Package 'crmPack'

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Title Object-oriented implementation of CRM designs

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Description Object-oriented implementation of CRM designs

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Collate 'Data-class.R' 'Data-methods.R' 'helpers.R' 'Rules-class.R' 'Model-class.R' 'Design-class.R' 'McmcOptions-class.R' 'McmcOptions-methods.R' 'Samples-class.R' 'Model-methods.R' 'Rules-methods.R' 'Samples-methods.R' 'Simulations-class.R' 'Simulations-methods.R' 'crmPack-package.R' 'fromQuantiles.R' 'mcmc.R' 'simulate.R'

R topics documented:

`crmPack-package` *Object-oriented implementation of CRM designs*

Description

Object-oriented implementation of CRM designs

Author(s)

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as.list,Data-method *as.list method for the "Data" class*

Description

as.list method for the "Data" class

Usage

```
## S4 method for signature 'Data'
as.list(x, ...)
```

Arguments

x	the Data object we want to convert
...	objects, possibly named.

Value

a list of all slots in x

CohortSize-class *The virtual class for cohort sizes*

Description

The virtual class for cohort sizes

See Also

CohortSizeMax, CohortSizeMin, CohortSizeRange, CohortSizeDLT, CohortSizeConst

CohortSizeConst-class *Constant cohort size*

Description

This class is used when the cohort size should be kept constant.

Slots

size the constant integer size

CohortSizeDLT-class *Cohort size based on number of DLTs*

Description

Cohort size based on number of DLTs

Slots

`DLTintervals` a vector with the bounds of the relevant DLT intervals of length `n`

`cohortSize` an integer vector of length `n-1` with the cohort sizes in the `DLTintervals`

CohortSizeMax-class *Size based on maximum of multiple cohort size rules*

Description

This class can be used to combine multiple cohort size rules with the MAX operation.

Details

`cohortSizeList` contains all cohort size rules, which are again objects of class `CohortSize`. The maximum of these individual cohort sizes is taken to give the final cohort size.

Slots

`cohortSizeList` list of cohort size rules

CohortSizeMin-class *Size based on minimum of multiple cohort size rules*

Description

This class can be used to combine multiple cohort size rules with the MIN operation.

Details

`cohortSizeList` contains all cohort size rules, which are again objects of class `CohortSize`. The minimum of these individual cohort sizes is taken to give the final cohort size.

Slots

`cohortSizeList` list of cohort size rules

CohortSizeRange-class *Cohort size based on dose range*

Description

Cohort size based on dose range

Slots

`intervals` a vector with the bounds of the relevant dose intervals of length `n`

`cohortSize` an integer vector of length `n-1` with the cohort sizes in the `intervals`

Data-class *Class for the data input*

Description

Class for the data input

Slots

`x` the doses for the patients

`y` the vector of toxicity events (0 or 1 integers)

`ID` unique patient IDs (integer vector)

`cohort` the cohort indices (sorted values from 0, 1, 2, ...)

`doseGrid` the vector of all possible doses (sorted), i.e. the dose grid

`nObs` number of observations

`nGrid` number of gridpoints

`xLevel` the levels for the doses the patients have been given

DataDual-class *Class for the dual endpoint data input*

Description

This is a subclass of `Data`, so contains all slots from `Data`, and in addition biomarker values.

Slots

`w` the continuous vector of biomarker values

Design-class *Class for the CRM design*

Description

Class for the CRM design

Slots

`model` the model to be used, an object of class `Model`

`nextBest` how to find the next best dose, an object of class `NextBest`

`stopping` stopping rule(s) for the trial, an object of class `Stopping`

`increments` how to control increments between dose levels, an object of class `Increments`

`cohortSize` rules for the cohort sizes, an object of class `CohortSize`

`data` what is the dose grid, any previous data, etc., contained in an object of class `Data`

`startingDose` what is the starting dose? Must lie on the grid in `data`

dose *Compute the doses for a given probability, given model and samples*

Description

Compute the doses for a given probability, given model and samples

Usage

```
dose(prob, model, samples, ...)
```

Arguments

`prob`	the probability
`model`	the `Model`
`samples`	the `Samples`
`...`	unused

`dose,numeric,Model,Samples-method`
Compute the doses for a given probability, given model and samples

---

Description

Compute the doses for a given probability, given model and samples

Usage

```
## S4 method for signature 'numeric,Model,Samples'
dose(prob, model, samples, ...)
```

Arguments

`prob`	the probability
`model`	the `Model`
`samples`	the `Samples`
`...`	unused

`DualEndpoint-class` *Dual endpoint model*

Description

todo: describe the model

Slots

`mu` For the probit toxicity model, `mu` contains the prior mean vector

`Sigma` For the probit toxicity model, contains the prior covariance matrix

`sigma2betaW` For the biomarker model, contains the prior variance factor of the random walk prior. If it is not a single number, it can also contain a vector with elements `a` and `b` for the inverse-gamma prior on `sigma2betaW`.

`sigma2W` Either a fixed value for the biomarker variance, or a vector with elements `a` and `b` for the inverse-gamma prior parameters.

`rho` Either a fixed value for the correlation (between -1 and 1), or a vector with elements `a` and `b` for the Beta prior on the transformation kappa = (rho + 1) / 2, which is in (0, 1). For example, `a=1,b=1` leads to a uniform prior on rho.

`useRW1` for specifying the random walk prior on the biomarker level: if `TRUE`, RW1 is used, otherwise RW2.

`useFixed` a list with logical value for each of the three parameters `sigma2betaW`, `sigma2W` and `rho` indicating whether a fixed value is used or not.

extract *Extract something from an object and produce a data.frame*

Description

Extract something from an object and produce a data.frame

Usage

```
extract(object, ...)
```

Arguments

object	the object
...	unused

Value

the data frame

extract,Samples-method *Extract certain parameter from Samples object*

Description

Extract certain parameter from Samples object

Usage

```
## S4 method for signature 'Samples'
extract(object, parameter, ...)
```

Arguments

object	the Samples object
parameter	the name of the parameter
...	unused

Value

the data frame suitable for use with ggmcmc

fitted,Samples-method *Fit method for the Samples class*

Description

Fit method for the Samples class

Usage

```
## S4 method for signature 'Samples'
fitted(object, model, data, quantiles = c(0.025, 0.975),
  middle = mean, ...)
```

Arguments

object	the Samples object
model	the Model object
data	the Data object
quantiles	the quantiles to be calculated (default: 0.025 and 0.975)
middle	the function for computing the middle point. Default: mean
...	other arguments.

