RDS Library Intro

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Bibliotecas

```
# install.packages(renv)
# renv::init()
# renv::install("tidyverse")
# renv::install("RDS")
# renv::snapshot()
# renv::status()
```

```
library(renv)
library(tidyverse)
library(RDS)
```

Documentación

as.char

converts to character with minimal loss of precision for numeric variables

Description

converts to character with minimal loss of precision for numeric variables

Usage

as.char(x, ...) #### Arguments x the value ... passed to either format or as.character.

as.rds.data.frame

Coerces a data.frame object into an rds.data.frame object.

Description

This function converts a regular R data frame into an rds.data.frame. The greatest advantage of this is that it performs integrity checks and will fail if the recruitment information in the original data frame is incomplete.

Usage

as.rds.data.frame(df, id = if (is.null(attr(df, “id”))) “id” else attr(df, “id”), recruiter.id = if (is.null(attr(df, “recruiter.id”))) { “recruiter.id” } else attr(df, “recruiter.id”), network.size = if (is.null(attr(df, “network.size.variable”))) { “network.size.variable” } else attr(df, “network.size.variable”), population.size = if (all(is.na(get.population.size(df, FALSE)))) { NULL } else get.population.size(df, FALSE), max.coupons = if (is.null(attr(df, “max.coupons”))) { NULL } else attr(df, “max.coupons”), notes = if (is.null(attr(df, “notes”))) { NULL } else attr(df, “time”), time = if (is.null(attr(df, “time”))) { NULL } else attr(df, “time”), check.valid = TRUE)

Arguments

df A data.frame representing an RDS sample. id The unique identifier. recruiter.id The unique identifier of the recruiter of this row. network.size The number of alters (i.e. possible recruitees). population.size The size of the population from which this RDS sample has been drawn. Either a single number, or a vector of length three indicating low, mid and high estimates. max.coupons The number of recruitment coupons distributed to each enrolled subject (i.e. the maximum number of recruitees for any subject). notes Data set notes. time the name of the recruitment time variable. optional. check.valid If true, validity checks are performed to ensure that the data is well formed. Value An rds.data.frame object

Examples

```
dat <- data.frame(id=c(1,2,3,4,5), recruiter.id=c(2,-1,2,-1,4), network.size.variable=c(4,8,8
dat
```

```
  id recruiter.id network.size.variable
1  1            2                     4
2  2           -1                     8
3  3            2                     8
```

```
4  4           -1                    2
5  5            4                    3
```

```
as.rds.data.frame(dat)
```

```
An object of class "rds.data.frame"

id:  1 2 3 4 5

recruiter.id:  2 -1 2 -1 4

  id recruiter.id network.size.variable
1  1            2                    4
2  2           -1                    8
3  3            2                    8
4  4           -1                    2
5  5            4                    3
```

```
dat
```

```
  id recruiter.id network.size.variable
1  1            2                    4
2  2           -1                    8
3  3            2                    8
4  4           -1                    2
5  5            4                    3
```

assert.valid.rds.data.frame

Does various checks and throws errors if x is not a valid rds.data.frame

Description

Does various checks and throws errors if x is not a valid rds.data.frame

Usage

assert.valid.rds.data.frame(x, ...)

Arguments

x an rds.data.frame … unused

Details

Throws an informative message if x is malformed.

bootstrap.contingency.test

Performs a bootstrap test of independance between two categorical variables

Description

Performs a bootstrap test of independance between two categorical variables

Usage

bootstrap.contingency.test(rds.data, row.var, col.var, number.of.bootstrap.samples = 1000, weight.type = c("HCG", "RDS-II", "Arithmetic Mean"), table.only = FALSE, verbose = TRUE, …)

Arguments

rds.data an rds.data.frame row.var the name of the first categorical variable col.var the name of the second categorical variable number.of.bootstrap.samples The number of simulated booot-strap populations weight.type The type of weighting to use for the contningency table. Only large sample methods are allowed. table.only only returns the weighted table, without boot-strap. verbose level of output … Additional parameters for compute_weights

Details

This function first estimates a Homophily Configuration Graph model for the underlying network under the assumption that the two variables are independant and that the population size is large. It then draws bootstrap RDS samples from this population distribution and calculates the chi.squared statistic on the weighted contingency table. Weights are calculated using the HCG estimator assuming a large population size.

Examples

```
data(faux)
bootstrap.contingency.test(rds.data=faux, row.var="X", col.var="Y", number.of.bootstrap.sampl
```

```
    RDS Bootstrap Test of X versus Y

data:
X-squared = 9.5503, p-value = 0.32
```

bootstrap.incidence

Calculates incidence and bootstrap confidence intervals for immunoassay data collected with RDS

Description

Calculates incidence and bootstrap confidence intervals for immunoassay data collected with RDS

Usage

bootstrap.incidence(rds.data, recent.variable, hiv.variable, N = NULL, weight.type = c("Gile's SS", "RDS-I", "RDS-I (DS)", "RDS-II", "Arithmetic Mean", "HCG"), mean.duration = 200, frr = 0.01, post.infection.cutoff = 730, number.of.bootstrap.samples = 1000, se.mean.duration = 0, se.frr = 0, confidence.level = 0.95, verbose = TRUE, ...)

Arguments

rds.data an rds.data.frame recent.variable The name of the variable indicating recent infection hiv.variable The name of the variable indicating of hiv infection N Population size weight.type A string giving the type of estimator to use. The options are "Gile's SS", "RDS-I", "RDS-II", "RDS-I/DS", and "Arithemic Mean". It defaults to "Gile's SS". mean.duration Estimated mean duration of recent infection (MDRI) (days) frr Estimated false-recent rate (FRR) post.infection.cutoff Post-infection time cut-off T, separating "true-recent" from "false-recent" results (days) number.of.bootstrap.samples The number of bootstrap samples used to construct the interval. se.mean.duration The standard error of the mean.duration estimate se.frr The standard error of the false recency estimate confidence.level The level of confidence for the interval verbose verbosity control ... additional arguments to compute.weights

Details

The recent.variable and hiv should be the names of logical variables. Otherwise they are converted to logical using as.numeric(x) > 0.5. This function estimates incidence using RDS sampling wieghts. Confidence intervals are constucted using HCG bootstraps. See http://www.incidence-estimation.org/ for additional information on (non-RDS) incidence estimation.

Examples

```
data(faux)
faux$hiv <- faux$X == "blue"
faux$recent <- NA
faux$recent[faux$hiv] <- runif(sum(faux$hiv)) < .2
faux$recent[runif(nrow(faux)) > .5] <- NA
faux$hiv[is.na(faux$recent)][c(1,6,10,21)] <- NA
attr(faux,"time") <- "wave"
bootstrap.incidence(faux,"recent","hiv",weight.type="RDS-II", number.of.bootstrap.samples=10
```

```
10% completed ...
20% completed ...
30% completed ...
40% completed ...
50% completed ...
60% completed ...
70% completed ...
80% completed ...
90% completed ...
100% completed ...
```

```
       Incidence         SE     Lower     Upper
recent 0.1572932 0.05451127 0.0504531 0.2641334
```

bottleneck.plot

Bottleneck Plot

Description

Bottleneck Plot

Usage

bottleneck.plot(rds.data, outcome.variable, est.func = RDS.II.estimates, as.factor = FALSE, n.eval.points = 25, ...)

Arguments

rds.data An rds.data.frame. outcome.variable A character vector of outcome variables. est.func A function taking rds.data and outcome.variable as parameters and returning an rds.weighted.estimate object. as.factor Convert all outcome variables to factors n.eval.points number of evaluation points to calculate the estimates at ... additional parameters for est.func.

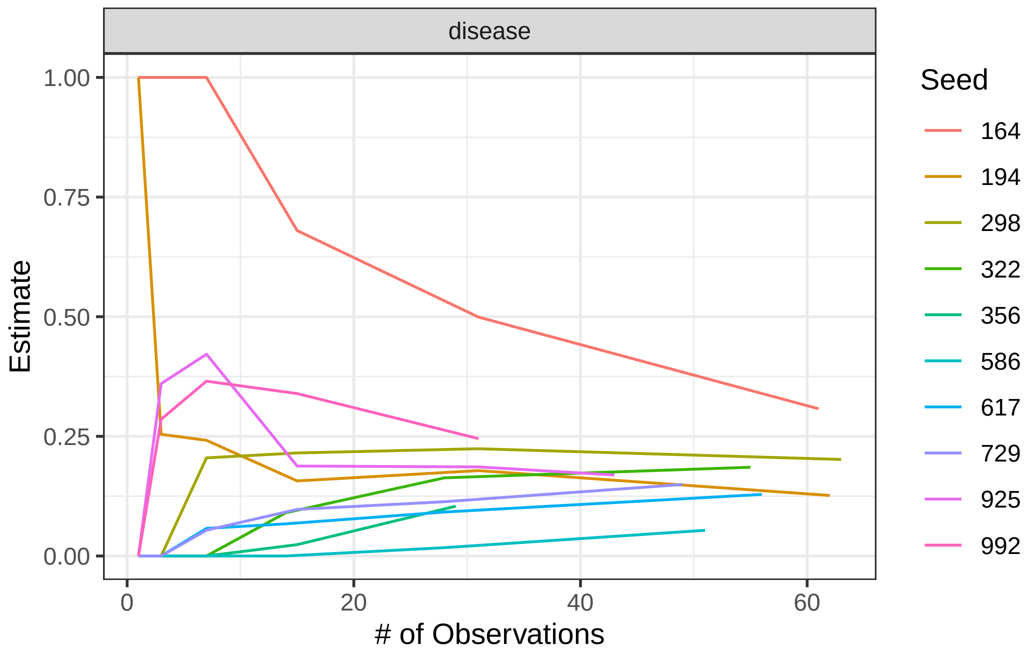
References

Krista J. Gile, Lisa G. Johnston, Matthew J. Salganik Diagnostics for Respondent-driven Sampling eprint arXiv:1209.6254, 2012

Examples

```
data(fauxmadrona)
bottleneck.plot(fauxmadrona,"disease")
```

```
[1] "194"
[1] "298"
[1] "164"
[1] "617"
[1] "586"
[1] "322"
[1] "729"
[1] "925"
[1] "992"
[1] "356"
```



compute.weights

Compute estimates of the sampling weights of the respondent's observations based on various estimators

Description

Compute estimates of the sampling weights of the respondent's observations based on various estimators

Usage

compute.weights(rds.data, weight.type = c("Gile's SS", "RDS-I", "RDS-I (DS)", "RDS-II", "Arithmetic Mean", "HCG"), N = NULL, subset = NULL, control = control.rds.estimates(), ...)

Arguments

rds.data An rds.data.frame that indicates recruitment patterns by a pair of attributes named "id" and "recruiter.id". weight.type A string giving the type of estimator to use. The options are "Gile's SS", "RDS-I", "RDS-II", "RDS-I/DS", and "Arithemic Mean". It defaults to "Gile's SS". N An estimate of the number of members of the population being sampled. If NULL it is read as the population.size.mid attribute of the rds.data frame. If that is missing, the weights will sum to 1. Note that this parameter is required for Gile's SS. subset An optional criterion to subset rds.data by. It is an R expression which, when evaluated, subset the data. In plain English, it can be something like subset = seed > 0 to exclude seeds. It can also be the name of a logical vector of the same length of the outcome variable where TRUE means include it in the analysis. If NULL then no subsetting is done. control A list of control parameters for algorithm tuning. Constructed using control.rds.estimates. … Additional parameters passed to the individual weighting algorithms. Value A vector of weights for each of the respondents. It is of the same size as the number of rows in rds.data. See Also rds.I.weights, gile.ss.weights, vh.weights

control.list.accessor

Named element accessor for ergm control lists

Description

Utility method that overrides the standard '$' list accessor to disable partial matching for ergm control.list objects

Usage

*## S3 method for class 'control.list' object$name

Arguments

object list-coearceable object with elements to be searched name literal character name of list element to search for and return

Details

Executes getElement instead of $ so that element names must match exactly to be returned and partially matching names will not return the wrong object. Value Returns the named list element exactly matching name, or NULL if no matching elements found Author(s) Pavel N. Krivitsky See Also see getElement

control.rds.estimates

Auxiliary for Controlling RDS.bootstrap.intervals

Description

Auxiliary function as user interface for fine-tuning RDS.bootstrap.intervals algorithm, which computes interval estimates for via bootstrapping.

Usage

control.rds.estimates(confidence.level = 0.95, SS.infinity = 0.01, lowprevalence = c(8, 14), discrete.cutoff = 0.8, useC = TRUE, number.of.bootstrap.samples = NULL, hcg.reltol = sqrt(.Machine*double.eps*), *hcg.BS.reltol* = 1*e*+05 ∗ *sqrt*(.*Machine*double.eps), hcg.max.optim = 500, seed = NULL)

Arguments

confidence.level The confidence level for the confidence intervals. The default is 0.95 for 95%. SS.infinity The sample proportion, n/N, below which the computation of the SS weights should simplify to that of the RDS-II weights. lowprevalence Standard confidence interval procedures can be inaccurate when the outcome expected count is close to zero. This sets conditions where alternatives to the standard are used for the ci.type="hmg" option. See Details for its use. discrete.cutoff The minimum proportion of the values of the outcome variable that need to be unique before the variable is judged to be continuous. useC Use a C-level implementation of Gile's bootstrap (rather than the R level). The implementations should be computational equivalent (except for speed). number.of.bootstrap.samples The number of bootstrap samples to take in estimating the uncertainty of the estimator. If NULL it defaults to the number necessary to compute the standard error to accuracy 0.001. hcg.reltol Relative convergence tolerance for the HCG estimator. The algorithm stops if it is unable to reduce the log-likelihood by a factor of reltol * (abs(log-likelihood) + reltol) at a step. Defaults to sqrt(.Machine$double.eps), typically about 1e-8. hcg.BS.reltol Relative convergence tolerance for the bootstrap of the HCG estimator. It has the same interpretation as hcg.reltol except it is applied to each bootstrap sample. It is typically the same or larger than hcg.reltol. hcg.max.optim The number of iterations on the likelihood optimization for the HCG estimator. seed Seed value (integer) for the random number generator. See set.seed

Details

This function is only used within a call to the RDS.bootstrap.intervals function. Some of the arguments are not yet fully implemented. It will evolve slower to incorporate more arguments as the package develops. Standard confidence interval procedures can be inaccurate when the outcome expected count is close to zero. In these cases the combined Agresti-Coull and the bootstrap-t interval of Mantalos and Zografos (2008) can be used. The lowprevalence argument is a two vector parameter setting the conditions under which the approximation is used. The first is the penalty term on the differential activity. If the observed number of the rare group minus the product of the first parameter and the differential activity is lower than the second parameter, the low prevalence approximation is used. Value A list with arguments as components. See Also RDS.bootstrap.intervals

convergence.plot

Convergence Plots

Description

This function creates diagnostic convergence plots for RDS estimators. Usage convergence.plot(rds.data, outcome.variable, est.func = RDS.II.estimates, as.factor = FALSE, n.eval.points = 25, ...)

