

Package ‘svisits’

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Type Package

Title Shared Clinic Visit Dates Identify Steady HIV Positive Partnerships for Research

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Description This package helps to find some stable HIV-infected partnerships in cohort studies basing on the assumption that some patients frequently attend the clinical visits together. These pairs are useful for biological and epidemiological research.

License GPL (≥ 2)

Depends Rcpp ($\geq 0.12.5$), compiler, parallel, chron, data.table

Imports Rcpp ($\geq 0.12.5$), compiler, parallel, chron, data.table

LinkingTo Rcpp

Suggests knitr, rmarkdown

VignetteBuilder knitr

R topics documented:

svisits-package	2
adjust_Rcpp_min	2
adjust_R_Rcpp_short_binomial	3
adjust_visits	4
barcode	4
Bonferroni_m	5
chooseC	6
getPairs	6
get_observed_pairs	7
prepare_db	8
Shuffling_simulation	8
simulated_data	9

Index	11
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svisits-package	<i>svisits: finding HIV transmission and serosorting pairs using shared clinic visit dates</i>
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Description

This package helps to find some stable HIV-infected partnerships in cohort studies basing on the assumption that some patients frequently attend the clinical visits together. These pairs are useful for biological and epidemiological research.

Details

This section should provide a more detailed overview of how to use the package, including the most important functions.

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References

This optional section can contain literature or other references for background information.

See Also

Optional links to other man pages

adjust_Rcpp_min	<i>adjustment function</i>
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Description

This is the C++ adjustment function that is called by adjust_visits

Arguments

mat	matrix to adjust
prob	probability of sharing a single visit, default 1/75

Details

written in C++

Value

returns the adjusted matrix, the column "Corrected" is the adjusted number of shared visits per pair

Examples

```
# load data
data("simulated_data")
db_dates<-prepare_db(your_database = simulated_data,ids_column = "subject",dates_column = "sim_dates")

# first get unadjusted pairs
unadjusted_observed_pairs<-get_observed_pairs(db_dates)
ids<- data.table(ids=as.character(names(table(db_dates$subject))),
                 N_visits=as.character(as.numeric(table(db_dates$subject))))
setkey(ids, "ids")

# now adjust the pairs
adjusted_observed<-adjust_visits(unadjusted_pairs=unadjusted_observed_pairs,ids=ids,prob = 1/75)
head(adjusted_observed)
```

adjust_R_Rcpp_short_binomial

Probabilites of sharing a given number of visits

Description

this is the C++ function that is called by Bonferroni_m

Arguments

mat	pairs as found by the function get_observed_pairs
prob	probability of sharing a single visit, default 1/75

Details

written in C++

Value

returns a matrix with a probability to share the given number of visits for each pair

Examples

```
# load data
data("simulated_data")
db_dates<-prepare_db(your_database = simulated_data,ids_column = "subject",dates_column = "sim_dates")

# first get unadjusted pairs
unadjusted_observed_pairs<-get_observed_pairs(db_dates)
# prepare ids
ids<- data.table(ids=as.character(names(table(db_dates$subject))),
                 N_visits=as.character(as.numeric(table(db_dates$subject))))
setkey(ids, "ids")

# run
Bonferroni_m_output<-Bonferroni_m(unadjusted_observed_pairs,ids=ids,prob = 1/75,alpha =0.01)
length(Bonferroni_m_output[,1])
```

adjust_visits	<i>Adjust the number of shared visits</i>
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Description

Adjusts the total number of shared visits per pair

Usage

```
adjust_visits(unadjusted_pairs,ids=ids, prob = 1/75)
```

Arguments

unadjusted_pairs	The pairs
ids	patient ids
prob	probability of sharing a single visit, depends on the frequency of visits. Default 1/75 ~visit every three months.

Value

returns data.frame with the column "Corrected" representing the adjusted number of shared visits per pair

Examples

```
# load data
data("simulated_data")
db_dates<-prepare_db(your_database = simulated_data,ids_column = "subject",dates_column = "sim_dates")

# first get unadjusted pairs
unadjusted_observed_pairs<-get_observed_pairs(db_dates)
ids<- data.table(ids=as.character(names(table(db_dates$subject))),
                 N_visits=as.character(as.numeric(table(db_dates$subject))))
setkey(ids, "ids")

# now adjust the pairs
adjusted_observed<-adjust_visits(unadjusted_pairs=unadjusted_observed_pairs,ids=ids, prob = 1/75)
head(adjusted_observed)
```

barcode	<i>Unique pair identifier</i>
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Description

Makes a unique identifier for each pair. Each member's id should be numeric! For example id_1=6758 , id_2=3456 the barcode will be 3456_6758

Usage

```
barcode(raw_for_eval)
```

Arguments

```
raw_for_eval
```

Value

string of a form id1_id2

Examples

```
barcode(c(id_2=6578,id_1=3456))

## The function is currently defined as
function (raw_for_eval)
{
  return(as.character(paste0(min(as.numeric(raw_for_eval)),
    "_", max(as.numeric(raw_for_eval)))))
}
```

Bonferroni_m

Detecting the pairs using Bonferroni correction

Description

much faster than the shuffling

Usage

```
Bonferroni_m(unadjusted_pairs, ids=ids,prob = 1/75, alpha = 0.01, only_significant = TRUE)
```

Arguments

```
unadjusted_pairs      pairs as found by the function get_observed_pairs
ids                    patient ids
prob                   probability of sharing a single visit, default 1/75
alpha                  type 1 error
only_significant       return only significant pairs above the threshold (default) or all the pairs
```

