linkage events are independent of one another (i.e, linkage of case i to case j has no bearing on linkage of case i to any other sample).

Usage

```
prob_trans_mtml(eta, chi, rho, M, R)
```

Arguments

`eta`	scalar or vector giving the sensitivity of the linkage criteria
`chi`	scalar or vector giving the specificity of the linkage criteria
`rho`	scalar or vector giving the proportion of the final outbreak size that is sampled
`M`	scalar or vector giving the number of cases sampled
`R`	scalar or vector giving the effective reproductive number of the pathogen

Value

scalar or vector giving the probability of transmission between two cases given linkage by phylogeneitic criteria

Author(s)

John Giles, Shirlee Wohl, and Justin Lessler

See Also

Other prob_trans: `prob_trans_mtsl()`, `prob_trans_stsl()`

Examples

```
prob_trans_mtml(eta=1, chi=1, rho=0.5, M=100, R=1) # Perfect sensitivity and specificity

prob_trans_mtml(eta=0.99, chi=0.9, rho=1, M=50, R=1)

prob_trans_mtml(eta=0.99, chi=0.9, rho=0.5, M=100, R=1)
```

`prob_trans_mtsl` *Probability of transmission assuming multiple-transmission and single-linkage*

Description

This function calculates the probabilitiy that two cases are linked by direct transmission given that they have been linked by phylogenetic criteria. The multiple-transmission and single-linkage method assumes the following:

1. Each case i is, on average, the infector of `R` cases in the population (N)
2. Each case i is allowed to be linked by the linkage criteria to only one other case j in the sampled population (M).

Usage

```
prob_trans_mtsl(chi, eta, rho, M, R)
```

Arguments

`chi`	scalar or vector giving the specificity of the linkage criteria
`eta`	scalar or vector giving the sensitivity of the linkage criteria
`rho`	scalar or vector giving the proportion of the final outbreak size that is sampled
`M`	scalar or vector giving the number of cases sampled
`R`	scalar or vector giving the effective reproductive number of the pathogen

Value

scalar or vector giving the probability of transmission between two cases given linkage by phylogeneitic criteria

Author(s)

John Giles, Shirlee Wohl, and Justin Lessler

See Also

Other prob_trans: `prob_trans_mtml()`, `prob_trans_stsl()`

Examples

```
prob_trans_mtsl(eta=1, chi=1, rho=0.5, M=100, R=1) # Perfect sensitivity and specificity

prob_trans_mtsl(eta=0.99, chi=0.9, rho=1, M=50, R=1)

prob_trans_mtsl(eta=0.99, chi=0.9, rho=0.5, M=100, R=1)
```

`prob_trans_stsl` *Probability of transmission assuming single-transmission and single-linkage*

Description

This function calculates the probabilitiy that two cases are linked by direct transmission given that they have been linked by phylogenetic criteria. The single-transmission and single-linkage method assumes the following:

1. Each case i is linked by transmission to only one other case j in the population (N).
2. Each case i is linked by the linkage criteria to only one other case j in the sampled population (M).

Usage

```
prob_trans_stsl(eta, chi, rho, M)
```

Arguments

`eta`	scalar or vector giving the sensitivity of the linkage criteria
`chi`	scalar or vector giving the specificity of the linkage criteria
`rho`	scalar or vector giving the proportion of the final outbreak size that is sampled
`M`	scalar or vector giving the number of cases sampled

Details

For perfect sensitivity, set `eta = 1`.

Value

scalar or vector giving the probability of transmission between two cases given linkage by phylogeneitic criteria

Author(s)

John Giles, Shirlee Wohl, and Justin Lessler

See Also

Other prob_trans: `prob_trans_mtml()`, `prob_trans_mtsl()`

Examples

```
prob_trans_stsl(eta=1, chi=1, rho=0.2, M=100) # perfect sensitivity and specificity

prob_trans_stsl(eta=1, chi=0.95, rho=0.2, M=100) # perfect sensitivity only

prob_trans_stsl(eta=0.99, chi=0.95, rho=0.9, M=50)

prob_trans_stsl(eta=0.99, chi=0.95, rho=0.05, M=100)
```

`samplesize` *Calculate sample size*

Description

This function calculates the sample size needed to obtain at least a defined false disovery rate given a final outbreak size N.