Arguments

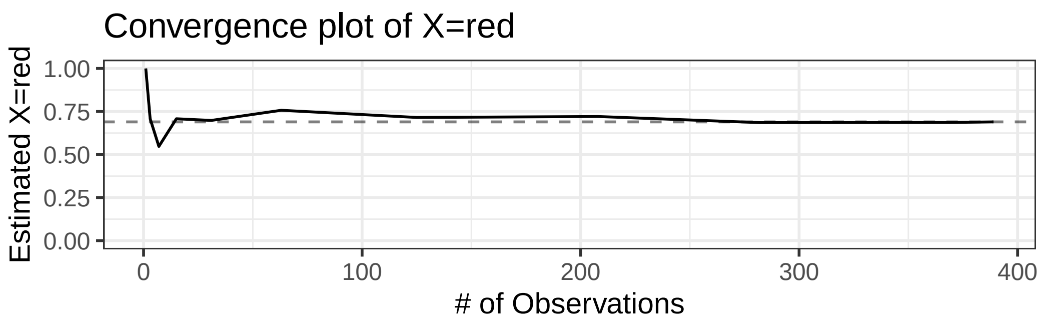
rds.data An rds.data.frame. outcome.variable A character vector of outcome variables. est.func A function taking rds.data and outcome.variable as parameters and returning an rds.weighted.estimate object. as.factor Convert all outcome variables to factors n.eval.points number of evaluation points to calculate the estimates at ... additional parameters for est.func.

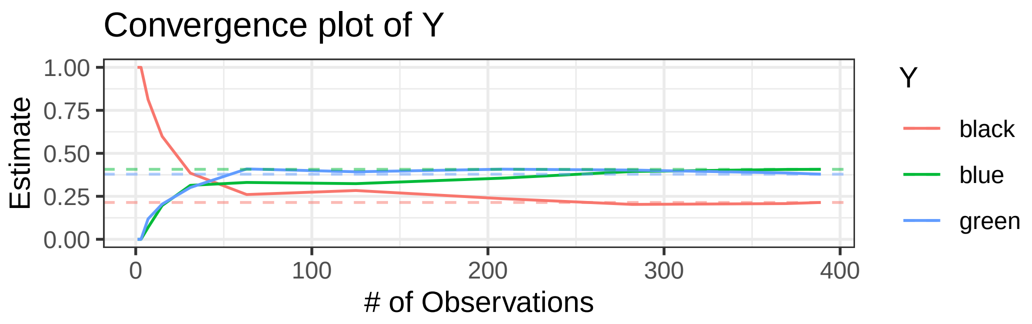
References

Krista J. Gile, Lisa G. Johnston, Matthew J. Salganik Diagnostics for Respondent-driven Sampling eprint arXiv:1209.6254, 2012

Examples

```r
data(faux)
convergence.plot(faux,c("X","Y"))
```





count.transitions

Counts the number or recruiter->recruitee transitions between different levels of the grouping variable.

Description

Counts the number or recruiter->recruitee transitions between different levels of the grouping variable.

Usage

count.transitions(rds.data, group.variable)

Arguments

rds.data An rds.data.frame group.variable The name of a categorical variable in rds.data

Examples

```
data(faux)
count.transitions(faux,"X")
```

```
      grp
rgrp   blue red
  blue   39  82
  red    79 188
```

cumulative.estimate

Calculates estimates at each successive wave of the sampling process

Description

Calculates estimates at each successive wave of the sampling process

Usage

cumulative.estimate(rds.data, outcome.variable, est.func = RDS.II.estimates, n.eval.points = 25, …)

Arguments

rds.data An rds.data.frame outcome.variable The outcome est.func A function taking rds.data and outcome.variable as parameters and returning an rds.weighted.estimate object n.eval.points number of evaluation points to calculate the estimates at … additional parameters for est.func

differential.activity.estimates

Differential Activity between groups

Description

Differential Activity between groups

Usage

differential.activity.estimates(rds.data, outcome.variable, weight.type = "Gile's SS", N = NULL, subset = NULL, …)

Arguments

rds.data An rds.data.frame object outcome.variable A character string of column names representing categorical variables. weight.type A string giving the type of estimator to use. The options are “Gile’s SS”, “RDS-I”, “RDS-II”, “RDS-I/DS”, and “Arithemic Mean”. It defaults to “Gile’s SS”. N The population size. subset An expression defining a subset of rds.data. ... Additional parameters passed to compute.weights.

Details

This function estimates the ratio of the average degree of one population group divided by the average degree of those in another population group.

Examples

```
data(faux)
differential.activity.estimates(faux,"X",weight.type="RDS-II")
```

```
The mean degree of those with value 1 divided by the mean degree of those without is 1.03342
```

export.rds.interval.estimate

Convert the output of print.rds.interval.estimate from a character data.frame to a numeric matrix

Description

Convert the output of print.rds.interval.estimate from a character data.frame to a numeric matrix

Usage

export.rds.interval.estimate(x, proportion = TRUE)

Arguments

x An object, typically the result of print.rds.interval.estimate. proportion logical, Should the outcome be treated as a proportion and converted to a percentage.

faux

A Simulated RDS Data Set

Description

This is a faux set used to demonstrate RDS functions and analysis. It is used is some simple examples and has categorical variables “X”, “Y” and “Z”. Format An rds.data.frame object

References

Gile, Krista J., Handcock, Mark S., 2010 Respondent-driven Sampling: An Assessment of Current Methodology, Sociological Methodology, 40, 285-327. See Also fauxsycamore, fauxmadrona

Examples

```
data(faux)
RDS.I.estimates(rds.data=faux,outcome.variable='X')
```

```
RDS-I Estimate for X
     Estimate         95% Interval Design Effect Std. Error     N
blue   0.3109 (  0.2681,   0.3537)          1.42     0.0219   118
red    0.6891 (  0.6463,   0.7319)          1.42     0.0219   271
                                                      Total   389
* Using population size estimate: 1000
```

fauxmadrona

A Simulated RDS Data Set with no seed dependency

Description

This is a faux set used to illustrate how the estimators perform under different populations and RDS schemes. Format An rds.data.frame

Details

The population had N=1000 nodes. In this case, the sample size is 500 so that there is a relatively small sample fraction (50%). There is homophily on disease status (R=5) and there is differential activity by disease status whereby the infected nodes have mean degree twice that of the uninfected (w=1.8). In the sampling, the seeds are chosen randomly from the full population, so there is no dependency induced by seed selection. Each sample member is given 2 uniquely identified coupons to distribute to other members of the target population in their acquaintance. Further each respondent distributes their coupons completely at random from among those they are connected to. Here are the results for this data set and the sister fauxsycamore data set: Name City Type Mean RDS I (SH) RDS II (VH) SS fauxsycamore Oxford seed dependency, 70% 0.2408 0.1087 0.1372 0.1814 fauxmadrona Seattle no seed dependency, 50% 0.2592 0.1592 0.1644 0.1941 Even with only 50% sample, the VH is substantially biased , and the SS does much better. Source The original network is included as fauxmadrona.network as a network object. The data set also includes the data.frame of the RDS data set as fauxmadrona. Use data(package="RDS") to get a full list of datasets.

References

Gile, Krista J., Handcock, Mark S., 2010 Respondent-driven Sampling: An Assessment of Current Methodology, Sociological Methodology, 40, 285-327. See Also fauxsycamore, faux

fauxsycamore

A Simulated RDS Data Set with extreme seed dependency

Description

This is a faux set used to demonstrate RDS functions and analysis. The population had N=715 nodes. In this case, the sample size is 500 so that there is a relatively large sample fraction (70%). There is homophily on disease status (R=5) and there is differential activity by disease status whereby the infected nodes have mean degree twice that of the uninfected (w=1.8).

Format

An rds.data.frame plus the original network as a network object

Details

In the sampling the seeds are chosen randomly from the infected population, so there is extreme dependency induced by seed selection. Each sample member is given 2 uniquely identified coupons to distribute to other members of the target population in their acquaintance. Further each respondent distributes their coupons completely at random from among those they are connected to. With 70% sample, the VH is substantially biased, so the SS (and presumably MA) do much better. We expect the MA to perform a bit better than the SS. It is network 702 and its sample from YesYes on mosix. Look for "extract702.R" The original network is included as fauxsycamore.network as a network object. The data set also includes the data.frame of the RDS data set as fauxsycamore. Use data(package="RDS") to get a full list of datasets.

References

Gile, Krista J., Handcock, Mark S., 2009. Respondent-driven Sampling: An Assessment of Current Methodology, Sociological Methodology, 40, 285-327. See Also faux, fauxmadrona

fauxtime

A Simulated RDS Data Set

Description

This is a faux set used to demonstrate RDS functions and analysis.

Format

An rds.data.frame object

References

Gile, Krista J., Handcock, Mark S., 2010 Respondent-driven Sampling: An Assessment of Current Methodology, Sociological Methodology, 40, 285-327. See Also fauxsycamore, fauxmadrona

get.h.hat

Get Horvitz-Thompson estimator assuming inclusion probability proportional to the inverse of network.var (i.e. degree).

Description

Get Horvitz-Thompson estimator assuming inclusion probability proportional to the inverse of network.var (i.e. degree).

Usage

get.h.hat(rds.data, group.variable, network.var = attr(rds.data, “network.size”))

Arguments

rds.data An rds.data.from group.variable The grouping variable. network.var The network.size variable.

get.id

Get the subject id

Description

Get the subject id

Usage

get.id(x, check.type = TRUE)

Arguments

x an rds.data.frame object check.type if true, x is required to be of type rds.data.frame

Details

returns the variable indicated by the ’id’ attribute, coercing to a character vector

get.net.size

Returns the network size of each subject (i.e. their degree).

Description

Returns the network size of each subject (i.e. their degree).

Usage

get.net.size(x, check.type = TRUE)

Arguments

x the rds.data.frame check.type if true, x is required to be of type rds.data.frame

get.number.of.recruits

Calculates the number of (direct) recuits for each respondent.

Description

Calculates the number of (direct) recuits for each respondent.

Usage

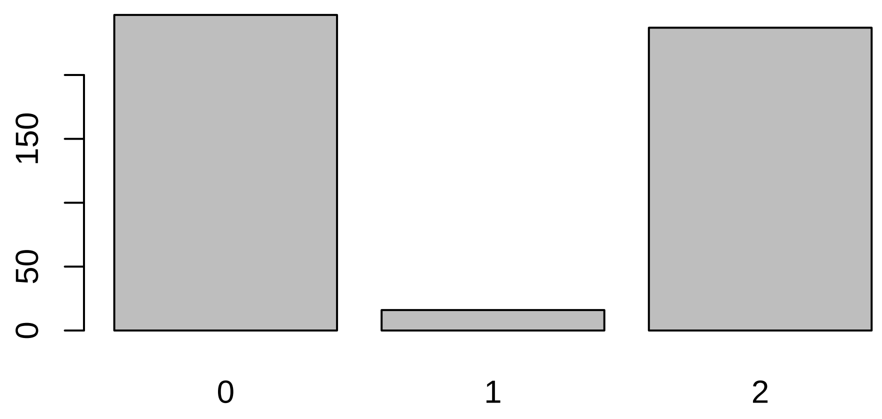
get.number.of.recruits(data)

Arguments

data An rds.data.frame

Examples

```
data(fauxmadrona)
nr <- get.number.of.recruits(fauxmadrona)
#frequency of number recruited by each id
barplot(table(nr))
```



get.population.size

Returns the population size associated with the data.

Description

Returns the population size associated with the data.

Usage

get.population.size(x, check.type = TRUE)

Arguments

x the rds.data.frame check.type if true, x is required to be of type rds.data.frame

get.recruitment.time

Returns the recruitment time for each subject

Description

Returns the recruitment time for each subject

Usage

get.recruitment.time(x, to.numeric = TRUE, wave.fallback = FALSE, check.type = TRUE)

Arguments

x the rds.data.frame to.numeric if true, time will be converted into a numeric variable. wave.fallback if true, subjects' recruitment times are ordered by wave and then by data.frame index if no recruitment time variable is available. check.type if true, x is required to be of type rds.data.frame

get.rid

Get recruiter id

Description

Get recruiter id

Usage

get.rid(x, check.type = TRUE)

Arguments

x an rds.data.frame object check.type if true, x is required to be of type rds.data.frame

Details

returns the variable indicated by the 'recruiter.id' attribute, coercing to a character vector

get.seed.id

Calculates the root seed id for each node of the recruitement tree.

Description

Calculates the root seed id for each node of the recruitement tree.