Value

data frame with dose, middle, lower and upper quantiles

Increments-class *The virtual class for controlling increments*

Description

The virtual class for controlling increments

See Also

IncrementsRelative, IncrementsRelativeDLT

IncrementsRelative-class *Increments control based on relative differences in intervals*

Description

Increments control based on relative differences in intervals

Slots

intervals a vector with the bounds of the relevant intervals of length n

increments a vector of length n-1 with the maximum allowable relative increments in the intervals

IncrementsRelativeDLT-class

Increments control based on relative differences in terms of DLTs

Description

Increments control based on relative differences in terms of DLTs

Slots

`DLTintervals` a vector with the bounds of the relevant DLT intervals of length `n`

`increments` a vector of length `n-1` with the maximum allowable relative increments in the `DLTintervals`

initialize,Data-method

Initialization method for the "Data" class

Description

This is the method for initializing a "Data" class object.

Usage

```
## S4 method for signature 'Data'
initialize(.Object, x = numeric(), y = integer(),
  ID = integer(), cohort = integer(), doseGrid = numeric(), ...)
```

Arguments

`.Object`	the `Data` we want to initialize
`x`	the doses for the patients
`y`	the vector of toxicity events (0 or 1 integers)
`ID`	unique patient IDs (integer vector)
`cohort`	the cohort indices (sorted values from 0, 1, 2, ...)
`doseGrid`	the vector of all possible doses
`...`	data to include in the new object. Named arguments correspond to slots in the class definition. Unnamed arguments must be objects from classes that this class extends.

Details

Note that `ID` and `cohort` can be missing, then a warning will be issued and the variables will be filled with default IDs and best guesses, respectively.

`initialize,DualEndpoint-method`

Initialization method for the "DualEndpoint" class

Description

Initialization method for the "DualEndpoint" class

Usage

```
## S4 method for signature 'DualEndpoint'
initialize(.Object, mu, Sigma, sigma2betaW, sigma2W,
  rho, smooth = c("RW1", "RW2"), ...)
```

Arguments

`.Object`	the `DualEndpoint` we want to initialize
`mu`	see `DualEndpoint`
`Sigma`	see `DualEndpoint`
`sigma2betaW`	see `DualEndpoint`
`sigma2W`	see `DualEndpoint`
`rho`	see `DualEndpoint`
`smooth`	either “RW1” (default) or “RW2”, for specifying the random walk prior on the biomarker level.
`...`	data to include in the new object. Named arguments correspond to slots in the class definition. Unnamed arguments must be objects from classes that this class extends.

`initialize,LogisticKadane-method`

Initialization method for the "LogisticKadane" class

Description

Initialization method for the "LogisticKadane" class

Usage

```
## S4 method for signature 'LogisticKadane'
initialize(.Object, theta, xmin, xmax, ...)
```

Arguments

.Object	the LogisticKadane we want to initialize
theta	the target toxicity probability
xmin	the minimum of the dose range
xmax	the maximum of the dose range
...	data to include in the new object. Named arguments correspond to slots in the class definition. Unnamed arguments must be objects from classes that this class extends.

---

initialize,LogisticLogNormal-method

Initialization method for the "LogisticLogNormal" class

Description

Initialization method for the "LogisticLogNormal" class

Usage

```
## S4 method for signature 'LogisticLogNormal'
initialize(.Object, mean, cov, refDose, ...)
```

Arguments

.Object	the LogisticLogNormal we want to initialize
mean	the prior mean vector
cov	the prior covariance matrix
refDose	the reference dose
...	data to include in the new object. Named arguments correspond to slots in the class definition. Unnamed arguments must be objects from classes that this class extends.

---

initialize,LogisticNormal-method

Initialization method for the "LogisticNormal" class

Description

Initialization method for the "LogisticNormal" class

Usage

```
## S4 method for signature 'LogisticNormal'
initialize(.Object, mean, cov, refDose, ...)
```

Arguments

.Object	the LogisticNormal we want to initialize
mean	the prior mean vector
cov	the prior covariance matrix
refDose	the reference dose
...	data to include in the new object. Named arguments correspond to slots in the class definition. Unnamed arguments must be objects from classes that this class extends.

---

initialize,McmcOptions-method *Initialization method for the "McmcOptions" class*

Description

Initialization method for the "McmcOptions" class

Usage

```
## S4 method for signature 'McmcOptions'
initialize(.Object, burnin = 10000L, step = 2L,
  samples = 10000L, ...)
```

Arguments

.Object	the McmcOptions we want to initialize
burnin	number of burn-in iterations which are not saved (default: 10,000)
step	only every step-th iteration is saved after the burn-in (default: 2)
samples	number of resulting samples (by default 10,000 will result)
...	data to include in the new object. Named arguments correspond to slots in the class definition. Unnamed arguments must be objects from classes that this class extends.

LogisticKadane-class *Reparametrized logistic model*

Description

This is the logistic model in the parametrization of Kadane et al. (1980).

Details

Let $\rho_0 = p(x_{min})$ be the probability of a DLT and the minimum dose x_{min}, and let γ be the dose with target toxicity probability θ, i.e. $p(\gamma) = \theta$. Then it can easily be shown that the logistic regression model has intercept

$$\frac{\gamma logit(\rho_0) - x_{min} logit(\theta)}{\gamma - x_{min}}$$

and slope

$$\frac{logit(theta) - logit(\rho_0)}{\gamma - x_{min}}$$

The prior is a uniform distribution for γ between x_{min} and x_{max}, and for ρ_0 as well a uniform distribution between 0 and θ.

The slots of this class, required for creating the model, are the target toxicity, as well as the minimum and maximum of the dose range. Note that these can be different from the minimum and maximum of the dose grid in the data later on.

Slots

`theta` the target toxicity probability θ

`xmin` the minimum of the dose range x_{min}

`xmax` the maximum of the dose range x_{max}

`LogisticLogNormal-class`

Standard logistic model with bivariate (log) normal prior

Description

This is the usual logistic regression model with a bivariate normal prior on the intercept and log slope.

Details

The covariate is the natural logarithm of the dose x divided by the reference dose x^*:

$$logit[p(x)] = \alpha + \beta \cdot \log(x/x^*)$$

where $p(x)$ is the probability of observing a DLT for a given dose x.

The prior is

$$(\alpha, \log(\beta)) \sim Normal(\mu, \Sigma)$$

The slots of this class contain the mean vector and the covariance matrix of the bivariate normal distribution, as well as the reference dose.

Slots

`mean` the prior mean vector μ

`cov` the prior covariance matrix Σ

`refDose` the reference dose x^*

LogisticNormal-class *Standard logistic model with bivariate normal prior*

Description

This is the usual logistic regression model with a bivariate normal prior on the intercept and slope.

Details

The covariate is the natural logarithm of the dose x divided by the reference dose x^*:

$$logit[p(x)] = \alpha + \beta \cdot \log(x/x^*)$$

where $p(x)$ is the probability of observing a DLT for a given dose x.

The prior is

$$(\alpha, \beta) \sim Normal(\mu, \Sigma)$$

The slots of this class contain the mean vector, the covariance and precision matrices of the bivariate normal distribution, as well as the reference dose.