Usage

```
samplesize(eta, chi, N, R = NULL, phi, min_pairs = 1, assumption = "mtml")
```

Arguments

`eta`	scalar or vector giving the sensitivity of the linkage criteria
`chi`	scalar or vector giving the specificity of the linkage criteria
`N`	scalar or vector giving the final outbreak size
`R`	scalar or vector giving the effective reproductive number of the pathogen
`phi`	scalar or vector giving the desired true discovery rate (1-false discovery rate)
`min_pairs`	minimum number of linked pairs observed in the sample, defaults to 1 pair (2 samples); this is to ensure reasonable results are obtained
`assumption`	a character vector indicating which assumptions about transmission and linkage criteria. Default = `'mtml'`. Accepted arguments are: 1. `'stsl'` for the single-transmission single-linkage assumption (`prob_trans_stsl`). 2. `'mtsl'` for the multiple-transmission single-linkage assumption (`prob_trans_mtsl`). 3. `'mtml'` for the multiple-transmission multiple-linkage assumption (`prob_trans_mtml`).

Value

scalar or vector giving the sample size needed to meet the given conditions

Author(s)

John Giles, Shirlee Wohl, and Justin Lessler

Examples

```
samplesize(eta=0.99, chi=0.995, N=100, R=1, phi=0.75)
```

`sens_spec_calc` *Calculate sensitivity and specificity*

Description

Function to calculate the sensitivity and specificity of a genetic distance cutoff given an underlying mutation rate and mean number of generations between cases

Usage

```
sens_spec_calc(
  cutoff,
  mut_rate,
  mean_gens_pdf,
  max_link_gens = 1,
  max_gens = NULL,
  max_dist = NULL
)
```

Arguments

`cutoff`	the maximum genetic distance at which to consider cases linked
`mut_rate`	mean number of mutations per generation, assumed to be poisson distributed
`mean_gens_pdf`	the density distribution of the mean number of generations between cases; the index of this vector is assumed to be the discrete distance between cases
`max_link_gens`	the maximium generations of separation for linked pairs
`max_gens`	the maximum number of generations to consider, if `NULL` (default) value set to the highest number of generations in mean_gens_pdf with a non-zero probability
`max_dist`	the maximum distance to calculate, if `NULL` (default) value set to max_gens * 99.9th percentile of mut_rate poisson distribution

Value

a data frame with the sensitivity and specificity for a particular genetic distance cutoff

Author(s)

Shirlee Wohl and Justin Lessler

See Also

Other mutrate_functions: `gen_dists()`, `get_optim_roc()`, `sens_spec_roc()`

Examples

```
# calculate the sensitivity and specificity for a specific genetic distance threshold of 2 mutations
sens_spec_calc(cutoff=2,
               mut_rate=1,
               mean_gens_pdf=c(0.02,0.08,0.15,0.75),
               max_link_gens=1)

# calculate the sensitivity and specificity for a a range of genetic distance thresholds
sens_spec_calc(cutoff=1:10,
               mut_rate=1,
               mean_gens_pdf=c(0.02,0.08,0.15,0.75),
               max_link_gens=1)
```

`sens_spec_roc` *Make ROC from sensitivity and specificity*

Description

This is a wrapper function that takes output from the ‘sens_spec_calc()‘ function and constructs values for the Receiver Operating Characteric (ROC) curve

Usage

```
sens_spec_roc(
  cutoff,
  mut_rate,
  mean_gens_pdf,
  max_link_gens = 1,
  max_gens = NULL,
  max_dist = NULL
)
```

Arguments

`cutoff`	the maximum genetic distance at which to consider cases linked
`mut_rate`	mean number of mutations per generation, assumed to be poisson distributed
`mean_gens_pdf`	the density distribution of the mean number of generations between cases; the index of this vector is assumed to be the discrete distance between cases
`max_link_gens`	the maximium generations of separation for linked pairs
`max_gens`	the maximum number of generations to consider, if `NULL` (default) value set to the highest number of generations in mean_gens_pdf with a non-zero probability
`max_dist`	the maximum distance to calculate, if `NULL` (default) value set to max_gens * 99.9th percentile of mut_rate poisson distribution