Usage

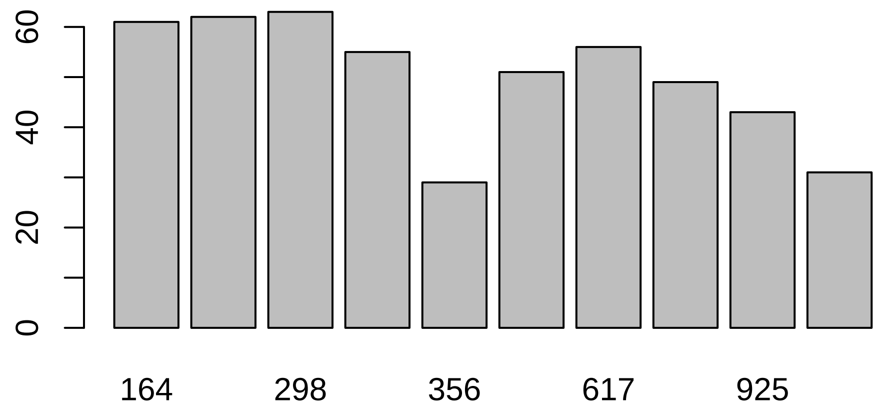
get.seed.id(data)

Arguments

data An rds.data.frame

Examples

```
data(fauxmadrona)
seeds <- get.seed.id(fauxmadrona)
#number recruited by each seed
barplot(table(seeds))
```



get.seed.rid

Gets the recruiter id associated with the seeds

Description

Gets the recruiter id associated with the seeds

Usage

get.seed.rid(x, check.type = TRUE)

Arguments

x an rds.data.frame object check.type if true, x is required to be of type rds.data.frame

Details

All seed nodes must have the same placeholder recruiter id.

get.stationary.distribution

Markov chain statistionary distribution

Description

Markov chain statistionary distribution

Usage

get.stationary.distribution(mle)

Arguments

mle The transition probabilities

Value

A vector of proportions representing the proportion in each group at the stationary distribution of the Markov chain.

get.wave

Calculates the depth of the recruitment tree (i.e. the recruitment wave) at each node.

Description

Calculates the depth of the recruitment tree (i.e. the recruitment wave) at each node.

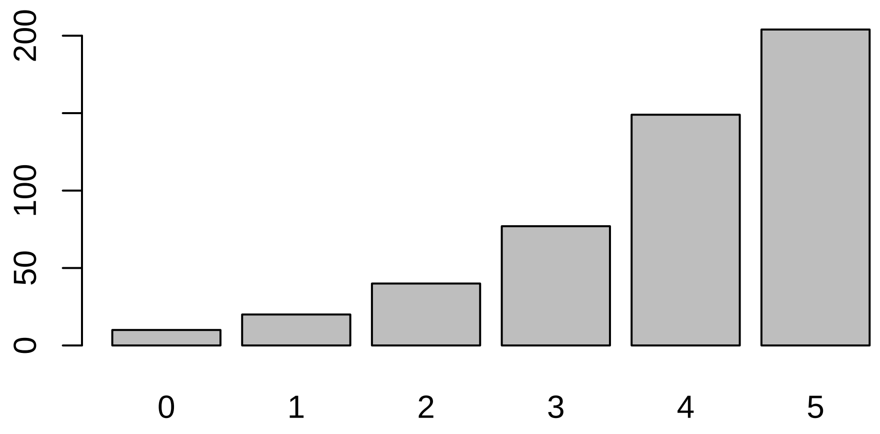
Usage

get.wave(data)

Arguments

data An rds.data.frame #### Examples

```
data(fauxmadrona)
#number subjects in each wave
w <- get.wave(fauxmadrona)
#number recruited in each wave
barplot(table(w))
```



gile.ss.weights

Weights using Giles SS estimator

Description

Weights using Giles SS estimator

Usage

gile.ss.weights(degs, N, number.ss.samples.per.iteration = 500, number.ss.iterations = 5, hajek = TRUE, SS.infinity = 0.04, se = FALSE, ...)

Arguments

degs subjects' degrees (i.e. network sizes). N Population size estimate. number.ss.samples.per.iteration The number of samples to use to estimate inclusion probabilities in a probability proportional to size without replacement design. number.ss.iterations number of iterations to use in giles SS algorithm. hajek Should the hajek estiamtor be used. If false, the HT estimator is used. SS.infinity The sample proportion, n/N, below which the computation of the SS weights should simplify to that of the RDS-II weights. se Should covariances be included. ... unused

has.recruitment.time RDS

data.frame has recruitment time information

Description

RDS data.frame has recruitment time information

Usage

has.recruitment.time(x, check.type = TRUE)

Arguments

x the rds.data.frame check.type if true, x is required to be of type rds.data.frame

hcg.replicate.weights

HCG parametric bootstrap replicate weights

Description

HCG parametric bootstrap replicate weights

Usage

hcg.replicate.weights(rds.data, outcome.variable, number.of.bootstrap.samples = 500, include.sample.weights = FALSE, N = NULL, small.fraction = FALSE)

Arguments

rds.data An rds.data.frame outcome.variable The column name of the variable defining the groups for the homophily configuration graph number.of.bootstrap.samples The number of bootstrap replicate weights to be generated include.sample.weights If TRUE, the first column of the returned frame are the HCG weights for the sample N The population size small.fraction If TRUE, the sample size is assumed to be small compared to the population size

Details

This function generates bootstrap replicate weights which may be used to analyze RDS data in other packages or software systems (e.g. the survey package with svrepdesign). Value A data.frame of replicate weights. If include.sample.weights is TRUE, the first column are the HCG weights for the observed sample.

Examples

```r
## Not run:
data("fauxmadrona")
set.seed(1)
# Generate replicate weights
result <- hcg.replicate.weights(fauxmadrona, "disease", 50, TRUE)
```

```
Note: Using the data's mid population size estimate: N = 1000
10% completed ...
20% completed ...
30% completed ...
40% completed ...
50% completed ...
60% completed ...
70% completed ...
80% completed ...
90% completed ...
100% completed ...
```

```
# Analyze with survey package and compare to internal function
if(require(survey)){
set.seed(1)
design <- svrepdesign(fauxmadrona, type = "bootstrap",
weights= result[[1]], repweights = result[-1])
svymean(~disease, design) |> print()
RDS.bootstrap.intervals(fauxmadrona, "disease", "HCG", "HCG",
number.of.bootstrap.samples = 50) |> print()
}
```

```
Loading required package: survey
```

```
Warning in library(package, lib.loc = lib.loc, character.only = TRUE,
logical.return = TRUE, : there is no package called 'survey'
```

```
## End(Not run)
```

hcg.weights

homophily configuration graph weights

Description

homophily configuration graph weights

Usage

hcg.weights(rds.data, outcome.variable, N = NULL, small.fraction = FALSE, reltol = sqrt(.Machine$double.eps), max.optim = 500, theta.start = NULL, weights.include.seeds = TRUE, ...)

Arguments

rds.data An rds.data.frame outcome.variable The variable used to base the weights on. N Population size small.fraction should a small sample fraction be assumed reltol Relative convergence tolerance for the HCG estimator. The algorithm stops if it is unable to reduce the log-likelihood by a factor of reltol * (abs(log-likelihood) + reltol) at a step. Defaults to sqrt(.Machine$double.eps), typically about 1e-8. max.optim The number of iterations on the likelihood optimization for the HCG estimator. theta.start The initial value of theta used in the likelihood optimization for the HCG estimator. If NULL, the default, it is the margin of the table of counts for the transitions. weights.include.seeds logical Should the weights be computed including the influence of the seeds? ... Unused

Examples

```
data(fauxtime)
hcg.weights(fauxtime,"var1",N=3000)
```

```
  [1]  1.761105 23.806193  1.108483 15.113171  1.953351  1.688959 10.272898
  [8] 12.392367  4.914937  2.672978  1.695138  2.727248  2.569408  0.994497
 [15] 13.746330  1.594635  8.700932  4.914937 15.113171 10.272898  9.423607
 [22]  2.368957  3.313720 23.806193  5.075373 23.806193  3.041840 12.392367
 [29]  1.366458  8.029119  2.269900  5.881672 13.746330  6.344322 23.806193
 [36]  4.715382  1.957166  3.881481  7.864439  2.138888  2.727248  2.080347
 [43]  2.876753  2.849817  4.340852  6.176714  8.700932  4.922156 10.272898
 [50]  1.695138 10.272898 14.770050  1.704199  4.582632  2.316540  3.755881
 [57]  1.911737  3.056253 14.770050 12.392367  3.217653  1.616240  7.501452
 [64]  2.120183  3.982948  2.236761 17.242483  1.834171  4.252920  1.218198
 [71]  1.834171  5.881672  3.593076  3.313720  2.812167  2.001736  2.368957
 [78]  1.010150  4.252920 12.392367  6.176714  1.911737  3.435104  1.332201
 [85]  3.982948  8.700932  6.344322  5.568843  3.982948  4.582632  1.237122
 [92]  5.568843  8.623437  4.582632 20.387189  4.340852  6.176714  4.914937
 [99]  5.568843  7.315576  7.501452  3.755881  1.792610  6.935876  4.922156
[106]  9.630868  6.176714  2.820837  3.056253  1.695138 23.806193  2.520294
[113]  2.866564  3.041840  4.001873  5.239649  1.634163  5.075373  8.700932
[120]  3.982948  8.029119  5.290225  2.762900  2.727248  8.700932  2.587988
[127]  6.181675  7.315576  5.881672  1.024610  2.298323 13.375651  2.001736
[134]  9.630868 10.272898  6.663421  3.907788  9.423607  1.304777  2.820837
[141]  4.358469  6.663421  3.982948 10.272898  2.063994 12.392367  2.001736
[148]  5.881672  5.437583  7.501452 10.272898 17.242483  2.520294  8.029119
[155]  1.177519  4.914937  1.204410  1.361507 10.272898  2.001736 10.272898
[162]  8.029119  2.000138  7.501452  1.595651 12.392367  7.864439  4.715382
[169]  4.001873  2.000138  9.630868  2.374571  1.210228  1.634163  1.077493
[176]  1.957166  1.708072 10.272898  5.190031 11.282250 20.387189  4.922156
[183]  2.820837  2.414624  4.001873  2.680527  2.820837  4.001873  5.437583
[190]  4.340852  8.700932  9.630868  2.120183  8.700932  2.389655  6.113411
[197]  4.922156  4.582632  2.001736  1.700488  1.964841  1.911737  1.911737
[204]  7.315576  8.700932  4.252920  3.041840  2.236761  5.881672  7.864439
[211]  2.770059  1.093962  7.864439  2.820837  6.935876  2.727248  1.201521
[218] 10.272898  1.291326  7.864439  5.881672  6.935876  4.715382  6.181675
[225]  3.982948  7.501452 13.746330 13.746330  9.630868  2.866564  3.593076
```

```
[232]  5.568843 20.566170  8.700932  5.568843  8.029119  5.568843  4.715382
[239] 29.894580  1.968701  3.907788  1.704199  4.922156  8.003904  3.041840
[246]  3.915466  9.630868  7.864439  6.344322  2.866564  2.447482  2.587988
[253] 11.282250  4.922156  1.708072  4.358469  6.176714  3.435104  6.344322
[260]  4.914937  5.075373  1.380260  3.351401  2.368957  6.663421  7.501452
[267]  4.252920  2.866564  8.029119  3.055088 17.242483  2.520294  2.123027
[274]  1.695138  4.582632  5.568843  3.056253  5.568843  2.473372  4.715382
[281]  1.101175  5.881672  2.997215  6.663421  2.820837  6.176714  3.593076
[288]  2.876753  1.748811  1.642736  2.000138  4.922156  3.041840  4.914937
[295]  2.482827 10.004880 11.282250  4.922156  1.595651  4.715382  1.594635
[302]  5.437583 23.806193 11.282250  4.914937  3.982948  2.368957  4.358469
[309]  4.715382  7.501452  2.473372  3.351401  6.176714  7.864439 12.392367
[316]  5.075373  9.630868  6.663421  7.501452  2.447482  8.029119  3.055088
[323]  1.911737 13.375651  5.568843  3.055088  2.520294  8.700932  1.634163
[330]  2.770059  3.881481  2.447482  5.042945  6.344322  4.592101  6.176714
[337]  5.437583  1.366458 13.746330 12.392367  6.176714  7.334294 11.300357
[344]  3.907788  5.568843  8.029119  9.423607  2.849817 11.282250 13.746330
[351]  4.922156  2.812167  3.412623  6.181675  8.700932  7.864439  4.922156
[358]  2.412686 42.255919  3.707443 17.242483  3.565245 15.113171  4.715382
[365]  6.663421 10.272898  5.881672 23.806193  3.593076  1.594635  3.041840
[372] 13.746330  4.914937 11.282250  8.700932 13.240710  6.663421 13.746330
[379]  4.554324 10.272898  3.313720 23.806193  5.075373  6.663421 20.566170
[386]  8.029119  7.864439  1.811793  1.911737  4.340852  2.722639  4.922156
[393]  4.358469  4.592101  5.075373  1.442093 12.392367  6.181675  4.715382
[400]  2.094918 20.566170  1.834171 13.240710  4.715382 11.282250 12.392367
[407]  2.473372 10.272898  4.922156  2.680527  5.881672  6.181675  4.922156
[414]  4.340852 11.282250 17.242483  3.462232  3.982948  1.908977  2.770059
[421]  2.482827  2.770059  7.501452  8.029119  2.722639  2.680527  3.056253
[428]  3.041840  8.700932  1.177519  4.001873  2.727248  1.668261  3.593076
[435]  3.217653  6.344322  4.358469  2.150363  7.334294  5.290225  4.582632
[442]  2.120183  6.935876  8.700932  2.491215  2.316540  2.403867  8.029119
[449]  3.351401  2.094918 10.272898  2.032594  9.630868  2.094918  2.866564
[456]  9.423607  2.997215  3.755881  2.236761  6.935876  3.462232  3.435104
[463] 10.272898  5.239649  6.663421  2.569408  9.630868  6.935876  4.914937
[470]  7.501452  6.663421  4.252920  7.501452  2.672978  5.881672  7.864439
[477]  3.755881  2.403867  6.663421  6.181675  2.236761  2.063994  2.770059
[484]  4.922156  3.055088  5.881672  3.982948  2.316540  7.501452  3.982948
[491]  3.055088  5.568843  7.315576  6.176714  3.056253  3.435104  7.501452
[498]  2.138888  4.922156  5.881672  4.340852  2.319604  3.707443  2.770059
[505]  4.914937  3.881481  2.820837  5.568843  2.403867  1.668261  1.704199
```

```r
fauxtime$NETWORK[c(1,100,40,82,77)] <- NA
```

homophily.estimates

This function computes an estimate of the population homophily and the recruitment homophily based on a categorical variable.