Slots

`mean` the prior mean vector μ

`cov` the prior covariance matrix Σ

`prec` the prior precision matrix Σ^{-1}

`refDose` the reference dose x^*

logit *Shorthand for logit function*

Description

Shorthand for logit function

Usage

```
logit(x)
```

Arguments

`x`	the function argument

Value

the logit(x)

maxDose *Determine the maximum possible next dose*

Description

Determine the upper limit of the next dose based on the increments rule.

Usage

```
maxDose(increments, data, ...)
```

Arguments

increments	The rule, an object of class Increments
data	The data input, an object of class Data
...	further arguments

Details

This function outputs the maximum possible next dose, based on the corresponding rule `increments` and the `data`.

Value

the maximum possible next dose

maxDose,IncrementsRelative,Data-method *Determine the maximum possible next dose based on relative increments*

Description

Determine the maximum possible next dose based on relative increments

Usage

```
## S4 method for signature 'IncrementsRelative,Data'
maxDose(increments, data, ...)
```

Arguments

increments	The rule, an object of class Increments
data	The data input, an object of class Data
...	further arguments

`maxDose,IncrementsRelativeDLT,Data-method`
Determine the maximum possible next dose based on relative increments determined by DLTs so far

---

Description

Determine the maximum possible next dose based on relative increments determined by DLTs so far

Usage

```
## S4 method for signature 'IncrementsRelativeDLT,Data'
maxDose(increments, data, ...)
```

Arguments

`increments`	The rule, an object of class `Increments`
`data`	The data input, an object of class `Data`
`...`	further arguments

`maxSize` *"MAX" combination of cohort size rules*

Description

This function combines cohort size rules by taking the maximum of all sizes.

Usage

```
maxSize(...)
```

Arguments

`...`	Objects of class `CohortSize`

Value

the combination as an object of class `CohortSizeMax`

See Also

`minSize`

maxSize,CohortSize-method

The method combining cohort size rules by taking maximum

Description

The method combining cohort size rules by taking maximum

Usage

```
## S4 method for signature 'CohortSize'
maxSize(...)
```

Arguments

...	Objects of class CohortSize

mcmc

Obtain posterior samples for all model parameters

Description

Obtain posterior samples for all model parameters

Usage

```
mcmc(data, model, options, ...)
```

Arguments

data	The data input, an object of class Data
model	The model input, an object of class Model
options	MCMC options, an object of class McmcOptions
...	unused

Details

This is the function to actually run the MCMC machinery to produce posterior samples from all model parameters and required derived values. It is a generic function, so that customized versions may be conveniently defined for specific subclasses of Data, Model, and McmcOptions input.

Value

The posterior samples, an object of class Samples.

`mcmc,Data,LogisticLogNormal,McmcOptions-method`
The fast method for the LogisticLogNormal class

Description

The fast method for the LogisticLogNormal class

Usage

```
## S4 method for signature 'Data,LogisticLogNormal,McmcOptions'
mcmc(data, model, options,
  verbose = FALSE, ...)
```

Arguments

`verbose`	shall messages be printed? (not default)
`data`	The data input, an object of class `Data`
`model`	The model input, an object of class `Model`
`options`	MCMC options, an object of class `McmcOptions`
`...`	unused

`mcmc,Data,LogisticNormal,McmcOptions-method`
The fast method for the LogisticNormal class

Description

The fast method for the LogisticNormal class

Usage

```
## S4 method for signature 'Data,LogisticNormal,McmcOptions'
mcmc(data, model, options,
  verbose = FALSE, ...)
```

Arguments

`verbose`	shall messages be printed? (not default)
`data`	The data input, an object of class `Data`
`model`	The model input, an object of class `Model`
`options`	MCMC options, an object of class `McmcOptions`
`...`	unused

mcmc,Data,Model,McmcOptions-method *Standard method which uses BUGS*

Description

Standard method which uses BUGS

Usage

```
## S4 method for signature 'Data,Model,McmcOptions'
mcmc(data, model, options,
  program = "OpenBUGS", verbose = FALSE, ...)
```

Arguments

program	the program which shall be used (see bugs for details)
verbose	shall messages be printed? (not default)
data	The data input, an object of class Data
model	The model input, an object of class Model
options	MCMC options, an object of class McmcOptions
...	unused

McmcOptions-class *Class for the three canonical MCMC options*

Description

Class for the three canonical MCMC options

Slots

iterations number of MCMC iterations

burnin number of burn-in iterations which are not saved

step only every step-th iteration is saved after the burn-in

MinimalInformative *Construct a minimally informative prior*

Description

This function constructs a minimally informative prior, which is captured in a LogisticNormal object.

Usage

```
MinimalInformative(dosegrid, refDose, threshmin = 0.2, threshmax = 0.3, ...)
```

Arguments

dosegrid	the dose grid
refDose	the reference dose
threshmin	Any toxicity probability above this threshold would be very unlikely (5%) at the minimum dose (default: 0.2)
threshmax	Any toxicity probability below this threshold would be very unlikely (5%) at the maximum dose (default: 0.3)
...	additional arguments for computations, see Quantiles2LogisticNormal

Details

Based on the proposal by Neuenschwander et al (2008, Statistics in Medicine), a minimally informative prior distribution is constructed. The required key input is the minimum (d_1 in the notation of the Appendix A.1 of that paper) and the maximum value (d_J) of the dose grid supplied to this function. Then threshmin is the probability threshold q_1, such that any probability of DLT larger than q_1 has only 5% probability. Likewise, threshmax is the probability threshold q_J, such that any probability of DLT smaller than q_J has only 5% probability. Subsequently, for all doses supplied in the dosegrid argument, Beta distributions are set up, and Quantiles2LogisticNormal is used to transform the resulting quantiles into an approximating LogisticNormal model.

Value

see Quantiles2LogisticNormal

minSize *"MIN" combination of cohort size rules*

Description

This function combines cohort size rules by taking the minimum of all sizes.

Usage

```
minSize(...)
```

Arguments

...	Objects of class CohortSize

Value

the combination as an object of class CohortSizeMin

See Also

maxSize

---

minSize,CohortSize-method *The method combining cohort size rules by taking minimum*

Description

The method combining cohort size rules by taking minimum

Usage

```
## S4 method for signature 'CohortSize'
minSize(...)
```

Arguments

...	Objects of class CohortSize

Model-class *Class for the model input*

Description

This is the general model class, from which all other specific models inherit.

Details

The datamodel must obey the convention that the data input is called exactly as in the Data class. All prior distributions for parameters should be contained in the model function priormodel. The background is that this can be used to simulate from the prior distribution, before obtaining any data.

The dose function has as first argument prob, a scalar toxicity probability which is targeted. Additional arguments are model parameters. Then it computes, using model parameter(s) (samples), the resulting dose. Note that the model parameters are called exactly as in the model and must be included in the sample vector. The vectors of all samples for these parameters will then be supplied to the function. So your function must be able to process vectors of the model parameters, i.e. it must vectorize over them.