Value

data frame with cutoff, sensitivity, and 1-specificity

Author(s)

Shirlee Wohl and Justin Lessler

See Also

Other mutrate_functions: `gen_dists()`, `get_optim_roc()`, `sens_spec_calc()`

Examples

```
# ebola-like pathogen
R <- 1.5
mut_rate <- 1

# use simulated generation distributions
data("gen_dist_sim")
mean_gens_pdf <- as.numeric(gen_dist_sim[gen_dist_sim$R == R, -(1:2)])

# get theoretical genetic distance dist based on mutation rate and generation parameters
dists <- as.data.frame(gen_dists(mut_rate = mut_rate,
                                 mean_gens_pdf = mean_gens_pdf,
                                 max_link_gens = 1))

dists <- reshape2::melt(dists,
                        id.vars = "dist",
                        variable.name = "status",
                        value.name = "prob")

# get sensitivity and specificity using the same paramters
roc_calc <- sens_spec_roc(cutoff = 1:(max(dists$dist)-1),
                          mut_rate = mut_rate,
                          mean_gens_pdf = mean_gens_pdf)
```

`truediscoveryrate` *Calculate true discovery rate of a sample*

Description

This function calculates the true discovery rate (proportion of true transmission pairs) in a sample given the sensitivity η and specificity χ of the linkage criteria, and sample size M. Assumptions about transmission and linkage (single or multiple) can be specified.

Usage

```
truediscoveryrate(eta, chi, rho, M, R = NULL, assumption = "mtml")
```

Arguments

`eta`	scalar or vector giving the sensitivity of the linkage criteria
`chi`	scalar or vector giving the specificity of the linkage criteria
`rho`	scalar or vector giving the proportion of the final outbreak size that is sampled
`M`	scalar or vector giving the number of cases sampled
`R`	scalar or vector giving the effective reproductive number of the pathogen (default=NULL)
`assumption`	a character vector indicating which assumptions about transmission and linkage criteria. Default = `'mtml'`. Accepted arguments are: 1. `'stsl'` for the single-transmission single-linkage assumption (`prob_trans_stsl`). 2. `'mtsl'` for the multiple-transmission single-linkage assumption (`prob_trans_mtsl`). 3. `'mtml'` for the multiple-transmission multiple-linkage assumption (`prob_trans_mtml`).

Value

scalar or vector giving the true discovery rate

Author(s)

John Giles, Shirlee Wohl, and Justin Lessler

See Also

Other discovery_rate: `falsediscoveryrate()`

Examples

```
# The simplest case: single-transmission, single-linkage, and perfect sensitivity
truediscoveryrate(eta=1, chi=0.9, rho=0.5, M=100, assumption='stsl')

# Multiple-transmission and imperfect sensitivity
truediscoveryrate(eta=0.99, chi=0.9, rho=1, M=50, R=1, assumption='mtsl')

# Small outbreak, larger sampling proportion
truediscoveryrate(eta=0.99, chi=0.95, rho=1, M=50, R=1, assumption='mtml')

# Large outbreak, small sampling proportion
truediscoveryrate(eta=0.99, chi=0.95, rho=0.5, M=1000, R=1, assumption='mtml')
```

`true_pairs` *Calculate expected number of true transmission pairs*

Description

This function calculates the expected number true transmission pairs in a sample of size `M`. Assumptions about transmission and linkage (single or multiple) can be specified.

Usage

```
true_pairs(eta, rho, M, R = NULL, assumption = "mtml")
```

Arguments

`eta`	scalar or vector giving the sensitivity of the linkage criteria
`rho`	scalar or vector giving the proportion of the final outbreak size that is sampled
`M`	scalar or vector giving the number of cases sampled
`R`	scalar or vector giving the effective reproductive number of the pathogen (default=NULL)
`assumption`	a character vector indicating which assumptions about transmission and linkage criteria. Default = `'mtml'`. Accepted arguments are: 1. `'stsl'` for the single-transmission single-linkage assumption (`prob_trans_stsl`). 2. `'mtsl'` for the multiple-transmission single-linkage assumption (`prob_trans_mtsl`). 3. `'mtml'` for the multiple-transmission multiple-linkage assumption (`prob_trans_mtml`).