Description

This function computes an estimate of the population homophily and the recruitment homophily based on a categorical variable.

Usage

homophily.estimates(rds.data, outcome.variable, weight.type = NULL, uncertainty = NULL, recruitment = FALSE, N = NULL, to.group0.variable = NULL, to.group1.variable = NULL, number.ss.samples.per.iteration = NULL, confidence.level = 0.95)

Arguments

rds.data An rds.data.frame that indicates recruitment patterns by a pair of attributes named "id" and "recruiter.id". outcome.variable A string giving the name of the variable in the rds.data that contains a categorical or numeric variable to be analyzed. weight.type A string giving the type of estimator to use. The options are "Gile's SS", "RDS-I", "RDS-II", "RDS-I/DS", "Good-Fellows" and "Arithemic Mean". If NULL it defaults to "Gile's SS". uncertainty A string giving the type of uncertainty estimator to use. The options are "Gile's SS" and "Salganik". This is usually determined by weight.type to be consistent with the estimator's origins (e.g., for "Gile's SS", "RDS-I", "RDS-II", "RDS-I/DS", and "Arithemic Mean"). Hence it's current functionality is limited. If NULL it defaults to "Gile's SS". recruitment A logical indicating if the homophily in the recruitment chains should be computed also. The default is FALSE. N An estimate of the number of members of the population being sampled. If NULL it is read as the population.size.mid attribute of the rds.data frame. If that is missing it defaults to 1000. to.group0.variable The number in the network of each survey respondent who have group variable value 0. Usually this is not available. The default is to not use this variable. to.group1.variable The number in the network of each survey respondent who have group variable value 1. Usually this is not available. The default is to not use this variable. number.ss.samples.per.iteration The number of samples to take in estimating the inclusion probabilites in each iteration of the sequential sampling algorithm. If NULL it is read as the number.ss.samples.per.iteration attribute of rds.data. If that is missing it defaults to 5000. confidence.level The confidence level for the confidence intervals. The default is 0.95 for 95%. Value If outcome.variable is binary then the homophily estimate of 0 verses 1 is returned, otherwise a vector of differential homophily estimates is returned. Recruitment Homophily The recruitment homophily is a homophily measure for the recruitment process. It addresses the question: Do respondents differential recruit people like themselves? That is, the homophily on a variable in the recruitment chains. Take as an example infection status. In this case, it is the ratio of number of recruits that have the same infection status as their recruiter to the number we would expect if there was no homophily on infection status. The difference with the Population Homophily (see below) is that this is in the recruitment chain rather than the population of social ties. For example, of the recruitment homophily on infection status is about 1, we see little effect of recruitment homophily on infection status (as the numbers of homophilous pairs are close to what we would expect by chance). Population Homophily This is an estimate the homophily of a given variable in the underlying networked population. For example, consider HIV status. The population homophily is the homophily in the HIV status of two people who are tied in the underlying population social network (a "couple"). Specifically, the population homophily is the ratio of the expected number of HIV discordant couples absent homophily to the expected number of HIV discordant couples with the homophily. Hence larger values of population homophily indicate more homophily on HIV status. For example, a value of 1 means the couple are random with respect to HIV status. A value of 2 means there are twice as many HIV discordant couples as we would expect if there was no homophily in the population. This measure is meaningful across different levels of differential activity. As we do not see most of the population network, we estimate the population homophily from the RDS data. As an example, suppose the population homophily on HIV is 0.75 so there are 25% more HIV discordant couples than expected due to chance. So their is actually heterophily on HIV in the population. If the population homophily on sex is 1.1, there are 10% more same-sex couples than expected due to chance. Hence there is modest homophily on sex. Author(s) Mark S. Handcock with help from Krista J. Gile

References

Gile, Krista J., Handcock, Mark S., 2010, Respondent-driven Sampling: An Assessment of Current Methodology. Sociological Methodology 40, 285-327.

Examples

```
# ## Not run:
# data(fauxmadrona)
# names(fauxmadrona)
# #
# # True value:
# #
# if(require(network)){
# a=as.sociomatrix(fauxmadrona.network)
# deg <- apply(a,1,sum)
# dis <- fauxmadrona.network \
# deg1 <- apply(a[dis==1,],1,sum)
# deg0 <- apply(a[dis==0,],1,sum)
# # differential activity
# mean(deg1)/ mean(deg0)
# p=mean(dis)
# N=1000
# # True homophily
# p*(1-p)*mean(deg0)*mean(deg1)*N/(mean(deg)*sum(a[dis==1,dis==0]))
# }
# # HT based estimators using the to.group information
# data(fauxmadrona)
# homophily.estimates(fauxmadrona,outcome.variable="disease",
# to.group0.variable="tonondiseased", to.group1.variable="todiseased",
# N=1000)
# # HT based estimators not using the to.group information
# homophily.estimates(fauxmadrona,outcome.variable="disease",
# N=1000,weight.type="RDS-II")
# ## End(Not run)
```

impute.degree

Imputes missing degree values

Description

Imputes missing degree values

Usage

impute.degree(rds.data, trait.variable = NULL, N = NULL, method = c("mean", "quantile"), quantile = 0.5, recruitment.lower.bound = TRUE, round.degree = TRUE)

Arguments

rds.data an rds.data.frame trait.variable the name of the variable in rds.data to stratify the imputation by N population size method If mean, the weighted mean value is imputed, otherwize a quantile is used. quantile If method is "quantile", this is the quantile that is used. Defaults to median recruitment.lower.bound If TRUE, then for each individual, the degree is taken to be the minimum of the number of recruits plus one, and the reported degree round.degree Should degrees be integer rounded.

Details

This function imputes degree values using the weighted mean or quantile values of the non-missing degrees. Weights are calcualted using Gile's SS if N is not NULL, or RDS-II if it is. If a trait variable is specified, means and quantile are calculated within the levels of the trait variable

Examples

```
data(faux)
rds.data <- faux
rds.data$network.size[c(1,2,30,52,81,101,108,111)] <- NA
impute.degree(rds.data)
```

```
  [1] 15 15 17 32 14 25 43 28 11 10 26 21 28 22 22 18 23 19 29 15 25 24 15 13 39
 [26] 26 17 21 16 15 21 23 19 19 14 18 36 17 34 13 17 15 18 13 17 16 20 20 26 17
 [51] 21 15 14 24 27 18 20 16 16 25  8 16 34 21 32  9 15 17 19 15 31 15 19 24 23
 [76] 18 13 22 18 20 15 24 18 21 14 13 20 22  8 15 22 21 15 19 13 32 21 29 43 15
[101] 15 14 12 17 20 16 16 15 27 12 15 14 13 24 19 22 21 14  8 14 14  6  6 25 29
[126]  8 18 10  9  8 14 14 23 26  8 11 29 13 18  6 11 19 22 22  9 13 13 14 20 16
[151] 10  9 21 16 23 23 15 15 14 29 12 23  7 17 14 16 18 15 14 12  4  4 22 17 10
[176] 17 18 28 30 14 22 18 11 22 12 16 12 14 21 23 28 15 18 24  9 11 28 13 16 12
[201] 25 13 11 22 18 17 16  5 14 15 17 25 12 15 25 15 12 13 15  9 13 15 38 16 10
[226] 14 15 17 24 26 20 17 13 14 21 12 17 15 17 11 14 16 12 23 14 13  7 19 11 13
[251] 15 20 16 20 22 17 24 19 16 12 23 24 20  6 13 16 20 20 16 15 14 22 15 22 17
[276] 16  9 29 27 15 14 15 20 15 13 15 17 18 15 22 17 13 13 13 11 15  9 15 14 17
[301] 14 13 13 14 11 31 17 15 13 15 12  9 16 32 17 10 20 19 10 18 17 22  9 16 18
[326] 21  9  8 19 17 12  5 10 13 16 12  9 10 18 23 17 16 19 10  8 11 17 12 18 22
[351] 11 11 23 23 16 17 21 23 11 21 16 19  4 17 16  9 16 22 27 12 11 22 15  9 24
[376] 27 20 13 11 17 13 10 18 22 18 16 25 11 18
```

```
impute.degree(rds.data,trait.variable="X")
```

```
  [1] 15 16 17 32 14 25 43 28 11 10 26 21 28 22 22 18 23 19 29 15 25 24 15 13 39
 [26] 26 17 21 16 16 21 23 19 19 14 18 36 17 34 13 17 15 18 13 17 16 20 20 26 17
 [51] 21 15 14 24 27 18 20 16 16 25  8 16 34 21 32  9 15 17 19 15 31 15 19 24 23
 [76] 18 13 22 18 20 15 24 18 21 14 13 20 22  8 15 22 21 15 19 13 32 21 29 43 15
[101] 15 14 12 17 20 16 16 15 27 12 15 14 13 24 19 22 21 14  8 14 14  6  6 25 29
[126]  8 18 10  9  8 14 14 23 26  8 11 29 13 18  6 11 19 22 22  9 13 13 14 20 16
[151] 10  9 21 16 23 23 15 15 14 29 12 23  7 17 14 16 18 15 14 12  4  4 22 17 10
[176] 17 18 28 30 14 22 18 11 22 12 16 12 14 21 23 28 15 18 24  9 11 28 13 16 12
```

```
[201] 25 13 11 22 18 17 16  5 14 15 17 25 12 15 25 15 12 13 15  9 13 15 38 16 10
[226] 14 15 17 24 26 20 17 13 14 21 12 17 15 17 11 14 16 12 23 14 13  7 19 11 13
[251] 15 20 16 20 22 17 24 19 16 12 23 24 20  6 13 16 20 20 16 15 14 22 15 22 17
[276] 16  9 29 27 15 14 15 20 15 13 15 17 18 15 22 17 13 13 13 11 15  9 15 14 17
[301] 14 13 13 14 11 31 17 15 13 15 12  9 16 32 17 10 20 19 10 18 17 22  9 16 18
[326] 21  9  8 19 17 12  5 10 13 16 12  9 10 18 23 17 16 19 10  8 11 17 12 18 22
[351] 11 11 23 23 16 17 21 23 11 21 16 19  4 17 16  9 16 22 27 12 11 22 15  9 24
[376] 27 20 13 11 17 13 10 18 22 18 16 25 11 18
```

```
impute.degree(rds.data,trait.variable="X",method="quantile")
```

```
  [1] 14 15 17 32 14 25 43 28 11 10 26 21 28 22 22 18 23 19 29 15 25 24 15 13 39
 [26] 26 17 21 16 15 21 23 19 19 14 18 36 17 34 13 17 15 18 13 17 16 20 20 26 17
 [51] 21 14 14 24 27 18 20 16 16 25  8 16 34 21 32  9 15 17 19 15 31 15 19 24 23
 [76] 18 13 22 18 20 14 24 18 21 14 13 20 22  8 15 22 21 15 19 13 32 21 29 43 15
[101] 14 14 12 17 20 16 16 14 27 12 14 14 13 24 19 22 21 14  8 14 14  6  6 25 29
[126]  8 18 10  9  8 14 14 23 26  8 11 29 13 18  6 11 19 22 22  9 13 13 14 20 16
[151] 10  9 21 16 23 23 15 15 14 29 12 23  7 17 14 16 18 15 14 12  4  4 22 17 10
[176] 17 18 28 30 14 22 18 11 22 12 16 12 14 21 23 28 15 18 24  9 11 28 13 16 12
[201] 25 13 11 22 18 17 16  5 14 15 17 25 12 15 25 15 12 13 15  9 13 15 38 16 10
[226] 14 15 17 24 26 20 17 13 14 21 12 17 15 17 11 14 16 12 23 14 13  7 19 11 13
[251] 15 20 16 20 22 17 24 19 16 12 23 24 20  6 13 16 20 20 16 15 14 22 15 22 17
[276] 16  9 29 27 15 14 15 20 15 13 15 17 18 15 22 17 13 13 13 11 15  9 15 14 17
[301] 14 13 13 14 11 31 17 15 13 15 12  9 16 32 17 10 20 19 10 18 17 22  9 16 18
[326] 21  9  8 19 17 12  5 10 13 16 12  9 10 18 23 17 16 19 10  8 11 17 12 18 22
[351] 11 11 23 23 16 17 21 23 11 21 16 19  4 17 16  9 16 22 27 12 11 22 15  9 24
[376] 27 20 13 11 17 13 10 18 22 18 16 25 11 18
```

impute.visibility

Estimates each person's personal visibility based on their selfreported degree and the number of their (direct) recruits. It uses the time the person was recruited as a factor in determining the number of recruits they produce.

Description

Estimates each person's personal visibility based on their self-reported degree and the number of their (direct) recruits. It uses the time the person was recruited as a factor in determining the number of recruits they produce.

