

# Package ‘ViralBottleneck’

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**Type** Package

**Title** Create transmission object and perform bottleneck size calculation

**Version** 0.1.0

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

**License** FALSE

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.3.1

**Imports** methods,  
utils,  
ggplot2,  
pbapply,  
rmutil

**Suggests** knitr,  
rmarkdown

**VignetteBuilder** knitr

**Depends** R (>= 2.10)

## R topics documented:

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Bottleneck\_size\_Calculation

*Calculate transmission bottleneck size*


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## Description

Calculate transmission bottleneck size

## Usage

```
Bottleneck_size_Calculation(
  transmission_ob,
  method,
  plot = FALSE,
  show_table = FALSE,
  transmission_pairs = NULL,
  donor_depth_threshold = 10,
  recipient_depth_threshold = 10,
  error_filtering = 0,
  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 (Emmett et al., 2015), 'Presence-Absence' method (Sacristán et al., 2003), 'Binomial' method (Sobel Leonard et al., 2017), 'Beta_binomial_Approximate' method (Sobel Leonard et al., 2017), 'Beta_binomial_Exact' method (Sobel Leonard et al., 2017) and 'Wright-Fisher' method (Poon et al., 2016)
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_filtering	is a numeric and filter. The proportion of the variants lower than error calling means the variant is difficult to distinguish from errors. After using that, the variants with values below this threshold would be zero.

log	is a logical value to show the log or not. The log would be stored in an individual folder.
variant_calling	is a threshold used for calling variant. The variants greater than this threshold would be trusted.
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

### References

- Emmett, K. J., Lee, A., Khiabani, H., & Rabadan, R. (2015) High-resolution genomic surveillance of 2014 Ebola virus using shared subclonal variants. *PLOS Currents Outbreaks* **7**, ecurrents.outbreaks.
- Sacristán, S., Malpica, J. M., Fraile, A., & García-Arenal, F. (2003) Estimation of population bottlenecks during systemic movement of tobacco mosaic virus in tobacco plants. *Journal of Virology* **77**(18), 9906–9911.
- Poon, L. L. M., Song, T., Rosenfeld, R., Lin, X., Rogers, M. B., Zhou, B., Sebra, R., Halpin, R., Guan, Y., Twaddle, A., DePasse, J., Stockwell, T., Wentworth, D., Holmes, E., Greenbaum, B., Peiris, J. S. M., Cowling, B. J., & Ghedin, E. (2016) Quantifying influenza virus diversity and transmission in humans. *Nature Genetics* **48**(2), 195–200.
- Sobel Leonard, A., Weissman, D. B., Greenbaum, B., Ghedin, E., & Koelle, K. (2017) Transmission bottleneck size estimation from pathogen deep-sequencing data, with an application to human influenza A virus. *Journal of Virology* **91**(14), e00171-17.

### 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")
```

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```
CreateTransmissionObject
```

*Create Transmission Object*

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### 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 containing 2 columns, Donor and Recipient

### Value

Transmission\_object, an environment containing all the information of transmission pairs

### Examples

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

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```
Summary_ob
```

*Summary\_ob*

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### Description

Summary\_ob

### Usage

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

### Arguments

transmission\_ob  
is an object created by 'CreateTransmissionObject' function  
save  
is a logical value to determine whether the table needs 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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