Package 'dejaVu'

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Type Package

Title Multiple Imputation for Recurrent Events

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Description Performs reference based multiple imputation of recurrent event data based on a negative binomial regression model, as described by Keene et al (2014) <doi:10.1002/pst.1624>.

License GPL (>= 2)

LazyData true

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VignetteBuilder knitr

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Contents

ConstantRateDrop   *Create a Dropout Mechanism with constant dropout rate*

Description

Creates an MCAR DropoutMechanism object where subject i dropout is exponentially distributed with rate Ri where Ri = C*exp(Xi) for constant C and Xi a random normal variable with mean 0 and standard deviation sigma

Usage

```
ConstantRateDrop(rate, var = 0)
```

Arguments

rate	C described in the details
var	sigma^2 described in the details section, by default = 0

Value

A `DropoutMechanism` object

See Also

[`DropoutMechanism.object`](#)

Examples

```
ConstantRateDrop(rate=0.0025)
ConstantRateDrop(rate=0.0025,var=1)
```

---

copy_reference   *Create a copy reference* `ImputeMechanism` *object*

Description

Missing counts for subjects in both arms are imputed by assuming the rate before and dropout are both equal to the control (reference) estimated rate. This corresponds to what is usually termed the copy reference assumption.

Usage

```
copy_reference(proper = TRUE)
```

Arguments

proper   If `proper=TRUE` then proper imputation is performed, in which each imputation is created based on parameters values drawn from the (approximate) posterior distribution of the imputation model. If `proper=FALSE`, improper imputation is performed. This means all imputed datasets are generated conditional on the maximum likelihood estimates of the parameters.

Value

An `ImputeMechanism` object

See Also

[`ImputeMechanism.object`](#)

Examples

```
sim <- SimulateComplete(study.time=365,number.subjects=50,
                        event.rates=c(0.01,0.005),dispersions=0.25)
sim.with.MCAR.dropout <- SimulateDropout(sim,
                                    drop.mechanism = ConstantRateDrop(rate = 0.0025))
fit <- Simfit(sim.with.MCAR.dropout)
imps <- Impute(fit, copy_reference(), 10)
```

CreateNewDropoutMechanism

A function which creates a DropOut Mechanism object

Description

A function which creates a DropOut Mechanism object

Usage

```
CreateNewDropoutMechanism(
  type,
  text,
  cols.needed = vector("character"),
  GetDropTime,
  parameters = NULL
)
```

Arguments

type	The type of mechanism (e.g. "MCAR" or "MNAR")
text	A short string describing the mechanism (only used for printing)
cols.needed	Which columns in the SingleSim$data data frame must be included for this drop out mechanism to work. This option could allow drop out mechanism which depend on covariates to be included.
GetDropTime	A function with two arguments event.times and data, the corresponding entries from the SingleSim object. This function should return a list of dropout times (if a subject does not dropout its dropout time should be their current censored.time (i.e. the study follow up time))
parameters	A list of named parameters for the mechanism (only used for printing) or NULL if none

Value

A `DropoutMechanism.object`

See Also

`DropoutMechanism.object`

```
CreateNewImputeMechanism
```
                    A function which creates an Impute Mechanism object

---

Description

A function which creates an Impute Mechanism object

Usage

```
CreateNewImputeMechanism(
  name,
  cols.needed = vector("character"),
  impute,
  parameters = NULL
)
```

Arguments

name	The method name (used for printing)
cols.needed	which columns of the SingleSim data frame are required by the method, typically c("censored.time","observed.events","arm")
impute	A function which takes a SingleSimFit object and outputs the details for a single imputed data set, specifically a list with two elements: new.censored.times - a vector of times subjects were censored (after taking into account imputation) and newevent.times - a list of vectors where the vectors contain the imputed event times for the subjects (these vectors do not contain the observed event times before subject drop out). If a subject has no imputed events then the vector numeric(0) is returned.
parameters	A list of named parameters describing the method (used for printing) - or NULL if none