Usage

impute.visibility(rds.data, max.coupons = NULL, type.impute = c("median", "distribution", "mode", "mean"), recruit.time = NULL, include.tree = FALSE, reflect.time = FALSE, parallel = 1, parallel.type = "PSOCK", interval = 10, burnin = 5000, mem.optimism.prior = NULL, df.mem.optimism.prior = 5, mem.scale.prior = 2, df.mem.scale.prior = 10, mem.overdispersion = 15, return.posterior.sample.visibilities = FALSE, verbose = FALSE)

Arguments

rds.data An rds.data.frame max.coupons The number of recruitment coupons distributed to each enrolled subject (i.e. the maximum number of recruitees for any subject). By default it is taken by the attribute or data, else the maximum recorded number of coupons. type.impute The type of imputation based on the conditional distribution. It can be of type distribution,mode,median, or mean with the first , the default, being a random draw from the conditional distribution. recruit.time vector; An optional value for the data/time that the person was interviewed. It needs to resolve as a numeric vector with number of elements the number of rows of the data with non-missing values of the network variable. If it is a character name of a variable in the data then that variable is used. If it is NULL then the sequence number of the recruit in the data is used. If it is NA then the recruitment is not used in the model. Otherwise, the recruitment time is used in the model to better predict the visibility of the person. include.tree logical; If TRUE, augment the reported network size by the number of recruits and one for the recruiter (if any). This reflects a more accurate value for the visibility, but is not the self-reported degree. In particular, it typically produces a positive visibility (compared to a possibility zero self-reported degree). reflect.time logical; If FALSE then the recruit.time is the time before the end of the study (instead of the time since the survey started or chronological time). parallel count; the number of parallel processes to run for the Monte-Carlo sample. This uses MPI or PSOCK. The default is 1, that is not to use parallel processing. parallel.type The type of parallel processing to use. The options are "PSOCK" or "MPI". This requires the corresponding type to be installed. The default is "PSOCK". interval count; the number of proposals between sampled statistics. burnin count; the number of proposals before any MCMC sampling is done. It typically is set to a fairly large number. mem.optimism.prior scalar; A hyper parameter being the mean of the distribution of the optimism parameter. df.mem.optimism.prior scalar; A hyper parameter being the degrees-of-freedom of the prior for the optimism parameter. This gives the equivalent sample size that would contain the same amount of information inherent in the prior. mem.scale.prior scalar; A hyper parameter being the scale of the concentration of baseline negative binomial measurement error model. df.mem.scale.prior scalar; A hyper parameter being the degrees-of-freedom of the prior for the standard deviation of the dispersion parameter in the visibility model. This gives the equivalent sample size that would contain the same amount of information inherent in the prior for the standard deviation. mem.overdispersion scalar; A parameter being the overdispersion of the negative binomial distribution that is the baseline for the measurement error model.

return.posterior.sample.visibilities logical; If TRUE then return a matrix of dimension sample-size by n of posterior draws from the visibility distribution for those in the survey. The sample for the ith person is the ith column. The default is FALSE so that the vector of imputes defined by type.impute is returned. verbose logical; if this is TRUE, the program will print out additional

References

McLaughlin, Katherine R.; Johnston, Lisa G.; Jakupi, Xhevat; Gexha-Bunjaku, Dafina; Deva, Edona and Handcock, Mark S. (2023) Modeling the Visibility Distribution for Respondent-Driven Sampling with Application to Population Size Estimation, Annals of Applied Statistics, doi:10.1093/ jrsssa/qnad031 #### Examples

```
# ## Not run:
# data(fauxmadrona)
# # The next line fits the model for the self-reported personal
# # network sizes and imputes the personal network sizes
# # It may take up to 60 seconds.
# visibility <- impute.visibility(fauxmadrona)
# # frequency of estimated personal visibility
# table(visibility)
# ## End(Not run)
```

impute.visibility_mle

Estimates each person's personal visibility based on their selfreported degree and the number of their (direct) recruits. It uses the time the person was recruited as a factor in determining the number of recruits they produce. #### Description Estimates each person's personal visibility based on their self-reported degree and the number of their (direct) recruits. It uses the time the person was recruited as a factor in determining the number of recruits they produce. #### Usage impute.visibility_mle(rds.data, max.coupons = NULL, type.impute = c("distribution", "mode", "median", "mean"), recruit.time = NULL, include.tree = FALSE, unit.scale = NULL, unit.model = c("cmp", "nbinom"), optimism = FALSE, guess = NULL, reflect.time = TRUE, maxit = 100, K = NULL, verbose = TRUE) #### Arguments rds.data An rds.data.frame max.coupons The number of recruitment coupons distributed to each enrolled subject (i.e. the maximum number of recruitees for any subject). By default it is taken by the attribute or data, else the maximum recorded number of coupons. type.impute The type of imputation based on the conditional distribution. It can be of type distribution,mode,median, or mean with the first , the default, being a random draw from the conditional distribution. recruit.time vector; An optional value for the data/time that the person was interviewed. It needs to resolve as a numeric vector with number of elements the number of rows of the data with non-missing values of the network variable. If it is a character name of a variable in the data then that variable is used. If it is NULL then the sequence number of the recruit in the data is used. If it is NA then the recruitment is not used in the model. Otherwise, the recruitment time is used in the model to better predict the visibility of the person. include.tree logical; If TRUE, augment the reported network size by the number of recruits and one for the recruiter (if any). This reflects a more accurate value for the visibility, but is not the self-reported degree. In particular, it typically produces a positive visibility (compared to a possibility zero self-reported degree). unit.scale numeric; If not NULL it sets the numeric value of the scale parameter of the distribution of the unit sizes. For the negative binomial, it is the multiplier on the variance of the negative binomial compared to a Poisson (via the PoissonGamma mixture representation). Sometimes the scale is unnaturally large (e.g. 40) so this give the option of fixing it (rather than using the MLE of it). The model is fit with the parameter fixed at this passed value. unit.model The type of distribution for the unit sizes. It can be of nbinom, meaning a negative binomial. In this case, unit.scale is the multiplier on the variance of the negative binomial compared to a Poisson of the same mean. The alternative is cmp, meaning a Conway-Maxwell-Poisson distribution. In this case, unit.scale is the scale parameter compared to a Poisson of the same mean (values less than one mean underdispersed and values over one mean overdispersed). The default is cmp. optimism logical; If TRUE then add a term to the model allowing the (proportional) inflation of the self-reported degrees relative to the unit sizes. guess vector; if not NULL, the initial parameter values for the MLE fitting. reflect.time logical; If FALSE then the recruit.time is the time before the end of the study (instead of the time since the survey started or chronological time). maxit integer; The maximum number of iterations in the likelihood maximization. By default it is 100. K integer; The maximum degree. All self-reported degrees above this are recorded as being at least K. By default it is the 95th percentile of the self-reported network sizes. verbose logical; if this is TRUE, the program will print out additional #### References McLaughlin, K.R., M.S. Handcock, and L.G. Johnston, 2015. Inference for the visibility distribution for respondent-driven sampling. In JSM Proceedings. Alexandria, VA: American Statistical Association. 2259-2267. #### Examples

```
# ## Not run:
# data(fauxmadrona)
# # The next line fits the model for the self-reported personal
# # network sizes and imputes the personal network sizes
# # It may take up to 60 seconds.
# visibility <- impute.visibility(fauxmadrona)
# # frequency of estimated personal visibility
# table(visibility)
# ## End(Not run)
```

is.rds.data.frame

Is an instance of rds.data.frame #### Description Is an instance of rds.data.frame #### Usage is.rds.data.frame(x) #### Arguments x An object to be tested. is.rds.interval.estimate Is an instance of rds.interval.estimate #### Description Is an instance of rds.interval.estimate #### Usage is.rds.interval.estimate(x) #### Arguments x An object to be tested

is.rds.interval.estimate.list

Is an instance of rds.interval.estimate.list This is a (typically time ordered) sequence of RDS estimates of a comparable quantity #### Description Is an instance of rds.interval.estimate.list This is a (typically time ordered) sequence of RDS estimates of a comparable quantity #### Usage is.rds.interval.estimate.list(x) #### Arguments x An object to be tested. ### LRT.trend.test Compute a test of trend in prevalences based on a likelihood-ratio statistic #### Description This function takes a series of point estimates and their associated standard errors and computes the p-value for the test of a monotone decrease in the population prevalences (in sequence order). The p-value for a monotone increase is also reported. An optional plot of the estimates and the null distribution of the test statistics is provided. More formally, let the K population prevalences in sequence order be p1, . . . , pK. We test the null hypothesis: H0 : p1 = . . . = pK vs H1 : p1 p2 . . . pK with at least one equality strict. The alternatie hypothesis is for a monotone decreasing trend. A likelihood ratio statistic for this test has been derived (Bartholomew 1959). The null distribution of the likelihood ratio statistic is very complex but can be determined by a simple Monte Carlo process. Alternatively, we can test the null hypothesis: H0 : p1 p2 . . . pK vs H1 : H0 The null distribution of the likelihood ratio statistic is very complex but can be determined by a simple Monte Carlo process. In both cases we also test for: H : p1 p2 . . . pK that is, a monotonically increasing trend. The function requires the isotone library. Usage LRT.trend.test(data, variables = colnames(data), null = "monotone", confidence.level = 0.95, number.of.bootstrap.samples = 5000, plot = NULL, seed = 1) #### Arguments data A two row matrix or data.frame of prevalence estimates and their standard errors. The first row is the prevalence estimates and the second are the standard errors. The column are the comparison groups in the order (e.g., time) there are to be assessed. The row names of data should be "estimate" and "sigma". This is variables A character vector of column names it select from data. null A character string indicating the null hypothesis to use. The value "monotone" uses the various monotone hypotheses as the nulls. If not "monotone", the null is chosen to be that of equality of the means over all periods. confidence.level The confidence level for the confidence intervals. The default is 0.95 for 95%. number.of.bootstrap.samples The number of Monte Carlo draws to determine the null distribution of the likelihood ratio statistic. plot A character vector of choices, a subset of estimates, distributions. If estimates is given then a plot of the estimates and nominal 95% confidence bands (as error bars) is produced. If distributions is given then a plot is produced of the null distributions of the likelihood ratio statistic with the observed likelihood ratio statistics plotted as a vertical dashed line. seed The value of the random number seed. Preset by default to allow reproducibility. Value A list with components • pvalue.increasing: The p-value for the test of a monotone increase in population prevalence. • pvalue.decreasing: The p-value for the test of a monotone decrease in population prevalence. • L: The value of the likelihood-ratio statistic. • x: The passed vector of prevalence estimates in the order (e.g., time). • sigma The passed vector of standard error estimates corresponding to x. Author(s) Mark S. Handcock #### References Bartholomew, D. J. (1959). A test of homogeneity for ordered alternatives. Biometrika 46 36-48. #### Examples

```
d <- t(data.frame(estimate=c(0.16,0.15,0.3), sigma=c(0.04,0.04,0.1)))
colnames(d) <- c("time_1","time_2","time_3")
LRT.trend.test(d,number.of.bootstrap.samples=1000)
```

```
In a test of the null hypothesis of an increasing trend in proportions against the complemen
We do not reject the null hypothesis of an increasing trend (at the 5% level).

In a test of the null hypothesis of an decreasing trend in proportions against the complemen
We do not reject the null hypothesis of an decreasing trend (at the 5% level).

In a test of the null hypothesis of a monotone trend in proportions against the complementar
We do not reject the null hypothesis of a monotone trend (at the 5% level).
```

LRT.value.trend

Compute a test of trend in prevalences based on a likelihood-ratio statistic #### Description This function takes a series of point estimates and their associated standard errors and computes the p-value for the test of a monotone decrease in the population prevalences (in sequence order). The p-value for a monotone increase is also reported. More formally, let the K population prevalences in sequence order be p1, . . . , pK. We test the null hypothesis: H0 : p1 = . . . = pK vs H1 : p1   p2 . . .   pK with at least one equality strict. A likelihood ratio statistic for this test has been derived (Bartholomew 1959). The null distribution of the likelihood ratio statistic is very complex but can be determined by a simple Monte Carlo process. We also test the null hypothesis: H0 : p1   p2 . . .   pK vs H1 : H0 The null distribution of the likelihood ratio statistic is very complex but can be determined by a simple Monte Carlo process. The function requires the isotone library. Usage LRT.value.trend(x, sigma) #### Arguments x A vector of prevalence estimates in the order (e.g., time). sigma A vector of standard error estimates corresponding to x. Value A list with components • pvalue.increasing: The p-value for the test of a monotone increase in population prevalence. • pvalue.decreasing: The p-value for the test of a monotone decrease in population prevalence. • L: The value of the likelihood-ratio statistic. • x: The passed vector of prevalence estimates in the order (e.g., time). • sigma The passed vector of standard error estimates corresponding to x. Author(s) Mark S. Handcock #### References Bartholomew, D. J. (1959). A test of homogeneity for ordered alternatives. Biometrika 46 36-48. #### Examples

```
# ## Not run:
# x <- c(0.16,0.15,0.3)
# sigma <- c(0.04,0.04,0.1)
# LRT.value.trend(x,sigma)
# ## End(Not run)
```