The prob function has as first argument dose, which is a scalar dose. Additional arguments are model parameters. Then it computes, using model parameter(s) (samples), the resulting probability of toxicity at that dose. Again here, the function must vectorize over the model parameters.

If you work with multivariate parameters, then please assume that your the two functions receive either one parameter value as a row vector, or a samples matrix where the rows correspond to the sampling index, i.e. the layout is then nSamples x dimParameter.

Note that dose and prob are the inverse functions of each other.

Slots

datamodel a function representing the BUGS data model specification (see the details above)

priormodel a function representing the BUGS prior specification (see the details above)

datanames The names of all Data slots that are used in the datamodel and/or priormodel definition. Note that you cannot specify more variables than those that are really used in the model!

modelspecs a function computing the list of the data model and prior model specifications that are required for fully specifying them (e.g. prior parameters, reference dose, etc.), based on the Data slots that are then required as arguments of this function. This will then be passed to BUGS for the computations.

dose a function computing the dose reaching a specific target probability, based on the model parameters and additional prior settings (see the details above)

prob a function computing the probability of toxicity for a specific dose, based on the model parameters and additional prior settings (see the details above)

init a function computing the list of starting values for parameters required to be initialized in the MCMC sampler, based on the Data slots that are then required as arguments of this function

sample names of all parameters from which you would like to save the MCMC samples. These must include the ones required by the dose and prob functions.

See Also

LogisticNormal, LogisticLogNormal, LogisticKadane, DualEndpoint

---

nextBest *Find the next best dose*

Description

Compute the recommended next best dose.

Usage

```
nextBest(nextBest, doselimit, samples, model, data, ...)
```

Arguments

nextBest	The rule, an object of class NextBest
doselimit	The maximum allowed next dose
samples	the Samples object
model	The model input, an object of class Model
data	The data input, an object of class Data
...	possible additional arguments without method dispatch

Details

This function outputs the next best dose recommendation based on the corresponding rule `nextBest`, the posterior `samples` from the `model` and the underlying `data`.

Value

a list with the next best dose (element `value`) on the grid defined in `data`, and a plot depicting this recommendation (element `plot`)

`nextBest,NextBestDualEndpoint,numeric,Samples,DualEndpoint,Data-method`

Find the next best dose based on the dual endpoint model

Description

Find the next best dose based on the dual endpoint model

Usage

```
  ## S4 method for signature
## 'NextBestDualEndpoint,numeric,Samples,DualEndpoint,Data'
nextBest(nextBest,
  doselimit, samples, model, data, ...)
```

Arguments

`nextBest`	The rule, an object of class `NextBest`
`doselimit`	The maximum allowed next dose
`samples`	the `Samples` object
`model`	The model input, an object of class `Model`
`data`	The data input, an object of class `Data`
`...`	possible additional arguments without method dispatch

`nextBest,NextBestMTD,numeric,Samples,Model,Data-method`

Find the next best dose based on the MTD rule

Description

Find the next best dose based on the MTD rule

Usage

```
## S4 method for signature 'NextBestMTD,numeric,Samples,Model,Data'
nextBest(nextBest, doselimit,
  samples, model, data, ...)
```

Arguments

nextBest	The rule, an object of class NextBest
doselimit	The maximum allowed next dose
samples	the Samples object
model	The model input, an object of class Model
data	The data input, an object of class Data
...	possible additional arguments without method dispatch

---

nextBest,NextBestNCRM,numeric,Samples,Model,Data-method *Find the next best dose based on the NCRM method*

Description

Find the next best dose based on the NCRM method

Usage

```
## S4 method for signature 'NextBestNCRM,numeric,Samples,Model,Data'
nextBest(nextBest,
  doselimit, samples, model, data, ...)
```

Arguments

nextBest	The rule, an object of class NextBest
doselimit	The maximum allowed next dose
samples	the Samples object
model	The model input, an object of class Model
data	The data input, an object of class Data
...	possible additional arguments without method dispatch

NextBest-class *The virtual class for finding next best dose*

Description

The virtual class for finding next best dose

See Also

NextBestMTD, NextBestNCRM, NextBestDualEndpoint

NextBestDualEndpoint-class

The class with the input for finding the next dose based on the dual endpoint model

Description

The class with the input for finding the next dose based on the dual endpoint model

Slots

`target` the biomarker level, relative to the maximum, that needs to be reached. For example, 0.9 means that a dose with 90 of the maximum biomarker level is considered as having reached sufficient biomarker level.

`overdose` the overdose toxicity interval

`maxOverdoseProb` maximum overdose probability that is allowed

NextBestMTD-class

The class with the input for finding the next best MTD estimate

Description

The class with the input for finding the next best MTD estimate

Slots

`target` the target toxicity probability

`derive` the function which derives from the input, a vector of posterior MTD samples called `mtdSamples`, the final next best MTD estimate.

NextBestNCRM-class

The class with the input for finding the next dose in target interval

Description

The class with the input for finding the next dose in target interval

Slots

`target` the target toxicity interval

`overdose` the overdose toxicity interval

`maxOverdoseProb` maximum overdose probability that is allowed

or-Stopping-Stopping *The method combining two atomic stopping rules*

Description

The method combining two atomic stopping rules

Usage

```
## S4 method for signature 'Stopping,Stopping'
e1 | e2
```

Arguments

e1	First Stopping object
e2	Second Stopping object

Value

The StoppingAny object

or-Stopping-StoppingAny *The method combining a stopping list and an atomic*

Description

The method combining a stopping list and an atomic

Usage

```
## S4 method for signature 'StoppingAny,Stopping'
e1 | e2
```

Arguments

e1	StoppingAny object
e2	Stopping object

Value

The modified StoppingAny object

`or-StoppingAny-Stopping`

The method combining an atomic and a stopping list

Description

The method combining an atomic and a stopping list

Usage

```
## S4 method for signature 'Stopping,StoppingAny'
e1 | e2
```

Arguments

`e1`	`Stopping` object
`e2`	`StoppingAny` object

Value

The modified `StoppingAny` object

`plot,Data,missing-method`

Plot method for the "Data" class

Description

Plot method for the "Data" class

Usage

```
## S4 method for signature 'Data,missing'
plot(x, y, ...)
```

Arguments

`x`	the `Data` object we want to plot
`y`	the y coordinates of points in the plot, *optional* if `x` is an appropriate structure.
`...`	Arguments to be passed to methods, such as graphical parameters (see `par`). Many methods will accept the following arguments:
	`type` what type of plot should be drawn. Possible types are
	• `"p"` for **p**oints,
	• `"l"` for **l**ines,
	• `"b"` for **b**oth,
	• `"c"` for the lines part alone of `"b"`,
	• `"o"` for both '**o**verplotted',

- "h" for '**h**istogram' like (or 'high-density') vertical lines,
- "s" for stair **s**teps,
- "S" for other **s**teps, see 'Details' below,
- "n" for no plotting.