Value

A [ImputeMechanism.object](#)

See Also

[ImputeMechanism.object](#)

CreateScenario   *Create* Scenario *object from list of Fit Summaries*

Description

Create Scenario object from list of Fit Summaries

Usage

```
CreateScenario(object, description = "")
```

Arguments

object	Either a list of summary.SingleSimFit or summary.ImputeSimFit objects
description	A character string describing the scenario (used for printing)

Value

A Scenario object

See Also

[Scenario.object](#)

DejaData.object   *Data frame of covariates for simulating recurrent events*

Description

This object allows covariates to be included in the simulation procedure The object is created using the [MakeDejaData](#) function

Arguments

data	A data frame containing the subject
arm	character the column name of the treatment arm for each subject
rate	character the column name of the rate to be used when simulating
Id	character the column name of subject Id

Structure

The above components must be included in a DejaData Object

DropoutMechanism.object

DropoutMechanism object

Description

An object which defines a specific mechanism which takes a complete `SingleSim` object and returns a set of drop out times for subjects

Arguments

type
: The type of mechanism (e.g. "MCAR" or "MNAR")

text
: A short string describing the mechanism (only used for printing)

cols.needed
: Which columns in the SingleSim$data data frame must be included for this drop out mechanism to work. This option could allow drop out mechanism which depend on covariates to be included.

GetDropTime
: A function with two arguments event.times and data, the corresponding entries from the SingleSim object. This function should return a list of dropout times (if a subject does not dropout its dropout time should be their current censored.time (i.e. the study follow up time))

parameters
: A list of named parameters for the mechanism (only used for printing) or NULL if none

Details

It is possible to create user defined mechanisms, however, certain common mechanisms have already been implemented. For example see [ConstantRateDrop](#) and [LinearRateChangeDrop](#)

Only the GetDropTime and cols.needed entries are required for calculation, the other entries are used for printing the object

`print.DropoutMechanism` methods is defined.

Structure

The following components must be included in a DropoutMechanism Object

---

expandEventCount   *Expand event counts into a list of event times*

Description

This function exists to allow clinical trial data which typically gives event counts over time to be plugged into this software, which relies on actual event counts.

Usage

```
expandEventCount(count, time)
```

Arguments

count	a vector of event counts. All entries must be non-negative.
time	a matching (strictly positive) vector of followup times.

Details

This function always produces a warning: anyone relying on this function to actually analyze data should take great care.

Value

a list of vectors of event times

Examples

```
expandEventCount(count=c(0, 20), time=c(10, 20))
```

---

extract_results	*Extract the results of running a scenario*

Description

This function is a wrapper around [CreateScenario](#) See the user guide vignette for an example of using this function

Usage

```
extract_results(answer, name, description)
```

Arguments

answer	A named list of lists
name	The name of the lists of answer which should be extracted and put together into a sc
description	The description parameter to be passed into the CreateScenario function

Value

A Scenario object

See Also

[CreateScenario](#)

GetImputedDataSet   *Output a single imputed data set*

Description

Output a single imputed data set

Usage

```
GetImputedDataSet(imputeSim, index)
```

Arguments

imputeSim	A ImputeSim object which contains multiple imputed data sets
index	numeric, which of the multiple imputed data sets to output

Value

A SingleSim object with status="imputed"

See Also

[ImputeSim.object](#)

Examples

```
sim <- SimulateComplete(study.time=365,number.subjects=50,
event.rates=c(0.01,0.005),dispersions=0.25)
sim.with.MCAR.dropout <- SimulateDropout(sim,
  drop.mechanism = ConstantRateDrop(rate = 0.0025))
fit <- Simfit(sim.with.MCAR.dropout)
imps <- Impute(fit, copy_reference(), 10)
imp1 <- GetImputedDataSet(imps, 1)
```

ImportSim   *Import an existing data frame for use with the package*

Description

Import an existing data frame for use with the package

Usage

```
ImportSim(
  dejaData,
  event.times,
  status,
  study.time,
  censored.time = NULL,
  actual.events = NULL,
  allow.beyond.study = FALSE
)
```