Examples

```
# load data
data("simulated_data")
db_dates<-prepare_db(your_database = simulated_data,ids_column = "subject",dates_column = "sim_dates")

# first get unadjusted pairs
unadjusted_observed_pairs<-get_observed_pairs(db_dates)
# prepare ids
ids<- data.table(ids=as.character(names(table(db_dates$subject))),
                 N_visits=as.character(as.numeric(table(db_dates$subject))))
setkey(ids, "ids")

# run
Bonferroni_m_output<-Bonferroni_m(unadjusted_observed_pairs,ids=ids,prob = 1/75,alpha =0.01)
length(Bonferroni_m_output[,1])
```

chooseC

Binomial coefficient

Description

Calculates the Binomial coefficient

Arguments

n	size
k	number of unordered outcomes

Value

number

Examples

```
chooseC(n=6,k=2)
# 15
```

getPairs

Pairs that collided at a certain date

Description

Pairs that shared at least a single visit at a certain date

Usage

```
getPairs(ids)
```

Arguments

ids

Details

this function is called by get_observed_pairs which goes date by date for each unique date

Examples

```
# load data
data("simulated_data")
db_dates<-prepare_db(your_database = simulated_data,ids_column = "subject",dates_column = "sim_dates")

# get unadjusted pairs
unadjusted_observed_pairs<-get_observed_pairs(db_dates)
```

get_observed_pairs	<i>Find all the pairs that shared at least a single visit</i>
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Description

Find all the pairs that shared at least a single visit.

Usage

```
get_observed_pairs(tested_db)
```

Arguments

tested_db	visits in a long format, each row a visit date, see data("simulated_data") for an example
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Examples

```
# load data
data("simulated_data")
db_dates<-prepare_db(your_database = simulated_data,ids_column = "subject",dates_column = "sim_dates")

# get unadjusted pairs
unadjusted_observed_pairs<-get_observed_pairs(db_dates)
```

prepare_db	<i>Prepare the database</i>
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Description

Prepare the database for finding pairs.

Usage

```
prepare_db(your_database = simulated_data, ids_column = "subject", dates_column = "sim_dates")
```

Arguments

your_database	the data.frame to be analyzed
ids_column	column with the person identifiers
dates_column	column with the visit dates

Details

the dates are ordered in an increasing order within each subject

Value

returns the database with two columns "subject" and "dates"

Examples

```
data("simulated_data")
db_dates<-prepare_db(your_database = simulated_data, ids_column = "subject", dates_column = "sim_dates")
```

Shuffling_simulation	<i>Shuffling simulation to determine shared visits false-positive threshold</i>
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Description

Shuffling simulation to determine shared visits false-positive threshold, one run, use "replicate" for several, see example

Usage

```
Shuffling_simulation(db_dates, ids=ids, adjusted_observed)
```

Arguments

db_dates	visits to be shuffled (long format) an output from prepare_db, see data("simulated_data")
ids	patients ids
adjusted_observed	The dataset with adjusted observed number of visits

Details

Due to the multiple comparisons problem and a strongly simplifying assumptions about the uniform distribution of visits, the corrected number of shared visits is not an optimal test statistic. Instead, the visits are first shuffled within each quarter (such that the original distribution of the number of visits per individual was preserved) and the number of randomly collided shared visits per pair is counted and penalized using "adjust_visits". In other words, the observed visit dates from a given quarter were randomly re-assigned between the patients that attended during this quarter.

Define the number of desired shuffling simulations (ideally >100, but it will take some time) and run

Value

returns a numeric vector of size 10 with each value representing the false positive fraction for a cutoff of adjusted shared visits that corresponds to the position of the value in the order of the vector.

Examples

```
# load data
data("simulated_data")
db_dates<-prepare_db(your_database = simulated_data,ids_column = "subject",dates_column = "sim_dates")

# prepare 3 months periods for later shuffling
db_dates<-cbind(db_dates,month.day.year(db_dates$dates));periodMonths<-3
db_dates<-cbind(db_dates,fupdatePeriod=db_dates$year
               +round(floor((db_dates$month-1)/periodMonths) *periodMonths/12,2))

# first get unadjusted pairs
unadjusted_observed_pairs<-get_observed_pairs(db_dates)
ids<- data.table(ids=as.character(names(table(db_dates$subject))),
                N_visits=as.character(as.numeric(table(db_dates$subject))))
setkey(ids, "ids")

# now adjust the pairs
adjusted_observed<-adjust_visits(unadjusted_pairs=unadjusted_observed_pairs,ids=ids,prob = 1/75)
# number of simulations
n_shuffl<-2 # two
Shuffling_simulation_output<- replicate(n_shuffl,
                                       Shuffling_simulation(db_dates,ids=ids,adjusted_observed),
                                       simplify=FALSE)

head(Shuffling_simulation_output)
```

simulated_data

Simulated dataset of visit dates based on the SHCS

Description

Contains 20 pseudo transmission pairs that should be detected with the method

Usage

```
data("simulated_data")
```

Format

A data frame with 90266 observations on the following 3 variables.

`X` just indexing

`subject` a numeric vector with patient identifiers

`sim_dates` a factor with the visit dates

Examples

```
data(simulated_data)
```

Index

*Topic **package**

svisits-package, [2](#)

adjust_R_Rcpp_short_binomial, [3](#)

adjust_Rcpp_min, [2](#)

adjust_visits, [4](#)

barcode, [4](#)

Bonferroni_m, [5](#)

chooseC, [6](#)

get_observed_pairs, [7](#)

getPairs, [6](#)

prepare_db, [8](#)

Shuffling_simulation, [8](#)

simulated_data, [9](#)

svisits (svisits-package), [2](#)

svisits-package, [2](#)