MA.estimates

MA Estimates

Description

This function computes the sequential sampling (MA) estimates for a categorical variable or numeric variable. #### Usage MA.estimates(rds.data, trait.variable, seed.selection = "degree", number.of.seeds = NULL, number.of.coupons = NULL, number.of.iterations = 3, N = NULL, M1 = 25, M2 = 20, seed = 1, initial.sampling.probabilities = NULL, MPLE.samplesize = 50000, SAN.maxit = 5, SAN.nsteps = 2^19, sim.interval = 10000, number.of.cross.ties = NULL, max.degree = NULL, parallel = 1, parallel.type = "PSOCK", full.output = FALSE, verbose = TRUE) #### Arguments rds.data An rds.data.frame that indicates recruitment patterns by a pair of attributes named "id" and "recruiter.id". trait.variable A string giving the name of the variable in the rds.data that contains a categorical or numeric variable to be analyzed. seed.selection An estimate of the mechanism guiding the choice of seeds. The choices are "allwithtrait" indicating that all the seeds had the trait; "random" meaning they were, as if, a simple random sample of individuals from the population; "sample" indicating that the seeds are taken as those in the sample (and resampled for the population with that composition if necessary); "degree" is proportional to the degree of the individual; "allwithtraitdegree" indicating that all the seeds had the trait and the probability of being a seed is proportional to the degree of the respondent. number.of.seeds The number of seeds chosen to initiate the sampling. number.of.coupons The number of coupons given to each respondent. number.of.iterations The number of iterations used at the core of the algorithm. N An estimate of the number of members of the population being sampled. If NULL it is read as the pop.size.mid attribute of the rds.data frame. If that is missing it defaults to 1000. M1 The number of networked populations generated at each iteration. M2 The number of (full) RDS samples generated for each networked population at each iteration. seed The random number seed used to initiate the computations. initial.sampling.probabilities Initialize sampling probabilities for the algorithm. If missing, they are taken as proportional to degree, and this is almost always the best starting values. MPLE.samplesize Number of samples to take in the computation of the maximum pseudolikelihood estimator (MPLE) of the working model parameter. The default is almost always sufficient. SAN.maxit A ceiling on the number of simulated annealing iterations. SAN.nsteps Number of MCMC proposals for all the annealing runs combined. sim.interval Number of MCMC steps between each of the M1 sampled networks per iteration. number.of.cross.ties The expected number of ties between those with the trait and those without. If missing, it is computed based on the respondent's reports of the number of ties they have to population members who have the trait (i.e. ties.to.trait.variable) and do not have the trait (i.e. ties.not.to.trait.variable). max.degree Impose ceiling on degree size. parallel Number of processors to use in the computations. The default is 1, that is no parallel processing. parallel.type The type of cluster to start. e.g. 'PSOCK', 'MPI', etc. full.output More verbose output verbose Should verbose diagnostics be printed while the algorithm is running. Value If trait.variable is numeric then the model-assisted estimate of the mean is returned, otherwise a vector of proportion estimates is returned. If full.output=TRUE this leads to: If full.output=FALSE this leads to an object of class rds.interval.estimate which is a list with component estimate the numerical point estimate of proportion of thetrait.variable. interval a matrix with size columns and one row per category of trait.variable: point estimate The HT estimate of the population mean. 95% Lower Bound Lower 95% confidence bound 95% Upper Bound Upper 95% confidence bound Design Effect The design effect of the RDS s.e. standard error n count of the number of sample values with that value of the trait rds.data an rds.data.frame that indicates recruitment patterns by a pair of attributes named "id" and "recruiter.id". N an estimate of the number of members of the population being sampled. If NULL it is read as the pop.size.mid attribute of the rds.data frame. If that is missing it defaults to 1000. M1 the number of networked populations generated at each iteration. M2 the number of (full) RDS populations generated for each networked population at each iteration. seed the random number seed used to initiate the computations. seed.selection an estimate of the mechanism guiding the choice of seeds. The choices are "allwithtrait" indicating that all the seeds had the trait; "random" meaning they were, as if, a simple random sample of individuals from the population; "sample" indicating that the seeds are taken as those in the sample (and resampled for the population with that composition if necessary); "degree" is proportional to the degree of the individual; "allwithtraitdegree" indicating that all the seeds had the trait and the probability of being a seed is proportional to the degree of the respondent. number.of.seeds The number of seeds chosen to initiate the sampling. number.of.coupons The number of coupons given to each respondent. number.of.iterations The number of iterations used at the core of the algorithm. outcome.variable The name of the outcome variable weight.type The type of weighting used (i.e. MA) uncertainty The type of weighting used (i.e. MA) details A list of other diagnostic output from the computations. varestBS Output from the bootstrap procedure. A list with two elements: var is the bootstrap variance, and BSest is the vector of bootstrap estimates themselves. coefficient estimate of the parameter of the ERGM for the network. Author(s) Krista J. Gile with help from Mark S. Handcock #### References Gile, Krista J. 2011 Improved Inference for Respondent-Driven Sampling Data with Application to HIV Prevalence Estimation, Journal of the American Statistical Association, 106, 135-146. Gile, Krista J., Handcock, Mark S., 2010. Respondent-driven Sampling: An Assessment of Current Methodology, Sociological Methodology, 40, 285-327. doi:10.1111/j.1467-9531.2010.01223.x Gile, Krista J., Beaudry, Isabelle S.

and Handcock, Mark S., 2018 Methods for Inference from Respondent-Driven Sampling Data, Annual Review of Statistics and Its Application doi:10.1146/annurevstatistics-031017-100704. See Also RDS.I.estimates, RDS.I.estimates #### Examples

```
# ## Not run:
# data(faux)
# MA.estimates(rds.data=faux,trait.variable='X')
# ## End(Not run)
```

plot.rds.data.frame

Diagnostic plots for the RDS recruitment process #### Description Diagnostic plots for the RDS recruitment process #### Usage *## S3 method for class 'rds.data.frame' plot(x, plot.type = c("Recruitment tree", "Network size by wave", "Recruits by wave", "Recruits per seed", "Recruits per subject"), stratify.by = NULL, ...) #### Arguments x An rds.data.frame object. plot.type the type of diagnostic. stratify.by A factor used to color or stratify the plot elements. ... Additional arguments for the underlying plot function if applicable. Details Several types of diagnostics are supported by the plot.type argument. 'Recruitment tree' displays a network plot of the RDS recruitment process. 'Network size by wave' monitors systematic changes is network size based on how far subjects are from the seed 'Recruits by wave' displays counts of subjects based on how far they rare from their seed. 'Recruit per seed' shows the total tree size for each seed. 'Recruits per subject' shows counts of how many subjects are recruited by each subject who are non-terminal. Value Either nothing (for the recruitment tree plot), or a ggplot2 object. #### Examples

```
# data(fauxmadrona)
# ## Not run:
# plot(fauxmadrona)
# ## End(Not run)
# plot(fauxmadrona, plot.type='Recruits by wave')
# plot(fauxmadrona, plot.type='Recruits per seed')
# plot(fauxmadrona, plot.type='Recruits per subject')
# plot(fauxmadrona, plot.type='Recruits by wave', stratify.by='disease')
# plot(fauxmadrona, plot.type='Recruits per seed', stratify.by='disease')
# plot(fauxmadrona, plot.type='Recruits per subject', stratify.by='disease')
```

print.differential.activity.estimate

Prints an differential.activity.estimate object #### Description Prints an differential.activity.estimate object #### Usage ## *S3 method for class 'differential.activity.estimate' print(x, ...) #### Arguments x an differential.activity.estimate object ... unused ###*

print.pvalue.table Displays a pvalue.table #### Description Displays a pvalue.table Usage ## S3 method for class 'pvalue.table' print(x, ...) Arguments x a pvalue.table object ... additional parameters passed to print.data.frame.

print.rds.contin.bootstrap

Displays an rds.contin.bootstrap Description Displays an rds.contin.bootstrap Usage *## S3 method for class 'rds.contin.bootstrap' print(x, show.table = FALSE, ...) Arguments x an rds.contin.bootstrap object show.table Display weighted contingency table ... additional parameters passed to print.matrix. ### print.rds.data.frame Displays an rds.data.frame Description Displays an rds.data.frame Usage* ## S3 method for class 'rds.data.frame' print(x, ...) Arguments x an rds.data.frame object ... additional parameters passed to print.data.frame.

print.rds.interval.estimate

Prints an rds.interval.estimate object Description Prints an rds.interval.estimate object Usage *## S3 method for class 'rds.interval.estimate' print(x, as.percentage = NULL, ...) Arguments x an rds.interval.estimate object as.percentage logical. Print the interval estimates as percentages (as distinct from proportions). The default, NULL, means that it will determine if the variable is discrete or continuous and only print them as percentages if they are discrete. ... unused ### print.summary.svyglm.RDS Summarizing Generalized Linear Model Fits with Odds Ratios Description print.summary.svyglm.RDS is a version of print.summary.svyglm that reports odds-ratios in place of coefficients in the summary table. This only applies for the binomial family. Otherwise it is identical to print.summary.svyglm. The default in print.summary.svyglm is to display the log-odds-ratios and this displays the exponetiated from and a 95 p-values are still displayed. Usage* ## S3 method for class 'summary.svyglm.RDS' print(x, digits = max(3, getOption("digits") - 3), symbolic.cor = x$symbolic.cor, signif.stars = getOption("show.signif.stars"), ...) Arguments x an object of class "summary.svyglm.RDS", usually, a result of a call to RDS::summary.svyglm. digits the number of significant digits to use when printing. symbolic.cor logical. If TRUE, print the correlations in a symbolic form (see symnum) rather than as numbers. signif.stars logical. If TRUE, 'significance stars' are printed for each coefficient. ... further arguments passed to or from other methods. See Also svyglm, summary.svyglm. #### Examples

```
## For examples see example(svyglm)
```

RDS.bootstrap.intervals

RDS Bootstrap Interval Estimates Description This function computes an interval estimate for one or more categorical variables. It optionally uses attributes of the RDS data set to determine the type of estimator and type of uncertainty estimate to use. Usage RDS.bootstrap.intervals(rds.data, outcome.variable, weight.type = NULL, uncertainty = NULL, N = NULL, subset = NULL, confidence.level = 0.95, number.of.bootstrap.samples = NULL, fast = TRUE, useC = TRUE, ci.type = "t", control = control.rds.estimates(), to.factor = FALSE, cont.breaks = 3, ...) Arguments rds.data An rds.data.frame that indicates recruitment patterns by a pair of attributes named "id" and "recruiter.id". outcome.variable A string giving the name of the variable in the rds.data that contains a categorical or numeric variable to be analyzed. weight.type A string giving the type of estimator to use. The options are "Gile's SS", "RDS-I", "RDS-II", "RDS-I (DS)", and "Arithemic Mean". If NULL it defaults to "Gile's SS". uncertainty A string giving the type of uncertainty estimator to use. The options are "SRS", "Gile" and "Salganik". This is usually determined by weight.type to be consistent with the estimator's origins. The estimators RDS-I, RDS-I (DS), and RDS-II default to "Salganik", "Arithmetic Mean" defaults to "SRS" and "Gile's SS" defaults to the "Gile" bootstrap. N An estimate of the number of members of the population being sampled. If NULL it is read as the population.size.mid attribute of the rds.data frame. If that is missing it defaults to 1000. subset An optional criterion to subset rds.data by. It is a character string giving an R expression which, when evaluated, subset the data. In plain English, it can be something like "seed > 0" to exclude seeds. It can be the name of a logical vector of the same length of the outcome variable where TRUE means include it in the analysis. If NULL then no subsetting is done. confidence.level The confidence level for the confidence intervals. The default is 0.95 for 95%. number.of.bootstrap.samples The number of bootstrap samples to take in estimating the uncertainty of the estimator. If NULL it defaults to the number necessary to compute the standard error to accuracy 0.001. outcome.variable. Otherwise it will compute the population frequencies of each value of the outcome.variable. fast Use a fast bootstrap where the weights are reused from the estimator rather than being recomputed for each bootstrap sample. useC Use a C-level implementation of Gile's bootstrap (rather than the R level). The implementations should be a computational equivalent estimator (except for speed). ci.type Type of confidence interval to use, if possible. If "t", use lower and upper confidence interval values based on the standard deviation of the bootstrapped values and a t multiplier. If "pivotal", use lower and upper confidence interval values based on the basic bootstrap (also called the pivotal confidence interval). If "quantile", use lower and upper confidence interval values based on the quantiles of the bootstrap sample. If "proportion", use the "t" unless the estimated proportion is less than 0.15 or the bounds are outside [0,1 . In this case, try the "quantile" and constrain the bounds to be compatible with [0,1]. control A list of control parameters for algorithm tuning. Constructed using control.rds.estimates. to.factor force variable to be a factor cont.breaks For continuous variates, some bootstrap proceedures require categorical data. In these cases, in order to contruct each bootstrap replicate, the outcome variable is split into cont.breaks categories. ... Additional arguments for RDS.*.estimates. Value An object of class rds.interval.estimate summarizing the inference. The confidence interval and standard error are based on the bootstrap procedure. In additon, the object has attribute bsresult which provides details of the bootstrap procedure. The contents of the bsresult attribute depends on the uncertainty used. If uncertainty=="Salganik" then bsresult is a vector of standard deviations of the bootstrap samples. If uncertainty=="Gile's SS" then bsresult is a list with components for the bootstrap point estimate, the bootstrap samples themselves and the standard deviations of the bootstrap samples. If uncertainty==“SRS” then bsresult is NULL. References Gile, Krista J. 2011 Improved Inference for Respondent-Driven Sampling Data with Application to HIV Prevalence Estimation, Journal of the American Statistical Association, 106, 135-146. Gile, Krista J., Handcock, Mark S., 2010. Respondent-driven Sampling: An Assessment of Current Methodology, Sociological Methodology, 40, 285-327. doi:10.1111/j.1467-9531.2010.01223.x Gile, Krista J., Beaudry, Isabelle S. and Handcock, Mark S., 2018 Methods for Inference from Respondent-Driven Sampling Data, Annual Review of Statistics and Its Application doi:10.1146/annurevstatistics-031017-100704. Examples

```
# ## Not run:
# data(fauxmadrona)
# RDS.bootstrap.intervals(rds.data=fauxmadrona,weight.type="RDS-II",
# uncertainty="Salganik",
# outcome.variable="disease",N=1000,number.of.bootstrap.samples=50)
# data(fauxtime)
# RDS.bootstrap.intervals(rds.data=fauxtime,weight.type="HCG",
# uncertainty="HCG",
# outcome.variable="var1",N=1000,number.of.bootstrap.samples=10)
# ## End(Not run)
```

RDS.compare.proportions

Compares the rates of two variables against one another. Description Compares the rates of two variables against one another. Usage RDS.compare.proportions(first.interval, second.interval, M = 10000) Arguments first.interval An rds.interval.estimate object fit with either “Gile” or “Salganik” uncertainty. second.interval An rds.interval.estimate object fit with either “Gile” or “Salganik” uncertainty. M The number of bootstrap resamplings to use Details This function preforms a bootstrap test comparing the the rates of two variables against one another. Examples

```
# ## Not run:
# data(faux)
# int1 <- RDS.bootstrap.intervals(faux, outcome.variable=c("X"),
# weight.type="RDS-II", uncertainty="Salganik", N=1000,
# number.ss.samples.per.iteration=1000,
# confidence.level=0.95, number.of.bootstrap.samples=100)
# int2 <- RDS.bootstrap.intervals(faux, outcome.variable=c("Y"),
# weight.type="RDS-II", uncertainty="Salganik", N=1000,
# number.ss.samples.per.iteration=1000,
# confidence.level=0.95, number.of.bootstrap.samples=100)
# RDS.compare.proportions(int1,int2)
# ## End(Not run)
```