Arguments

dejaData   a `DejaData` object contain the subject covariates and treatment arm

event.times   A list of vectors, containing the observed event times of each subject. If no events are observed then numeric(0) should be used. See example in this help file for more details

status   The status of the data set imported, either "complete" (if all subjects complete their follow up period) or "dropout" (if not)

study.time   The total follow up time according to study protocol

censored.time   If status is "dropout", this is a vector of the times at which each subject is censored

actual.events   If status is "dropout" and the total number of events (i.e. not just the number observed) is known (e.g. if a different simulation procedure was used) a vector of total number of events should be included. If the number is not known or status is "complete" then this should be set to NULL

allow.beyond.study
                Whether or not to allow imported data with events after the nominal end of study.

Value

A SingleSim object

Examples

```
covar.df <- data.frame(Id=1:6,
                       arm=c(rep(0,3),rep(1,3)),
                       Z=c(0,1,1,0,1,0))

dejaData <- MakeDejaData(covar.df,arm="arm",Id="Id")


event.times <- list(c(25,100,121,200,225),
                    c(100,110),c(55),numeric(0),
                    150,45)

complete.dataset <- ImportSim(dejaData, event.times,
                    status="complete",
```

```
                            study.time=365)

censored.time  <- c(365,178,100,245,200,100)

dropout.dataset <- ImportSim(dejaData, event.times,
                      status="dropout",
                      study.time=365,
                      censored.time=censored.time)
```

Impute   *Produce imputed data sets*

Description

Given a `SingleSimFit` object (with impute.parameters not NULL) and an imputation mechanism, create a collection of imputed data sets

Usage

```
Impute(fit, impute.mechanism, N)
```

Arguments

fit   A `SingleSimFit` object

impute.mechanism
                  An `ImputeMechanism` object

N   The number of data sets to impute

Value

An `ImputeSim` object

Examples

```
sim <- SimulateComplete(study.time=365,number.subjects=50,
    event.rates=c(0.01,0.005),dispersions=0.25)
sim.with.MCAR.dropout <- SimulateDropout(sim,
    drop.mechanism = ConstantRateDrop(rate = 0.0025))
fit <- Simfit(sim.with.MCAR.dropout)
imps <- Impute(fit, copy_reference(), 10)
```

```
ImputeMechanism.object
```
ImputeMechanism object

Description

An object which defines a mechanism for taking a `SingleSimFit` object and imputing missing data to create a `ImputeSim`

Arguments

name	The method name (used for printing)
cols.needed	which columns of the SingleSim data frame are required by the method, typically `c("censored.time","observed.events","arm")`
impute	A function which takes a `SingleSimFit` object and outputs the details for a single imputed data set, specifically a list with two elements: `new.censored.times` - a vector of times subjects were censored (after taking into account imputation) and `newevent.times` - a list of vectors where the vectors contain the imputed event times for the subjects (these vectors do not contain the observed event times before subject drop out). If a subject has no imputed events then the vector `numeric(0)` is returned.
parameters	A list of named parameters describing the method (used for printing) - or NULL if none

Details

It is possible to create user defined mechanisms, however, common mechanisms have already been implemented. For example see [weighted_j2r](#)

A `print.ImputeMechanism` method is defined.