All other types give a warning or an error; using, e.g., type = "punkte" being equivalent to type = "p" for S compatibility. Note that some methods, e.g. plot.factor, do not accept this.

main an overall title for the plot: see title.

sub a sub title for the plot: see title.

xlab a title for the x axis: see title.

ylab a title for the y axis: see title.

asp the y/x aspect ratio, see plot.window.

Value

the ggplot object

---

plot,DataDual,missing-method

Plot method for the "DataDual" class

Description

Plot method for the "DataDual" class

Usage

```
## S4 method for signature 'DataDual,missing'
plot(x, y, ...)
```

Arguments

x	the DataDual object we want to plot
y	the y coordinates of points in the plot, *optional* if x is an appropriate structure.
...	Arguments to be passed to methods, such as graphical parameters (see par). Many methods will accept the following arguments:

type what type of plot should be drawn. Possible types are

- "p" for **p**oints,
- "l" for **l**ines,
- "b" for **b**oth,
- "c" for the lines part alone of "b",
- "o" for both '**o**verplotted',
- "h" for '**h**istogram' like (or 'high-density') vertical lines,
- "s" for stair **s**teps,
- "S" for other **s**teps, see 'Details' below,
- "n" for no plotting.

All other types give a warning or an error; using, e.g., type = "punkte" being equivalent to type = "p" for S compatibility. Note that some methods, e.g. plot.factor, do not accept this.

main an overall title for the plot: see title.

sub a sub title for the plot: see title.

xlab a title for the x axis: see title.

ylab a title for the y axis: see title.

asp the y/x aspect ratio, see plot.window.

Value

the ggplot object

---

plot,Samples,DualEndpoint-method

Plot method for the "Samples" object, when we have the dual endpoint model

---

Description

Plot method for the "Samples" object, when we have the dual endpoint model

Usage

```
## S4 method for signature 'Samples,DualEndpoint'
plot(x, y, data, extrapolate = TRUE, ...)
```

Arguments

x	the Samples object
y	the DualEndpoint object
data	the DataDual object
extrapolate	should the biomarker fit be extrapolated to the whole dose grid? (default)
...	Arguments to be passed to methods, such as graphical parameters (see par). Many methods will accept the following arguments:

type what type of plot should be drawn. Possible types are

- "p" for **p**oints,
- "l" for **l**ines,
- "b" for **b**oth,
- "c" for the lines part alone of "b",
- "o" for both '**o**verplotted',
- "h" for '**h**istogram' like (or 'high-density') vertical lines,
- "s" for stair **s**teps,
- "S" for other **s**teps, see 'Details' below,
- "n" for no plotting.

All other types give a warning or an error; using, e.g., type = "punkte" being equivalent to type = "p" for S compatibility. Note that some methods, e.g. plot.factor, do not accept this.

`main` an overall title for the plot: see `title`.
`sub` a sub title for the plot: see `title`.
`xlab` a title for the x axis: see `title`.
`ylab` a title for the y axis: see `title`.
`asp` the y/x aspect ratio, see `plot.window`.

Value

the `ggplot` object

`plot,Samples,Model-method`
Plot method for the "Samples" and "Model" object

Description

Plot method for the "Samples" and "Model" object

Usage

```
## S4 method for signature 'Samples,Model'
plot(x, y, data, ...)
```

Arguments

`x`	the `Samples` object
`y`	the `Model` object
`data`	the `Data` object
`...`	Arguments to be passed to methods, such as graphical parameters (see `par`). Many methods will accept the following arguments: `type` what type of plot should be drawn. Possible types are • `"p"` for **p**oints, • `"l"` for **l**ines, • `"b"` for **b**oth, • `"c"` for the lines part alone of `"b"`, • `"o"` for both '**o**verplotted', • `"h"` for '**h**istogram' like (or 'high-density') vertical lines, • `"s"` for stair **s**teps, • `"S"` for other **s**teps, see 'Details' below, • `"n"` for no plotting. All other `type`s give a warning or an error; using, e.g., `type = "punkte"` being equivalent to `type = "p"` for S compatibility. Note that some methods, e.g. `plot.factor`, do not accept this. `main` an overall title for the plot: see `title`. `sub` a sub title for the plot: see `title`. `xlab` a title for the x axis: see `title`. `ylab` a title for the y axis: see `title`. `asp` the y/x aspect ratio, see `plot.window`.

Value

the ggplot object

`plot,Simulations,missing-method`
Plot simulations

Description

Summarize the simulations with plots

Usage

```
## S4 method for signature 'Simulations,missing'
plot(x, y, type = c("trajectory",
  "dosesTried"), ...)
```

Arguments

x	the Simulations object we want to plot from
type	the type of plots you want to obtain.
y	the y coordinates of points in the plot, *optional* if x is an appropriate structure.
...	Arguments to be passed to methods, such as graphical parameters (see par). Many methods will accept the following arguments: type what type of plot should be drawn. Possible types are • "p" for **p**oints, • "l" for **l**ines, • "b" for **b**oth, • "c" for the lines part alone of "b", • "o" for both '**o**verplotted', • "h" for '**h**istogram' like (or 'high-density') vertical lines, • "s" for stair **s**teps, • "S" for other **s**teps, see 'Details' below, • "n" for no plotting. All other types give a warning or an error; using, e.g., type = "punkte" being equivalent to type = "p" for S compatibility. Note that some methods, e.g. plot.factor, do not accept this. main an overall title for the plot: see title. sub a sub title for the plot: see title. xlab a title for the x axis: see title. ylab a title for the y axis: see title. asp the y/x aspect ratio, see plot.window.

Details

This plot method can be applied to Simulations objects in order to summarize them graphically. Possible types of plots at the moment are:

trajectory Summary of the trajectory of the simulated trials

dosesTried Average proportions of the doses tested in patients

You can specify one or both of these in the type argument.

Value

A single ggplot2 object if a single plot is asked for, otherwise a gridExtra{gTree} object. The first can be plotted with the print command, the latter with the grid.draw command.

---

plot,Simulations-summary,missing-method

Plot summaries of the simulations

Description

Graphical display of the simulation summary

Usage

```
## S4 method for signature 'Simulations-summary,missing'
plot(x, y, type = c("nObs",
  "doseSelected", "propDLTs", "nAboveTarget", "meanFit"), ...)
```

Arguments

x	the Simulations-summary object we want to plot from
type	the types of plots you want to obtain.
y	the y coordinates of points in the plot, *optional* if x is an appropriate structure.
...	Arguments to be passed to methods, such as graphical parameters (see par). Many methods will accept the following arguments:

type what type of plot should be drawn. Possible types are

- "p" for **p**oints,
- "l" for **l**ines,
- "b" for **b**oth,
- "c" for the lines part alone of "b",
- "o" for both '**o**verplotted',
- "h" for '**h**istogram' like (or 'high-density') vertical lines,
- "s" for stair **s**teps,
- "S" for other **s**teps, see 'Details' below,
- "n" for no plotting.