Value

scalar or vector giving the expected number of true transmission pairs in the sample

Author(s)

John Giles, Shirlee Wohl, and Justin Lessler

See Also

Other true_pairs: `true_pairs_mtml()`, `true_pairs_mtsl()`, `true_pairs_stsl()`

Examples

```
true_pairs(eta=0.99, rho=0.75, M=100, R=1)
```

`true_pairs_mtml` *Expected number of true transmission pairs assuming multiple-transmission and multiple-linkage*

Description

This function calculates the expected number of true transmission pairs in a sample of size `M`. The multiple-transmission and multiple-linkage method assumes the following:

1. Each case i is, on average, the infector of `R` cases in the population (N)
2. Each case i is allowed to be linked by the linkage criteria to multiple cases j in the sampled population (M).
3. Linkage events are independent of one another (i.e, linkage of case i to case j has no bearing on linkage of case i to any other sample).

Usage

```
true_pairs_mtml(eta, rho, M, R)
```

Arguments

`eta`	scalar or vector giving the sensitivity of the linkage criteria
`rho`	scalar or vector giving the proportion of the final outbreak size that is sampled
`M`	scalar or vector giving the number of cases sampled
`R`	scalar or vector giving the effective reproductive number of the pathogen

Value

scalar or vector giving the expected number of true transmission pairs in the sample

Author(s)

John Giles, Shirlee Wohl and Justin Lessler

See Also

Other true_pairs: `true_pairs_mtsl()`, `true_pairs_stsl()`, `true_pairs()`

Examples

```
true_pairs_mtml(eta=0.95, rho=0.2, M=1000, R=1)
```

`true_pairs_mtsl` *Expected number of true transmission pairs assuming multiple-transmission and single-linkage*

Description

This function calculates the expected number true transmission pairs in a sample of size `M`. The multiple-transmission and single-linkage method assumes the following:

1. Each case i is, on average, the infector of `R` cases in the population (N)
2. Each case i is allowed to be linked by the linkage criteria to only one other case j in the sampled population (M).

Usage

```
true_pairs_mtsl(eta, rho, M, R)
```

Arguments

`eta`	scalar or vector giving the sensitivity of the linkage criteria
`rho`	scalar or vector giving the proportion of the final outbreak size that is sampled
`M`	scalar or vector giving the number of cases sampled
`R`	scalar or vector giving the effective reproductive number of the pathogen

Value

scalar or vector giving the expected number of true transmission pairs in the sample

Author(s)

John Giles, Shirlee Wohl and Justin Lessler

See Also

Other true_pairs: `true_pairs_mtml()`, `true_pairs_stsl()`, `true_pairs()`

Examples

```
true_pairs_mtsl(eta=0.95, rho=0.2, M=200, R=1)
```

`true_pairs_stsl` *Expected number of true transmission pairs assuming single-transmission and single-linkage*

Description

This function calculates the expected number of true transmission pairs in a sample of size `M`. The single-transmission and single-linkage method assumes the following:

1. Each case i is linked by transmissino to only one other case j in the population (N).
2. Each case i is linked by the linkage criteria to only one other case j in the sampled population (M).

Usage

```
true_pairs_stsl(eta, rho, M)
```

Arguments

`eta`	scalar or vector giving the sensitivity of the linkage criteria
`rho`	scalar or vector giving the proportion of the final outbreak size that is sampled
`M`	scalar or vector giving the number of cases sampled

Value

scalar or vector giving the expected number of true transmission pairs in the sample

Author(s)

John Giles, Shirlee Wohl, and Justin Lessler

See Also

Other true_pairs: `true_pairs_mtml()`, `true_pairs_mtsl()`, `true_pairs()`

Examples

```
true_pairs_stsl(eta=0.95, rho=0.2, M=200)
```

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