Structure

The following components must be included in an ImputeMechanism Object

Examples

```
j2r <- weighted_j2r(trt.weight=0)
```

ImputeSim.object   *ImputeSim object*

Description

This object contains a collection of imputed data sets derived from a `SingleSimFit` object and `ImputeMechanism`

Arguments

singleSim   The `SingleSim` object from which the imputed data sets have been derived

impute.mechanism

     The `ImputeMechanism` object used to perform the imputation

imputed.values   A matrix with 1 column per imputed data set and two rows: newevent.times a list of vectors containing the imputed event times (not including the events which were observed) and new.censored.times - a vector containing the times at which subjects (with imputed data) are now censored

dropout   A vector containing the number of subjects who have dropped out in each arm, for whom data is to be imputed

     Use [GetImputedDataSet](#) to extract a single imputed data set and use `Simfit` to fit a model to the set of data sets

See Also

[GetImputedDataSet](#)

ImputeSimFit.object   *ImputeSimFit object*

Description

An object which contains both a set of imputed data sets (`ImputeSim` object) and a set of models fitted to them

Arguments

imputeSim   The `ImputeSim` object for which models have been fitted

summaries   A list of `summary.SingleSimFit` objects containing the model fits for each of the imputed data sets

Details

Calling `summary.ImputeSimFit` will apply Rubin's formula to calculate estimates for the treatment effect and standard error

Functions `summary.ImputeSimFit` and `as.data.frame.ImputeSimFit` have been implemented

See Also

summary.ImputeSimFit summary.SingleSimFit

LinearRateChangeDrop   *Create a Dropout Mechanism with drop out rate which changes by a fixed constant after every event*

Description

Creates an MAR DropoutMechanism object where subject i has piecewise exponential dropout rate where the rate changes by a constant amount after each event, specifically after j events the subject has rate $Rij = Cj*exp(Xij)$ where $Cj=C+j*D$ for constants C, D and Xij is a standard normal variable with mean 0 and standard deviation sigma

Usage

```
LinearRateChangeDrop(starting.rate, rate.change, var = 0)
```

Arguments

starting.rate	C, see description section.
rate.change	D, see description section. Note if D<0, Cj could be negative for large j, this is not possible and the rate remains constant if the next change would set Cj<=0
var	sigma^2, see description section

Value

A DropoutMechanism object

See Also

DropoutMechanism.object

Examples

```
LinearRateChangeDrop(starting.rate=0.0025,rate.change=0.0005)
LinearRateChangeDrop(starting.rate=0.0025,rate.change=-0.00001,var=1)
```

MakeDejaData	*Create a* `DejaData` *object*

Description

This object is can be used to create a `SingleSim` object with subject specific rates

Usage

```
MakeDejaData(data, arm, Id, rate = NULL)
```

Arguments

data	A data frame containing the subject
arm	character the column name of the treatment arm for each subject
Id	character the column name of subject Id
rate	character the column name of the rate to be used when simulating (or NULL, if using DejaData to import a data set, see [ImportSim](#))

Value

A `DejaData` object

Examples

```
set.seed(232)

my.df <- data.frame(Id=1:100,
                    arm=c(rep(0,50),rep(1,50)),
                    covar=rbinom(n=100,size=1,prob=0.5))

my.df$rate <- 0.0025 + my.df$covar*0.002 + (1-my.df$arm)*0.002

my.dejaData <- MakeDejaData(my.df,arm="arm",rate="rate",Id="Id")
```

---

numberSubjects	*S3 generic to output the number of subjects in a given object*

Description

S3 generic to output the number of subjects in a given object

Usage

```
numberSubjects(x)
```

Arguments

x   The object

Value

The number of subjects

Examples

```
sim <- SimulateComplete(study.time=365,number.subjects=50,
event.rates=c(0.01,0.005),dispersions=0.25)
numberSubjects(sim)
```

Scenario.object   *Scenario object*

Description

This class contains a collection of model fit summaries and summarizing this object will calculate overall summary statistics such as power/type I error

Arguments

description   A string containing a description of the scenario

summaries   A list of either summary.ImputeSimFit or summary.SingleSimFit objects

Details

Functions as.data.frame.Scenario and summary.Scenario have been implemented

See Also

[CreateScenario]

---

simData   *Simulated recurrent event data.*

Description

A simulated dataset containing a randomised treatment group, follow-up time, and number of events, for 500 patients. The planned follow-up period for the study was 1 year, but some patients dropped out early and so their follow-up ended prematurely (i.e. before 1 year)

Usage

simData

Format

A data frame with 500 rows and 3 variables:

z a binary variable indicating randomised treatment group

y number of events observed during patient's follow-up

fupTime the time in years the patient was followed up for ...