All other types give a warning or an error; using, e.g., type = "punkte" being equivalent to type = "p" for S compatibility. Note that some methods, e.g. plot.factor, do not accept this.

`main` an overall title for the plot: see `title`.

`sub` a sub title for the plot: see `title`.

`xlab` a title for the x axis: see `title`.

`ylab` a title for the y axis: see `title`.

`asp` the y/x aspect ratio, see `plot.window`.

Details

This plot method can be applied to `Simulations` objects in order to summarize them graphically. Possible `type`s of plots at the moment are:

nObs Distribution of the number of patients in the simulated trials

doseSelected Distribution of the final selected doses in the trials

propDLTs Distribution of the proportion of patients with DLTs in the trials

nAboveTarget Distribution of the number of patients treated at doses which are above the target toxicity interval (as specified by the `truth` and `target` arguments to `summary,Simulations-method`)

meanFit Plot showing the average fitted dose-toxicity curve across the trials, together with 95% credible intervals, and comparison with the assumed truth (as specified by the `truth` argument to `summary,Simulations-method`)

You can specify any subset of these in the `type` argument.

Value

A single `ggplot2` object if a single plot is asked for, otherwise a `gridExtra{gTree}` object. The first can be plotted with the `print` command, the latter with the `grid.draw` command.

`prob` *Compute the probability for a given dose, given model and samples*

Description

Compute the probability for a given dose, given model and samples

Usage

```
prob(dose, model, samples, ...)
```

Arguments

`dose`	the dose
`model`	the `Model`
`samples`	the `Samples`
`...`	unused

`prob,numeric,Model,Samples-method`

Compute the probability for a given dose, given model and samples

---

Description

Compute the probability for a given dose, given model and samples

Usage

```
## S4 method for signature 'numeric,Model,Samples'
prob(dose, model, samples, ...)
```

Arguments

`dose`	the dose
`model`	the `Model`
`samples`	the `Samples`
`...`	unused

`Quantiles2LogisticNormal`

Convert prior quantiles (lower, median, upper) to LogisticNormal model

---

Description

This function uses generalised simulated annealing to optimise a `LogisticNormal` model to be as close as possible to the given prior quantiles.

Usage

```
Quantiles2LogisticNormal(dosegrid, refDose, lower, median, upper,
  level = 0.95, parstart = NULL, parlower = c(-10, -10, 0, 0, -0.95),
  parupper = c(10, 10, 10, 10, 0.95), control = list(threshold.stop = 0.01,
  maxit = 50000, temperature = 50000, max.time = 600, verbose = TRUE))
```

Arguments

`dosegrid`	the dose grid
`refDose`	the reference dose
`lower`	the lower quantiles
`median`	the medians
`upper`	the upper quantiles
`level`	the credible level of the (lower, upper) intervals (default: 0.95)
`parstart`	starting values for the parameters. By default, these are determined from the medians supplied.

parlower	lower bounds on the parameters (intercept alpha and the slope beta, the corresponding standard deviations and the correlation.)
parupper	upper bounds on the parameters
control	additional options for the optimisation routine, see GenSA for more details

Value

a list with the best approximating LogisticNormal model, the resulting quantiles, the required quantiles and the distance to the required quantiles, as well as the final parameters (which could be used for running the algorithm a second time)

Samples-class *Class for the MCMC output*

Description

Class for the MCMC output

Slots

data a list where each entry contains the samples of a (vector-valued) parameter in a vector/matrix in the format (number of samples) x (dimension of the parameter).

options the McmcOptions which have been used

---

sampleSize *Compute the number of samples for a given MCMC options triple*

Description

Compute the number of samples for a given MCMC options triple

Usage

```
sampleSize(mcmcOptions)
```

Arguments

mcmcOptions	the McmcOptions object

Value

the resulting sample size

---

show,Simulations-summary-method

Show the summary of the simulations

Description

Show the summary of the simulations

Usage

```
## S4 method for signature 'Simulations-summary'
show(object)
```

Arguments

object	the Simulations-summary object we want to print

---

simulate,Design-method

Simulate outcomes from a CRM design

Description

Simulate outcomes from a CRM design

Usage

```
## S4 method for signature 'Design'
simulate(object, truth, args = NULL, nsim = 1L,
  mcmcOptions = new("McmcOptions"), seed = NULL, parallel = FALSE, ...)
```

Arguments

object	the Design object we want to simulate data from
truth	a function which takes as input a dose (vector) and returns the true probability (vector) for toxicity. Additional arguments can be supplied in args.
args	data frame with arguments for the truth function. The column names correspond to the argument names, the rows to the values of the arguments. The rows are appropriately recycled in the nsim simulations. In order to produce outcomes from the posterior predictive distribution, e.g, pass an object that contains the data observed so far, truth contains the prob function from the model in object, and args contains posterior samples from the model.
nsim	the number of simulations (default: 1)
mcmcOptions	object of class McmcOptions, giving the MCMC options for each evaluation in the trial. By default, the standard options are used

seed	an object specifying if and how the random number generator should be initialized ("seeded"). Either NULL (default) or an integer that will be used in a call to set.seed before simulating the response vectors. If set, the value is saved as the seed slot of the returned object. The default, NULL will not change the random generator state, and .Random.seed will be saved.
parallel	should the simulation runs be parallelized across the clusters of the computer? (not default)
...	additional optional arguments.

Value

an object of class Simulations

Simulations-class *Class for the simulations output*

Description

This class captures the trial simulations.

Details

Here also the random generator state before starting the simulation is saved, in order to be able to reproduce the outcome. For this just use set.seed with the seed as argument before running simulate,Design-method.

Slots

data list of produced Data objects

doses the vector of final dose recommendations

fit list with the final fits

stopReasons list of stopping reasons for each simulation run

seed random generator state before starting the simulation

Simulations-summary-class
Class for the summary of simulations output

Description

Class for the summary of simulations output

Slots

`target` target toxicity interval

`targetDoseInterval` corresponding target dose interval

`nsim` number of simulations

`propDLTs` proportions of DLTs in the trials

`meanToxRisk` mean toxicity risks for the patients

`doseSelected` doses selected as MTD

`toxAtDosesSelected` true toxicity at doses selected

`propAtTarget` Proportion of trials selecting target MTD

`doseMostSelected` dose most often selected as MTD

`obsToxRateAtDoseMostSelected` observed toxicity rate at dose most often selected

`fitAtDoseMostSelected` fitted toxicity rate at dose most often selected

`meanFit` list with the average, lower (2.5 quantiles of the mean fitted toxicity at each dose level

`nObs` number of patients overall

`nAboveTarget` number of patients treated above target tox interval

`doseGrid` the dose grid that has been used

`size` *Determine the size of the next cohort*

Description

This function determines the size of the next cohort.

