Package 'ViralBottleneck'

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Type Package

Title Create transmission object and perform bottleneck size calculation

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Description Create transmission object and apply different methods on transmission object to estimate bottlenecksize

License FALSE

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Imports methods,
utils,
ggplot2,
pbapply,
rmutil

R topics documented:

Bottleneck_size_Calculation

Calculate transmission bottleneck size

Description

Calculate transmission bottleneck size

Usage

```
Bottleneck_size_Calculation(
  transmission_ob,
  method = "KL",
  plot = FALSE,
  show_table = FALSE,
  transmission_pairs = NULL,
  donor_depth_threshold = 500,
  recipient_depth_threshold = 500,
  error_calling = 0.01,
  log = FALSE,
  variant_calling = 0.03,
  Nbmin = 1,
  Nbmax = 1000,
  NonSyn_or_Syn = "All"
)
```

Arguments

transmission_ob

> is a transmission object created by,'CreateTransmissionObject'.

method

> is characters containing 'KL' method, 'Presence-Absence' method, 'Binomial' method, 'Beta_binomial_Approximate' method, 'Beta_binomial_Exact' method and 'Wright-Fisher' method

plot

> is a logical value to determine plot the likelihood or not. Each plot would be stored in an individual folder named by transmission id.

show_table

> is a logical value to determine output a result table as 'csv' format.

transmission_pairs

> is a dataframe which is the subset of the transmission pairs table during the object creation.

donor_depth_threshold

> is a integer to filter variants in donor with the lower sequencing coverage

recipient_depth_threshold

> is a integer to filter variants in recipient with the lower sequencing coverage

error_calling

> is a numeric and filter. The proportion of the variant sites lower than error calling means the variant is difficult to distinguish from PCR errors. Then, the sites with lower proportion than error calling would be filtered.

log

> is a logical value to show the log or not. The log would be stored in an individual folder.

variant_calling

> is a parameter used for 'Presence-absence'method, 'Binomial' method, 'Beta_binomial' method to determine the variants is absent in recipient or not. Proportion of variant site lower than variant calling means this site is absent in recipient.

Nbmin

> is a integer representing the minimum number in likelihood range.

Nbmax

> is a integer representing the maximum number in likelihood range.

NonSyn_or_Syn

> is a filter to keep the variant sites which meet the requirements. If user need the mutation of variant sites are synonymous mutation, then 'NonSyn_or_Syn="Synonymous"'. If user need the mutation of variant sites are non-synonymous mutation, then 'NonSyn_or_Syn="Non-Synonymous"'. The default is "All"

Value

Bottleneck size table containing the transmission pairs, bottleneck size, the lower confidence interval and higher confidence interval

Examples

```
#The example can not be run directly
#Use different methods for estimation
#use KL method
KL_table = Bottleneck_size_calculation(transmission_object, method="KL")
#use presence-absence method
PA_table = Bottleneck_size_calculation(transmission_object, method="Presence-Absence")
#use Binomial method
Bi_table = Bottleneck_size_calculation(transmission_object, method="Binomial")
#use Beta-binomial approximate method
BB_App_table = Bottleneck_size_calculation(transmission_object, method="Beta_binomial_Approximate")
#use Beta-binomial approximate method
BB_Exact_table = Bottleneck_size_calculation(transmission_object, method="Beta_binomial_Exact")
#use wright-fisher method
BB_WF_table = Bottleneck_size_calculation(transmission_object, method="Wright-Fisher")
Take KL method as example to show other arguments
#Execute depth thresholds argument. The default of depth thresholds are 500.
KL_table = Bottleneck_size_calculation(transmission_object, method="KL"
                              ,donor_depth_threshold=1000, recipient_depth_threshold=1000)
#Execute error calling argument. The default of error calling threshold is 0.01.
KL_table = Bottleneck_size_calculation(transmission_object, method="KL",error_calling=0.02)
#Execute range argument. The default of Nbmin is 1 and Nbmax=1000. They are used for
#                                        methods excluding `Wright-Fisher` method.
KL_table = Bottleneck_size_calculation(transmission_object, method="KL",Nbmin=50,Nbmax=100)
#Execute variant calling argument. The argument only use
#              for `Presence-Absence`method, `Binomial` method, `Beta_binomial` method.
BB_Exact_table = Bottleneck_size_calculation(transmission_object,
                                  method="Beta_binomial_Exact",variant_calling=0.02)
#if user have the subset of the transmission pairs, `subset_transmissionpairs`which is the
#                                same dataframe as the input for `CreateTransmissionObject`.
KL_table = Bottleneck_size_calculation(transmission_object, method="KL"
                                      ,transmission_pairs=subset_transmissionpairs)
#If user need to output likelihood curve of transmission pairs in working directory,
#                                            excluding `Wright-Fisher` method.
KL_table = Bottleneck_size_calculation(transmission_object, method="KL",plot=TRUE)
#If user need to output table of transmission pairs in working directory.
KL_table = Bottleneck_size_calculation(transmission_object, method="KL",show_table=TRUE)
#If user need to output log of transmission pairs in working directory.
KL_table = Bottleneck_size_calculation(transmission_object, method="KL",log=TRUE)
```

```
CreateTransmissionObject
```
Create Transmission Object

Description

This function could check the input files and catch the files in working directory according to transmission pairs table to create a transmission object.

Usage

```
CreateTransmissionObject(transmission_pairs_table)
```

Arguments

```
transmission_pairs_table
```
                is a dataframe only contatining 2 columns, Donor and Recipient

Value

Transmission_object, a environment containing all the infomation of transmission pairs

Examples

```
mytransmission_object = CreateTransmissionObject(transmission_pairs_table)
```

Summary_ob   *Summary_ob*

Description

Summary_ob

Usage

```
Summary_ob(transmission_ob, save = FALSE, file_name = NULL)
```

Arguments

```
transmission_ob
```
                is a object created by 'CreateTransmissionObject' function

```
save
```
                is a logical value to determine whether the table need to be saved in path or not.

```
file_name
```
                is the name of file. It only would be used when 'save=TRUE'.

Value

would return a csv file containing the transmission pairs: donors, recipients and shared variant sites.

Examples

```
#The example can not be run directly
summary_table = Summary_ob(transmission_object)
```

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