RDS.compare.two.proportions

Compares the rates of two variables against one another. Description Compares the rates of two variables against one another. Usage RDS.compare.two.proportions(data, variables, confidence.level = 0.95, number.of.bootstrap.samples = 5000, plot = FALSE, seed = 1) Arguments data An object of class rds.interval.estimates.list with attribute variables containing a character vector of names of objects of class rds.interval.estimate. variables A character vector of column names to select from data. confidence.level The confidence level for the confidence intervals. The default is 0.95 for 95%. number.of.bootstrap.samples The number of Monte Carlo draws to determine the null distribution of the likelihood ratio statistic. plot Logical, if TRUE then a plot is produces of the null distribution of the likelihood ratio statistic with the observed statistics plotted as a vertical dashed line. seed The value of the random number seed. Preset by default to allow reproducability. Value An object of class pvalue.table containing the cross-tabulation of p-values for comparing the two classes ### RDS.HCG.estimates Homophily Configuration Graph Estimates Description This function computes the Homophily Configuration Graph type estimates for a categorical variable. Usage RDS.HCG.estimates(rds.data, outcome.variable, N = NULL, subset = NULL, small.fraction = FALSE, empir.lik = TRUE, to.factor = FALSE, cont.breaks = 3) Arguments rds.data An rds.data.frame with recruitment time set. outcome.variable A string giving the name of the variable in the rds.data that contains a categorical variable to be analyzed. N Population size to be used to calculate the empirical likelihood interval. If NULL, this value is taken to be the population.size.mid attribute of the data and if that is not set, no finite population correction is used. subset An optional criterion to subset rds.data by. It is an R expression which, when evaluated, subset the data. In plain English, it can be something like subset = seed > 0 to exclude seeds. It can also be the name of a logical vector of the same length of the outcome variable where TRUE means include it in the analysis. If NULL then no subsetting is done. small.fraction Should a small sample fraction be assumed empir.lik Should confidence intervals be estimated using empirical likelihood. to.factor force variable to be a factor cont.breaks If variable is numeric, how many discretization points should be used in the calculation of the weights. Value If the empir.lik is true, an object of class rds.interval.estimate is returned. This is a list with components • estimate: The numerical point estimate of proportion of the trait.variable. • interval: A matrix with six columns and one row per category of trait.variable: – point estimate: The HT estimate of the population mean. – 95% Lower Bound: Lower 95% confidence bound. – 95% Upper Bound: Upper 95% confidence bound. – Design Effect: The design effect of the RDS. – s.e.: Standard error. – n: Count of the number of sample values with that value of the trait. Otherwise an object of class rds.HCG.estimate object is returned. Author(s) Ian E. Fellows See Also RDS.I.estimates, RDS.II.estimates, RDS.SS.estimates Examples

```
# data(fauxtime)
# RDS.HCG.estimates(rds.data=fauxtime,outcome.variable='var1')
```

RDS.I.estimates

Compute RDS-I Estimates Description This function computes the RDS-I type estimates for a categorical variable. It is also referred to as the Salganik-Heckathorn estimator. Usage RDS.I.estimates(rds.data, outcome.variable, N = NULL, subset = NULL, smoothed = FALSE, empir.lik = TRUE, to.factor = FALSE, cont.breaks = 3) Arguments rds.data An rds.data.frame that indicates recruitment patterns by a pair of attributes named "id" and "recruiter.id". outcome.variable A string giving the name of the variable in the rds.data that contains a categorical variable to be analyzed. N Population size to be used to calculate the empirical likelihood interval. If NULL, this value is taken to be the population.size.mid attribute of the data and if that is not set, no finite population correction is used. subset An optional criterion to subset rds.data by. It is an R expression which, when evaluated, subset the data. In plain English, it can be something like subset = seed > 0 to exclude seeds. It can also be the name of a logical vector of the same length of the outcome variable where TRUE means include it in the analysis. If NULL then no subsetting is done. smoothed Logical, if TRUE then the "data smoothed" version of RDS-I is used, where it is assumed that the observed Markov process is reversible. empir.lik Should confidence intervals be estimated using empirical likelihood. to.factor force variable to be a factor cont.breaks The number of categories used for the RDS-I adjustment when the variate is continuous.

Value If the empir.lik is true, an object of class rds.interval.estimate is returned. This is a list with components • estimate: The numerical point estimate of proportion of the trait.variable. • interval: A matrix with six columns and one row per category of trait.variable: – point estimate: The HT estimate of the population mean. – 95% Lower Bound: Lower 95% confidence bound. – 95% Upper Bound: Upper 95% confidence bound. – Design Effect: The design effect of the RDS. – s.e.: Standard error. – n: Count of the number of sample values with that value of the trait. Otherwise an object of class rds.I.estimate object is returned. Author(s) Mark S. Handcock and W. Whipple Neely References Gile, Krista J., Handcock, Mark S., 2010. Respondent-driven Sampling: An Assessment of Current Methodology, Sociological Methodology, 40, 285-327. doi:10.1111/j.1467-9531.2010.01223.x Gile, Krista J., Beaudry, Isabelle S. and Handcock, Mark S., 2018 Methods for Inference from Respondent-Driven Sampling Data, Annual Review of Statistics and Its Application doi:10.1146/annurevstatistics-031017-100704. Neely, W. W., 2009. Bayesian methods for data from respondent driven sampling. Dissertation in-progress, Department of Statistics, University of Wisconsin, Madison. Salganik, M., Heckathorn, D. D., 2004. Sampling and estimation in hidden populations using respondent-driven sampling. Sociological Methodology 34, 193-239. Volz, E., Heckathorn, D., 2008. Probability based estimation theory for Respondent Driven Sampling. The Journal of Official Statistics 24 (1), 79-97. See Also RDS.II.estimates, RDS.SS.estimates Examples

```
# data(faux)
# RDS.I.estimates(rds.data=faux,outcome.variable='X')
# RDS.I.estimates(rds.data=faux,outcome.variable='X',smoothed=TRUE)
```

rds.I.weights

RDS-I weights Description RDS-I weights Usage rds.I.weights(rds.data, outcome.variable, N = NULL, smoothed = FALSE, ...) Arguments rds.data An rds.data.frame outcome.variable The variable used to base the weights on. N Population size smoothed Should the data smoothed RDS-I weights be computed. ... Unused

RDS.II.estimates

RDS-II Estimates Description This function computes the RDS-II estimates for a categorical variable or the RDS-II estimate for a numeric variable. Usage RDS.II.estimates(rds.data, outcome.variable, N = NULL, subset = NULL, empir.lik = TRUE, to.factor = FALSE)

Arguments rds.data An rds.data.frame that indicates recruitment patterns by a pair of attributes named “id” and “recruiter.id”. outcome.variable A string giving the name of the variable in the rds.data that contains a categorical or numeric variable to be analyzed. N Population size to be used to calculate the empirical likelihood interval. If NULL, this value is taken to be the population.size.mid attribute of the data and if that is not set, no finite population correction is used. subset An optional criterion to subset rds.data by. It is an R expression which, when evaluated, subset the data. In plain English, it can be something like subset = seed > 0 to exclude seeds. It can also be the name of a logical vector of the same length of the outcome variable where TRUE means include it in the analysis. If NULL then no subsetting is done. empir.lik If true, and outcome.variable is numeric, standard errors based on empirical likelihood will be given. to.factor force variable to be a factor Value If outcome.variable is numeric then the RDS-II estimate of the mean is returned, otherwise a vector of proportion estimates is returned. If the empir.lik is true, an object of class rds.interval.estimate is returned. This is a list with components • estimate: The numerical point estimate of proportion of the trait.variable. • interval: A matrix with six columns and one row per category of trait.variable: – point estimate: The HT estimate of the population mean. – 95% Lower Bound: Lower 95% confidence bound. – 95% Upper Bound: Upper 95% confidence bound. – Design Effect: The design effect of the RDS. – s.e.: Standard error. – n: Count of the number of sample values with that value of the trait. Otherwise, an object of class rds.II.estimate is returned. Author(s) Mark S. Handcock and W. Whipple Neely References Gile, Krista J., Handcock, Mark S., 2010. Respondent-driven Sampling: An Assessment of Current Methodology, Sociological Methodology, 40, 285-327. doi:10.1111/j.1467-9531.2010.01223.x Gile, Krista J., Beaudry, Isabelle S. and Handcock, Mark S., 2018 Methods for Inference from Respondent-Driven Sampling Data, Annual Review of Statistics and Its Application doi:10.1146/annurevstatistics-031017-100704.

Salganik, M., Heckathorn, D. D., 2004. Sampling and estimation in hidden populations using respondent-driven sampling. Sociological Methodology 34, 193-239. Volz, E., Heckathorn, D., 2008. Probability based estimation theory for Respondent Driven Sampling. The Journal of Official Statistics 24 (1), 79-97. See Also RDS.I.estimates, RDS.SS.estimates Examples

```
# data(faux)
# RDS.II.estimates(rds.data=faux,outcome.variable='X')
# RDS.II.estimates(rds.data=faux,outcome.variable='X',subset= Y!="blue")
```

rds.interval.estimate

An object of class rds.interval.estimate Description This function creates an object of class rds.interval.estimate. Usage rds.interval.estimate(estimate, outcome.variable, weight.type, uncertainty, weights, N = NULL, conf.level = 0.95, csubset = " ") Arguments estimate The numerical point estimate of proportion of the trait.variable. outcome.variable A string giving the name of the variable in the rds.data that contains a categorical variable to be analyzed. weight.type A string giving the type of estimator to use. The options are "Gile's SS", "RDS-I", "RDS-II", "RDS-I (DS)", and "Arithemic Mean". If NULL it defaults to "Gile's SS".

uncertainty A string giving the type of uncertainty estimator to use. The options are "SRS", "Gile" and "Salganik". This is usually determined by weight.type to be consistent with the estimator's origins. The estimators "RDS-I", "RDS-I (DS)", "RDS-II" default to "Salganik", "Arithmetic Mean" defaults to "SRS" and "Gile's SS" defaults to the "Gile" bootstrap. weights A numerical vector of sampling weights for the sample, in order of the sample. They should be inversely proportional to the first-order inclusion probabilites, although this is not assessed or inforced. N An estimate of the number of members of the population being sampled. If NULL it is read as the pop.size.mid attribute of the rds.data frame. If that is missing it defaults to 1000. conf.level The confidence level for the confidence intervals. The default is 0.95 for 95%. csubset A character string representing text to add to the output label. Typically this will be the expression used it define the subset of the data used for the estimate. Value An object of class rds.interval.estimate is returned. This is a list with components • estimate: The numerical point estimate of proportion of the trait.variable. • interval: A matrix with six columns and one row per category of trait.variable: – point estimate: The HT estimate of the population mean. – 95% Lower Bound: Lower 95% confidence bound. – 95% Upper Bound: Upper 95% confidence bound. – Design Effect: The design effect of the RDS. – s.e.: Standard error. – n: Count of the number of sample values with that value of the trait. Author(s) Mark S. Handcock References Gile, Krista J., Handcock, Mark S., 2010. Respondent-driven Sampling: An Assessment of Current Methodology, Sociological Methodology, 40, 285-327. doi:10.1111/j.1467-9531.2010.01223.x Gile, Krista J., Beaudry, Isabelle S. and Handcock, Mark S., 2018 Methods for Inference from Respondent-Driven Sampling Data, Annual Review of Statistics and Its Application doi:10.1146/annurevstatistics-031017-100704. Salganik, M., Heckathorn, D. D., 2004. Sampling and estimation in hidden populations using respondent-driven sampling. Sociological Methodology 34, 193-239. Volz, E., Heckathorn, D., 2008. Probability based estimation theory for Respondent Driven Sampling. The Journal of Official Statistics 24 (1), 79-97.