Usage

```
size(cohortSize, dose, data, ...)
```

Arguments

`cohortSize`	The rule, an object of class `CohortSize`
`dose`	the next dose
`data`	The data input, an object of class `Data`
`...`	additional arguments

Value

the size as integer value

size,CohortSizeConst,ANY,Data-method
Constant cohort size

Description

Constant cohort size

Usage

```
## S4 method for signature 'CohortSizeConst,ANY,Data'
size(cohortSize, dose, data, ...)
```

Arguments

cohortSize	The rule, an object of class CohortSize
dose	the next dose
data	The data input, an object of class Data
...	additional arguments

size,CohortSizeDLT,ANY,Data-method
Determine the cohort size based on the number of DLTs so far

Description

Determine the cohort size based on the number of DLTs so far

Usage

```
## S4 method for signature 'CohortSizeDLT,ANY,Data'
size(cohortSize, dose, data, ...)
```

Arguments

cohortSize	The rule, an object of class CohortSize
dose	the next dose
data	The data input, an object of class Data
...	additional arguments

`size,CohortSizeMax,ANY,Data-method`
Size based on maximum of multiple cohort size rules

Description

Size based on maximum of multiple cohort size rules

Usage

```
## S4 method for signature 'CohortSizeMax,ANY,Data'
size(cohortSize, dose, data, ...)
```

Arguments

`cohortSize`	The rule, an object of class `CohortSize`
`dose`	the next dose
`data`	The data input, an object of class `Data`
`...`	additional arguments

`size,CohortSizeMin,ANY,Data-method`
Size based on minimum of multiple cohort size rules

Description

Size based on minimum of multiple cohort size rules

Usage

```
## S4 method for signature 'CohortSizeMin,ANY,Data'
size(cohortSize, dose, data, ...)
```

Arguments

`cohortSize`	The rule, an object of class `CohortSize`
`dose`	the next dose
`data`	The data input, an object of class `Data`
`...`	additional arguments

size,CohortSizeRange,ANY,Data-method

Determine the cohort size based on the range into which the next dose falls into

Description

Determine the cohort size based on the range into which the next dose falls into

Usage

```
## S4 method for signature 'CohortSizeRange,ANY,Data'
size(cohortSize, dose, data, ...)
```

Arguments

cohortSize	The rule, an object of class CohortSize
dose	the next dose
data	The data input, an object of class Data
...	additional arguments

Stopping-class *The virtual class for stopping rules*

Description

The virtual class for stopping rules

See Also

StoppingList, StoppingMaxPatients, StoppingCohortsNearDose, StoppingPatientsNearDose, StoppingMinCohorts, StoppingTargetProb StoppingMTDdistribution, StoppingTargetBiomarker

StoppingAll-class *Stop based on fullfillment of all multiple stopping rules*

Description

This class can be used to combine multiple stopping rules with an AND operator.

Details

stopList contains all stopping rules, which are again objects of class Stopping. All stopping rules must be fulfilled in order that the result of this rule is to stop.

Slots

stopList list of stopping rules of the stopping rules into a single result

StoppingAny-class *Stop based on fullfillment of any stopping rule*

Description

This class can be used to combine multiple stopping rules with an OR operator.

Details

`stopList` contains all stopping rules, which are again objects of class `Stopping`. Any of these rules must be fulfilled in order that the result of this rule is to stop.

Slots

`stopList` list of stopping rules of the stopping rules into a single result

StoppingCohortsNearDose-class *Stop based on number of cohorts near to next best dose*

Description

Stop based on number of cohorts near to next best dose

Slots

`nCohorts` number of required cohorts

`percentage` percentage (between 0 and 100) within the next best dose the cohorts must lie

StoppingList-class *Stop based on multiple stopping rules*

Description

This class can be used to combine multiple stopping rules.

Details

`stopList` contains all stopping rules, which are again objects of class `Stopping`, and the `summary` is a function taking a logical vector of the size of `stopList` and returning a single logical value. For example, if the function `all` is given as `summary` function, then this means that all stopping rules must be fulfilled in order that the result of this rule is to stop.

Slots

`stopList` list of stopping rules

`summary` the summary function to combine the results of the stopping rules into a single result

StoppingMaxPatients-class

Stop based on maximum number of patients

Description

Stop based on maximum number of patients

Slots

`nPatients` maximum allowed number of patients

StoppingMinCohorts-class

Stop based on minimum number of cohorts

Description

Stop based on minimum number of cohorts

Slots

`nCohorts` minimum required number of cohorts

StoppingMTDdistribution-class

Stop based on MTD distribution

Description

Has 90% probability above a threshold of 50% of the current MTD been reached? This class is used for this question.

Slots

`target` the target toxicity probability (e.g. 0.33) defining the MTD

`thresh` the threshold relative to the MTD (e.g. 0.5)

`prob` required probability (e.g. 0.9)

StoppingPatientsNearDose-class

Stop based on number of patients near to next best dose

Description

Stop based on number of patients near to next best dose

Slots

`nPatients` number of required patients

`percentage` percentage (between 0 and 100) within the next best dose the patients must lie

StoppingTargetBiomarker-class

Stop based on probability of target biomarker

Description

Stop based on probability of target biomarker

Slots

`target` the biomarker level, relative to the maximum, that needs to be reached

`prob` required target probability for reaching sufficient precision

StoppingTargetProb-class

Stop based on probability of target tox interval

Description

Stop based on probability of target tox interval

Slots

`target` the target toxicity interval

`prob` required target toxicity probability for reaching sufficient precision

stopTrial *Stop the trial?*

Description

This function returns whether to stop the trial.

Usage

```
stopTrial(stopping, dose, samples, model, data, ...)
```

Arguments

stopping	The rule, an object of class Stopping
dose	the recommended next best dose
samples	the Samples object
model	The model input, an object of class Model
data	The data input, an object of class Data
...	additional arguments

Value

logical value: TRUE if the trial can be stopped, FALSE otherwise. It should have an attribute message which gives the reason for the decision.

stopTrial,StoppingAll,ANY,ANY,ANY,ANY-method *Stop based on fulfillment of all multiple stopping rules*

Description

Stop based on fulfillment of all multiple stopping rules

Usage

```
## S4 method for signature 'StoppingAll,ANY,ANY,ANY,ANY'
stopTrial(stopping, dose, samples,
  model, data, ...)
```

Arguments

stopping	The rule, an object of class Stopping
dose	the recommended next best dose
samples	the Samples object
model	The model input, an object of class Model
data	The data input, an object of class Data
...	additional arguments

`stopTrial,StoppingAny,ANY,ANY,ANY,ANY-method`

Stop based on fulfillment of any stopping rule

Description

Stop based on fulfillment of any stopping rule

Usage

```
## S4 method for signature 'StoppingAny,ANY,ANY,ANY,ANY'
stopTrial(stopping, dose, samples,
  model, data, ...)
```