Source

Simulated data

Simfit *S3 generic for fitting models*

Description

S3 generic for fitting models

Usage

```
Simfit(x, family = "negbin", equal.dispersion = TRUE, covar = NULL, ...)
```

Arguments

x	The S3 object
family	Either "negbin" for fitting a negative binomial model (using MASS::glm.nb), "poisson" for fitting a poisson model (glm) or "quasipoisson" for fitting a quasipoisson model glm
equal.dispersion	
	logical, should the arms have the same dispersion parameter when fitting negative binomial models
covar	A formula containing the additional covariates to be used when calling glm.nb if no covariates are included in the model this should be NULL, for example ~covar1 + covar2 See vignette for further details
...	Additional arguments to be passed to glm or glm.nb

Value

A SingleSimFit object

See Also

SingleSimFit.object

Examples

```
set.seed(1234)
sim <- SimulateComplete(study.time=1,number.subjects=50,
      event.rates=c(0.1,0.05),dispersions=0.1)
summary(Simfit(sim,equal.dispersion=TRUE))
```

SimulateComplete   *Simulate a complete data set*

Description

Simulate a complete data set of a recurrent event clinical trial without dropouts using a negative binomial model with given rates and dispersion parameters

Usage

```
SimulateComplete(
  study.time,
  dejaData = NULL,
  number.subjects = NULL,
  event.rates = NULL,
  dispersions
)
```

Arguments

study.time	The study follow up period
dejaData	If not NULL this should contain a `DejaData` object. If this is used then number.subjects and event.rates arguments are ignored
number.subjects	
	The number of subjects, if a vector `c(a,b)` then a subjects on the control arm and b subjects on the active arm. If `number.subjects` is a single number then both arms have the given number of subjects.
event.rates	The rate parameter(s) for the negative binomial model (if single parameter then it is used for both arms)
dispersions	The dispersion parameter(s) for the negative binomial model (if single parameter then it is used for both arms)

Details

Each subject's events are described by a Poisson process with a subject specific rate given by lambda/study.time where study.time is the study follow up period and lambda has a gamma distribution with shape=1/dispersion and scale=dispersion*event.rate*study.time

Different dispersions, event.rates and number of subjects can be specified for both arms of the trial

Value

A SingleSim object with status='complete'

See Also

[SingleSim.object](#)

Examples

```
sim <- SimulateComplete(study.time=365,number.subjects=50,
                        event.rates=c(0.01,0.005),dispersions=0.25)
sim2 <- SimulateComplete(study.time=365,number.subjects=c(50,75),
                        event.rates=c(0.01,0.005),dispersions=c(0,0.25))
```

SimulateDropout　　　　　*Simulate subject dropout*

Description

This function takes a complete recurrent event data set and drop out mechanism and creates a data set set with dropout

Usage

```
SimulateDropout(simComplete, drop.mechanism)
```

Arguments

simComplete　　　A SingleSim object (with status="complete")

drop.mechanism　A DropoutMechanism object

Value

A SingleSim object with status='dropout'

Examples

```
sim <- SimulateComplete(study.time=365,number.subjects=50,
                        event.rates=c(0.01,0.005),dispersions=0.25)

sim.with.MCAR.dropout <- SimulateDropout(sim,
                      drop.mechanism = ConstantRateDrop(rate = 0.0025))
sim.with.MAR.dropout <- SimulateDropout(sim,
                      drop.mechanism = LinearRateChangeDrop(
                                            starting.rate = 0.0025,
                                            rate.change = 0.0005))
```

SingleSim.object *SingleSim Object*

Description

A class containing the data for a single simulation. Depending on the value of status, this may be a complete data set, a set including subject dropouts or a data set after multiple imputation

print.SingleSim and summary.SingleSim methods are defined.