Examples

```
# data(faux)
# RDS.I.estimates(rds.data=faux,outcome.variable='X',smoothed=TRUE)
```

RDS.SS.estimates

Gile's SS Estimates Description This function computes the sequential sampling (SS) estimates for a categorical variable or numeric variable. Usage RDS.SS.estimates(rds.data, outcome.variable, N = NULL, subset = NULL, number.ss.samples.per.iteration = 500, number.ss.iterations = 5, control = control.rds.estimates(), hajek = TRUE, empir.lik = TRUE, to.factor = FALSE) Arguments rds.data An rds.data.frame that indicates recruitment patterns by a pair of attributes named "id" and "recruiter.id". outcome.variable A string giving the name of the variable in the rds.data that contains a categorical or numeric variable to be analyzed. N An estimate of the number of members of the population being sampled. If NULL it is read as the population.size.mid attribute of the rds.data frame. If that is missing it defaults to 1000. subset An optional criterion to subset rds.data by. It is an R expression which, when evaluated, subset the data. In plain English, it can be something like subset = seed > 0 to exclude seeds. It can also be the name of a logical vector of the same length of the outcome variable where TRUE means include it in the analysis. If NULL then no subsetting is done. number.ss.samples.per.iteration The number of samples to take in estimating the inclusion probabilites in each iteration of the sequential sampling algorithm. If NULL it is read as the eponymous attribute of rds.data. If that is missing it defaults to 5000.

number.ss.iterations The number of iterations of the sequential sampling algorithm. If that is missing it defaults to 5. control A list of control parameters for algorithm tuning. Constructed using control.rds.estimates. hajek logical; Use the standard Hajek-type estimator of Gile (2011) or the standard Hortitz-Thompson. The default is TRUE. empir.lik If true, and outcome.variable is numeric, standard errors based on empirical likelihood will be given. to.factor force variable to be a factor Value If outcome.variable is numeric then the Gile SS estimate of the mean is returned, otherwise a vector of proportion estimates is returned. If the empir.lik is true, an object of class rds.interval.estimate is returned. This is a list with components • estimate: The numerical point estimate of proportion of the trait.variable. • interval: A matrix with six columns and one row per category of trait.variable: – point estimate: The HT estimate of the population mean. – 95% Lower Bound: Lower 95% confidence bound. – 95% Upper Bound: Upper 95% confidence bound. – Design Effect: The design effect of the RDS. – s.e.: Standard error. – n: Count of the number of sample values with that value of the trait. Otherwise, an object of class rds.SS.estimate is returned. Author(s) Krista J. Gile with help from Mark S. Handcock References Gile, Krista J. 2011 Improved Inference for Respondent-Driven Sampling Data with Application to HIV Prevalence Estimation, Journal of the American Statistical Association, 106, 135-146. Gile, Krista J., Handcock, Mark S., 2010. Respondent-driven Sampling: An Assessment of Current Methodology, Sociological Methodology, 40, 285-327. doi:10.1111/j.1467-9531.2010.01223.x Gile, Krista J., Beaudry, Isabelle S. and Handcock, Mark S., 2018 Methods for Inference from Respondent-Driven Sampling Data, Annual Review of Statistics and Its Application doi:10.1146/annurevstatistics-031017-100704. Gile, Krista J., Handcock, Mark S., 2015 Network Model-Assisted Inference from Respondent-Driven Sampling Data, Journal of the Royal Statistical Society, A. doi:10.1111/rssa.12091. Salganik, M., Heckathorn, D. D., 2004. Sampling and estimation in hidden populations using respondent-driven sampling. Sociological Methodology 34, 193-239. Volz, E., Heckathorn, D., 2008. Probability based estimation theory for Respondent Driven Sampling. The Journal of Official Statistics 24 (1), 79-97.

See Also RDS.I.estimates, RDS.II.estimates Examples data(fauxmadrona) RDS.SS.estimates(rds.data=fauxmad

rdssampleC

Create RDS samples with given characteristics Description Create RDS samples with given characteristics Usage rdssampleC(net, nnodes = network.size(net), nsamp0, fixinitial, nsamp, replace, coupons, select = NULL, bias = NULL, rds.samp = NULL, seed.distribution = NULL, attrall = FALSE, trait.variable = “disease”, nsims = 1, seeds = NULL, prob.network.recall = 1, verbose = TRUE) Arguments net the network object from which to draw a sample nnodes the number of nodes in the network [at least as default] nsamp0 the number of seeds to be drawn (i.e. the size of the 0th wave of sampling) fixinitial a variable that indicates the distribution from which to draw the initial seeds, if the seeds variable is NULL and the seed.distribution variable is NULL nsamp number of individuals in each RDS sample

replace sampling with replacement coupons number of coupons select not used bias not used rds.samp not used seed.distribution a variable [what kind?] that indicates the distribution from which to draw the initial seeds attrall Whether all the information about the sample should be returned [??] trait.variable attribute of interest nsims number of RDS samples to draw seeds an array of seeds. Default is NULL, in which case the function draws the seeds from the nodes of the network. prob.network.recall simulates the probability that an individual will remember any particular link verbose Print verbose output Value A list with the following elements: nsample: vector of indices of sampled nodes wsample: vector of waves of each sampled node degsample: vector of degrees of sampled nodes attrsample: vector of attrs of sampled nodes toattr: vector of numbers of referrals to attrsd nodes tonoattr: vector of number of referrans to unattrsd nominators: recruiter of each sample read.rdsat Import data from the ’RDSAT’ format as an rds.data.frame Description This function imports RDSAT data files as rds.data.frame objects. Usage read.rdsat(file, delim = c(“”, “”̂,” “,”,“), N = NULL) Arguments file the name of the file which the data are to be read from. If it does not contain an *absolute* path, the file name is *relative* to the current working directory, 'getwd()'. Tilde-expansion is performed where supported. As from R 2.10.0 this can be a compressed file (see 'file') delim The seperator defining columns. will guess the delimitor based on the file. N The population size (Optional).

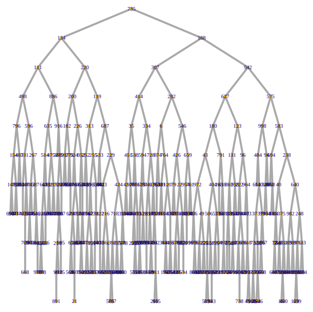
Examples fn <- paste0(path.package("RDS"),"/extdata/nyjazz.rdsat") rd <- read.rdsat(fn) plot(rd)

read.rdsobj

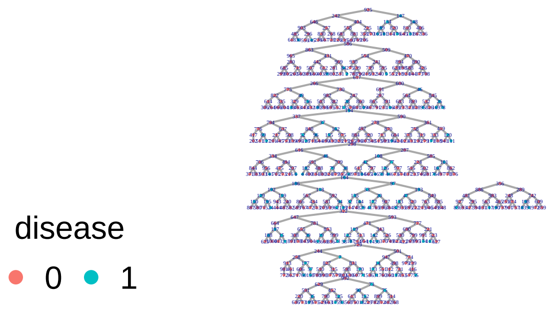
Import data saved using write.rdsobj Description Import data saved using write.rdsobj Usage read.rdsobj(file) Arguments file the name of the file which the data are to be read from. If it does not contain an *absolute* path, the file name is *relative* to the current working directory, 'getwd()'. Tilde-expansion is performed where supported. As from R 2.10.0 this can be a compressed file (see 'file') reingold.tilford.plot Plots the recruitment network using the Reingold Tilford algorithm. Description Plots the recruitment network using the Reingold Tilford algorithm. Usage reingold.tilford.plot(x, vertex.color = NULL, vertex.color.scale = hue_pal(), vertex.size = 2, vertex.size.range = c(1, 5), edge.arrow.size = 0, vertex.label.cex = 0.2, vertex.frame.color = NA, vertex.label = get.id(x), show.legend = TRUE, plot = TRUE, ...)

Arguments x An rds.data.frame vertex.color The name of the categorical variable in x to color the points with. vertex.color.scale The scale to create the color palette. vertex.size The size of the vertex points. either a number or the name of a column of x. vertex.size.range If vertex.size represents a variable, vertex.size.range is a vector of length 2 representing the minimum and maximum cex for the points. edge.arrow.size The size of the arrow from recruiter to recruitee. vertex.label.cex The size expansion factor for the vertex.labels. vertex.frame.color the color of the outside of the vertex.points. vertex.label The name of a variable to use as vertex labels. NA implies no labels. show.legend If true and either vertex.color or vertex.size represent variables, legends will be displayed at the bottom of the plot. plot Logical, if TRUE then a plot is produced of recruitment tree. ratio statistic with the observed statistics plotted as a vertical dashed line. ... Additional parameters passed to plot.igraph. Value A two-column vector of the positions of the nodes in the recruitment tree. Examples

```r
## Not run:
data(fauxmadrona)
data(faux)
reingold.tilford.plot(faux)
```



```
reingold.tilford.plot(fauxmadrona,vertex.color="disease")
```



```
## End(Not run)
```

rid.from.coupons

Determines the recruiter.id from recruitment coupon information Description Determines the recruiter.id from recruitment coupon information

Usage rid.from.coupons(data, subject.coupon = NULL, coupon.variables, subject.id = NULL, seed.id = “seed”) Arguments data a data.frame subject.coupon The variable representing the coupon returned by subject coupon.variables The variable representing the coupon ids given to the subject subject.id The variable representing the subject’s id seed.id The recruiter.id to assign to seed subjects. Examples

```
fpath <- system.file("extdata", "nyjazz.csv", package="RDS")
dat <- read.csv(fpath)
dat$recruiter.id <- rid.from.coupons(dat,"own.coupon",
paste0("coupon.",1:7),"id")
#create and rds.data.frame
rds <- as.rds.data.frame(dat,network.size="network.size")
```

set.control.class

Set the class of the control list Description This function sets the class of the control list, with the default being the name of the calling function. Usage set.control.class(myname = as.character(RDS::ult(sys.calls(), 2)[[1L]]), control = get(“control”, pos = parent.frame())) Arguments myname Name of the class to set. control Control list. Defaults to the control variable in the calling function.

Value The control list with class set. See Also check.control.class, print.control.list show.rds.data.frame Displays an rds.data.frame Description Displays an rds.data.frame Usage show.rds.data.frame(x, …) Arguments x an rds.data.frame object. … additional parameters passed to print.data.frame. ### summary.svyglm.RDS Summarizing Generalized Linear Model Fits with Odds Ratios for Survey Data Description RDS::summary.svyglm.RDS is a version of summary.svyglm that reports odds-ratios in place of coefficients in the summary table. This only applies for the binomial family. Otherwise it is identical to summary.svyglm. The default in summary.svyglm is to display the log-odds-ratios and this displays the exponetiated from and a 95 p-values are still displayed. Usage *## S3 method for class ‘svyglm.RDS’ summary(object, correlation = FALSE, df.resid = NULL, odds = TRUE, …) Arguments object an object of class “svyglm”, usually, a result of a call to svyglm. correlation logical; if TRUE, the correlation matrix of the estimated parameters is returned and printed. df.resid Optional denominator degrees of freedom for Wald tests. odds logical; Should the coefficients be reported as odds (rather than log-odds)? ... further arguments passed to or from other methods.

Details svyglm fits a generalised linear model to data from a complex survey design, with inverse-probability weighting and design-based standard errors. There is no anova method for svyglm as the models are not fitted by maximum likelihood. See the manual page on svyglm for detail of that function. Value RDS::summary.svyglm returns an object of class "summary.svyglm.RDS", a list with components call the component from object. family the component from object. deviance the component from object. contrasts the component from object. df.residual the component from object. null.deviance the component from object. df.null the component from object. deviance.resid the deviance residuals: see residuals.svyglm. coefficients the matrix of coefficients, standard errors, z-values and p-values. Aliased coefficients are omitted. aliased named logical vector showing if the original coefficients are aliased. dispersion either the supplied argument or the inferred/estimated dispersion if the latter is NULL. df a 3-vector of the rank of the model and the number of residual degrees of freedom, plus number of coefficients (including aliased ones). cov.unscaled the unscaled (dispersion = 1) estimated covariance matrix of the estimated coefficients. cov.scaled ditto, scaled by dispersion. correlation (only if correlation is true.) The estimated correlations of the estimated coefficients. symbolic.cor (only if correlation is true.) The value of the argument symbolic.cor. odds Are the coefficients reported as odds (rather than log-odds)? See Also svyglm, summary. Examples

```
## For examples see example(svyglm)
```

transition.counts.to.Markov.mle

calculates the mle. i.e. the row proportions of the transition matrix Description calculates the mle. i.e. the row proportions of the transition matrix Usage transition.counts.to.Markov.mle(transition.counts) Arguments transition.counts a matrix or table of transition counts Details depreicated. just use prop.table(transition.counts,1) ###ult Extract or replace the *ult*imate (last) element of a vector or a list, or an element counting from the end. Description Extract or replace the *ult*imate (last) element of a vector or a list, or an element counting from the end. Usage ult(x, i = 1L) Arguments x a vector or a list. i index from the end of the list to extract or replace (where 1 is the last element, 2 is the penultimate element, etc.). Value An element of 'x'.

Examples

```
x <- 1:5
(last <- ult(x))
```

```
[1] 5
```

```
(penultimate <- ult(x, 2)) # 2nd last.
```

```
[1] 4
```

vh.weights

Volz-Heckathorn (RDS-II) weights Description Volz-Heckathorn (RDS-II) weights Usage vh.weights(degs, N = NULL) Arguments degs The degrees (i.e. network sizes) of the sample units. N Population size write.graphviz writes an rds.data.frame recruitment tree as a GraphViz file Description writes an rds.data.frame recruitment tree as a GraphViz file Usage write.graphviz(x, file) Arguments x An rds.data.frame. file A character vector representing the file

write.netdraw

Writes out the RDS tree in NetDraw format Description Writes out the RDS tree in NetDraw format Usage write.netdraw(x, file = NULL, by.seed = FALSE) Arguments x An rds.data.frame. file a character vector representing a file. by.seed If true, seperate files will be created for each seed. Details If by.seed is false, two files are created using 'file' as a base name. paste0(file,".DL") contains the edge information, and paste0(file,".vna") contains the nodal attributes ### write.rdsat Writes out the RDS tree in RDSAT format Description Writes out the RDS tree in RDSAT format Usage write.rdsat(x, file = NULL) Arguments x An rds.data.frame. file a character vector representing a file.

write.rdsobj

Export an rds.data.frame to file Description Export an rds.data.frame to file Usage write.rdsobj(x, file) Arguments x The rds.data.frame to export file The name of the file to create. [.rds.data.frame indexing Description indexing Usage *## S3 method for class 'rds.data.frame' x[i, j, ..., drop, warn = TRUE] Arguments x object i indices j indices ... unused drop drop warn Warn if any new seeds are created Details Subsetting of RDS recruitment trees does not always yield a full RDS tree. In this case, subjects whose recruiter is no longer in the dataset are considered seeds. is issued if the 'warn' parameter is TRUE. dat <- data.frame(id=c(1,2,3,4,5), recruiter.id=c(2,-1,2,-1,4), network.size.variable=c(4,8,8,2,3)) r <- as.rds.data.frame(dat) r[1:3,] # A valid pruning of the RDS tree. r[c(1,5),warn=FALSE] # recruiter.id of last row set to -1 (i.e. a seed) to maintain validity of tree

[<-.rds.data.frame

indexing Description indexing Usage *## S3 replacement method for class ‘rds.data.frame’ x[i, j] <- value Arguments x object i indices j indices value value Details Indexed assignment. If the result is not a valid rds.data.frame, an error is emitted.