Arguments

`stopping`	The rule, an object of class `Stopping`
`dose`	the recommended next best dose
`samples`	the `Samples` object
`model`	The model input, an object of class `Model`
`data`	The data input, an object of class `Data`
`...`	additional arguments

`stopTrial,StoppingCohortsNearDose,numeric,ANY,ANY,Data-method`

Stop based on number of cohorts near to next best dose

Description

Stop based on number of cohorts near to next best dose

Usage

```
## S4 method for signature 'StoppingCohortsNearDose,numeric,ANY,ANY,Data'
stopTrial(stopping,
  dose, samples, model, data, ...)
```

Arguments

`stopping`	The rule, an object of class `Stopping`
`dose`	the recommended next best dose
`samples`	the `Samples` object
`model`	The model input, an object of class `Model`
`data`	The data input, an object of class `Data`
`...`	additional arguments

stopTrial,StoppingList,ANY,ANY,ANY,ANY-method

Stop based on multiple stopping rules

Description

Stop based on multiple stopping rules

Usage

```
## S4 method for signature 'StoppingList,ANY,ANY,ANY,ANY'
stopTrial(stopping, dose, samples,
  model, data, ...)
```

Arguments

stopping	The rule, an object of class Stopping
dose	the recommended next best dose
samples	the Samples object
model	The model input, an object of class Model
data	The data input, an object of class Data
...	additional arguments

stopTrial,StoppingMaxPatients,ANY,ANY,ANY,Data-method

Stop based on maximum number of patients

Description

Stop based on maximum number of patients

Usage

```
## S4 method for signature 'StoppingMaxPatients,ANY,ANY,ANY,Data'
stopTrial(stopping, dose,
  samples, model, data, ...)
```

Arguments

stopping	The rule, an object of class Stopping
dose	the recommended next best dose
samples	the Samples object
model	The model input, an object of class Model
data	The data input, an object of class Data
...	additional arguments

`stopTrial,StoppingMinCohorts,ANY,ANY,ANY,Data-method`

Stop based on minimum number of cohorts

Description

Stop based on minimum number of cohorts

Usage

```
## S4 method for signature 'StoppingMinCohorts,ANY,ANY,ANY,Data'
stopTrial(stopping, dose,
  samples, model, data, ...)
```

Arguments

`stopping`	The rule, an object of class `Stopping`
`dose`	the recommended next best dose
`samples`	the `Samples` object
`model`	The model input, an object of class `Model`
`data`	The data input, an object of class `Data`
`...`	additional arguments

`stopTrial,StoppingMTDdistribution,numeric,Samples,Model,ANY-method`

Stop based on MTD distribution

Description

Stop based on MTD distribution

Usage

```
## S4 method for signature 'StoppingMTDdistribution,numeric,Samples,Model,ANY'
stopTrial(stopping,
  dose, samples, model, data, ...)
```

Arguments

`stopping`	The rule, an object of class `Stopping`
`dose`	the recommended next best dose
`samples`	the `Samples` object
`model`	The model input, an object of class `Model`
`data`	The data input, an object of class `Data`
`...`	additional arguments

stopTrial,StoppingPatientsNearDose,numeric,ANY,ANY,Data-method

Stop based on number of patients near to next best dose

Description

Stop based on number of patients near to next best dose

Usage

```
## S4 method for signature 'StoppingPatientsNearDose,numeric,ANY,ANY,Data'
stopTrial(stopping,
  dose, samples, model, data, ...)
```

Arguments

stopping	The rule, an object of class Stopping
dose	the recommended next best dose
samples	the Samples object
model	The model input, an object of class Model
data	The data input, an object of class Data
...	additional arguments

stopTrial,StoppingTargetBiomarker,numeric,Samples,DualEndpoint,ANY-method

Stop based on probability of targeting biomarker

Description

Stop based on probability of targeting biomarker

Usage

```
  ## S4 method for signature
## 'StoppingTargetBiomarker,numeric,Samples,DualEndpoint,ANY'
stopTrial(stopping,
  dose, samples, model, data, ...)
```

Arguments

stopping	The rule, an object of class Stopping
dose	the recommended next best dose
samples	the Samples object
model	The model input, an object of class Model
data	The data input, an object of class Data
...	additional arguments

`stopTrial,StoppingTargetProb,numeric,Samples,Model,ANY-method`
Stop based on probability of target tox interval

Description

Stop based on probability of target tox interval

Usage

```
## S4 method for signature 'StoppingTargetProb,numeric,Samples,Model,ANY'
stopTrial(stopping,
  dose, samples, model, data, ...)
```

Arguments

`stopping`	The rule, an object of class `Stopping`
`dose`	the recommended next best dose
`samples`	the `Samples` object
`model`	The model input, an object of class `Model`
`data`	The data input, an object of class `Data`
`...`	additional arguments

`summary,Simulations-method`
Summarize the simulations, relative to a given truth

Description

Summarize the simulations, relative to a given truth

Usage

```
## S4 method for signature 'Simulations'
summary(object, truth, target = c(0.2, 0.35), ...)
```

Arguments

`object`	the `Simulations` object we want to summarize
`truth`	a function which takes as input a dose (vector) and returns the true probability (vector) for toxicity
`target`	the target toxicity interval (default: 20-35%)
`...`	additional arguments affecting the summary produced.

Value

an object of class `Simulations-summary`

update,Data-method *Update method for the "Data" class*

Description

Add new data to the Data object

Usage

```
## S4 method for signature 'Data'
update(object, x, y, ID, ...)
```

Arguments

object	the old Data object
x	the dose level (one level only!)
y	the DLT vector (0/1 vector), for all patients in this cohort
ID	the patient IDs
...	Additional arguments to the call, or arguments with changed values. Use name = NULL to remove the argument name.

Value

the new Data object

&,Stopping,Stopping-method *The method combining two atomic stopping rules*

Description

The method combining two atomic stopping rules

Usage

```
## S4 method for signature 'Stopping,Stopping'
e1 & e2
```

Arguments

e1	First Stopping object
e2	Second Stopping object

Value

The StoppingAll object

`&,Stopping,StoppingAll-method`

The method combining an atomic and a stopping list

Description

The method combining an atomic and a stopping list

Usage

```
## S4 method for signature 'Stopping,StoppingAll'
e1 & e2
```

Arguments

e1	Stopping object
e2	StoppingAll object

Value

The modified StoppingAll object

`&,StoppingAll,Stopping-method`

The method combining a stopping list and an atomic

Description

The method combining a stopping list and an atomic

Usage

```
## S4 method for signature 'StoppingAll,Stopping'
e1 & e2
```

Arguments

e1	StoppingAll object
e2	Stopping object

Value

The modified StoppingAll object

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