Arguments

data	The data frame, one row per subject containing (at least) the following columns Id, arm, censored.time, observed.events and actual.events
event.times	A list of event times. event.times[[1]] is a list of event times for subject with Id 1 The length of event.times[[1]] = the number of observed events of subject with Id 1
status	Either "complete", "dropout" or "imputed" denoting the status of the data set.
subject.rates	A vector of the specific rates used for the Poisson process for subjects when generating the data
dropout.mechanism	If status is not "complete" then this contains the DropoutMechanism object used to perform the subject dropout. See DropoutMechanism.object.
impute.mechanism	If the status is "imputed" then this contains the ImputeMechanism object used to perform the imputation. See ImputeMechanism.object
study.time	The study follow up period (see SimulateComplete)
event.rates	The control/active event rates (see SimulateComplete), if data set was generated without using these (e.g. the dejaData argument was used) then this is set to NULL
dispersions	The control/active dispersion rates (see SimulateComplete)

Structure

The above components must be included in a SingleSim Object

SingleSimFit.object   *SingleSimFit object*

Description

A `SingleSimFit` object is returned from calling `Simfit` with a `SingleSim` object. It can be used to both impute data sets or can be summarized

Arguments

singleSim   The `SingleSim` object to which a model has been fitted

model   The model which has been fitted

genCoeff.function

A function which returns a list of parameters from the model fit(s) which can be used when performing the gamma imputation. It takes one argument, use.uncertainty (by default is TRUE) which if TRUE stochastically incorporates uncertainty into the parameter estimates in preparation for use with imputation If a Poisson/quasi-Poisson model was fitted to the `SingleSimFit` object then this will be NULL

equal   dispersion whether equal dispersions were used when fitting model(s) to the data

Details

A `summary.SingleSimFit` method has been implemented

---

subjectsPerArm   *S3 generic to output the number of subjects in each arm for a given object*

Description

S3 generic to output the number of subjects in each arm for a given object

Usage

```
subjectsPerArm(x)
```

Arguments

x   The object

Value

A vector of the number of subjects in each arm

Examples

```
sim <- SimulateComplete(study.time=365,number.subjects=50,
event.rates=c(0.01,0.005),dispersions=0.25)
subjectsPerArm(sim)
```

---

summary.ImputeSimFit.object

summary.ImputeSimFit object

Description

The summary of a `ImputeSimFit` object. Rubin's formula is used to combine the test statistics into a single summary

Arguments

treatment.effect

> The mean of the estimated treatment.effect from the imputed data

se   The standard error of the (log) treatment effect calculated using Rubin's formula

df   The number of degrees of freedom used to calculate the p-value

adjusted.df   The number of degrees of freedom used to calculate the adjusted p-value (this should be used if the complete data number of degrees of freedom is small)

dispersion   The mean of the estimated dispersion parameter

pval   The p-value for the test log(treatment.effect)=0 using Rubin's formula

adjusted.pval   The p-value for the test log(treatment.effect)=0 using Rubin's formula and the adjusted number of degrees of freedom

dropout   The number of subjects who drop out (per arm) for this imputed data set

number.subjects

> The number of subjects (per arm) for this imputed data set

Details

A `print.summary.ImputeSimFit` object has been implemented

`summary.Scenario.object`

summary.Scenario object

Description

This object contains the overall summary statistics for a specific scenario. It is envisioned that multiple scenarios are run and a set of `summary.Scenario` objects are created and these can then be used for plotting

Arguments

`treatment.effect`

    The exp(mean(log(individual treatment effects))),

`se`   The mean standard error of the (log) treatment effect

`power`   The proportion of simulations for which the p-value is < `alpha`

`alpha`   The significance level used when calculating power, by default 0.05 use `summary(object,alpha=x)` to use a different p value

`use.adjusted.pval`

    logical, default FALSE should the p values calculated using Rubin's formula with the adjusted number of degrees of freedom be used. Use `summary(object,use.adjusted.pval=TRUE)` to use the adjusted p values

`description`   A string containing a description of the scenario

`dropout`   A list of summary statistics regarding number of subject dropouts

Details

A `print.summary.Scenario` function has been implemented

`summary.SingleSim.object`

summary.SingleSim object

Description

The object returned when calling the summary function on a `SingleSim` object

Arguments

`status`	The status of the SingleSim object
`study.time`	The study.time from the SingleSim object
`number.subjects`	
	The number of subjects on each arm
`number.dropouts`	
	The number of subjects who dropout on each arm
`total.events`	The total number of events for each arm
`time.at.risk`	The total time at risk for each arm
`empirical.rates`	
	total.events/time.at.risk
	The `print.summary.SingleSim` method has been implemented

`summary.SingleSimFit`	*summary.SingleSimFit*

Description

The summary object for a `SingleSimFit` object

Arguments

`model.summary`	The model summary from the fit
`treatment.effect`	
	The estimate of treatment effect from the model fit
`CI.limit`	The confidence interval limit (by default 0.95), call `summary(object,CI.limit=x)` to use CI of x instead.
`CI`	The confidence interval of the treatment effect
`se`	Estimate for the standard error of (log) treatment effect
`dispersion`	Estimate for the dispersion parameter or numeric(0) if Poisson/quasi-Poisson model used
`rate.estimate`	Estimate of the event rates from the model a vector c(control arm, treatment arm)
`pval`	The p value directly from the model fit (this is for the single model fit only, i.e. not using Rubin's formula)
`datastatus`	The status of SingleSim object to which the fit was applied
`df`	The number of degrees of freedom of the model
`dropout`	The number of dropouts of each arm
`number.subjects`	
	The number of subjects in each arm

Details

A `print.summary.SingleSimFit` method has been implemented

See Also

SingleSimFit.object

Examples

```
sim <- SimulateComplete(study.time=365,number.subjects=50,
event.rates=c(0.01,0.005),dispersions=0.25)
fit <- Simfit(sim)
summary(fit)
```

---

weighted_j2r *Create a weighted_j2r* ImputeMechanism *object*

Description

Missing counts for a subject in the active treatment arm will be imputed according to a point (determined by `trt.weight`) between the means of the placebo and treatment arms, conditioned on the number of events. Missing counts for subjects in the placebo arm will be imputed according to the mean of the placebo arm, conditioned on the subject's observed number of events.

Usage

```
weighted_j2r(trt.weight, delta = c(1, 1), proper = TRUE)
```

Arguments

trt.weight	See details
delta	If `trt.weight=1` then delta is a vector of length 2 (control.delta,treatment.delta) and the mean number of expected events for the imputed missing data is multiplied by the appropriate delta
proper	If `proper=TRUE` then proper imputation is performed, in which each imputation is created based on parameters values drawn from the (approximate) posterior distribution of the imputation model. If `proper=FALSE`, improper imputation is performed. This means all imputed datasets are generated conditional on the maximum likelihood estimates of the parameters.

Details

If `trt.weight = 0` then imputation using this mechanism will follow the jump to reference (j2r) model whereby missing counts for subjects in both arms will be imputed according to the mean of the placebo arm conditioned on the subject's observed number of events

If `trt.weight = 1` then imputation using this mechanism will follow the MAR model whereby missing counts for subjects in each arm will be imputed according to the event rate of subjects in its treatment group conditioned on the subject's observed number of events

See the User guide vignette for further details

Value

An `ImputeMechanism` object

See Also

ImputeMechanism.object

Examples

```
sim <- SimulateComplete(study.time=365,number.subjects=50,
event.rates=c(0.01,0.005),dispersions=0.25)
sim.with.MCAR.dropout <- SimulateDropout(sim,
                     drop.mechanism = ConstantRateDrop(rate = 0.0025))
fit <- Simfit(sim.with.MCAR.dropout)
imps <- Impute(fit, weighted_j2r(trt.weight=0), 10)
```

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