Package 'tipmap'

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Type Package

Title Tipping Point Analysis for Bayesian Dynamic Borrowing

Version 0.1.7

Description Tipping point analysis for clinical trials that employ Bayesian dynamic borrowing via robust meta-analytic predictive (MAP) priors. Mainly an implementation of an approach proposed by Best and colleagues (2021) is provided <doi:10.1002/pst.2093>. Intended use is the planning, analysis and interpretation of extrapolation studies in pediatric drug development, but applicability is generally wider.

License GPL (>= 3)

Encoding UTF-8

Imports dplyr, ggplot2, RBesT

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

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Depends R (>= 3.5.0)

NeedsCompilation no

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R topics documented:

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  createNewTrialData   *Data on new trial in target population*

Description

Creates a vector containing data on the new trial in the target population. This may be hypothetical data in the planning stage.

Usage

```
createNewTrialData(nTotal, treatmentEffectEstimate, standardError)
```

Arguments

nTotal   The total sample size.

treatmentEffectEstimate
                  Treatment effect estimate.

standardError   Standard error of the treatment effect estimate.

Value

A numeric vector with data on the new trial, incl. quantiles of an assumed normal data likelihood.

See Also

[createPosteriorData](), [createTippingPointData]()

Examples

```
newTrialData <- createNewTrialData(
  nTotal = 30, treatmentEffectEstimate = 1.27,
  standardError = 0.95
)
```

---

createPosteriorData	*Creates posterior distributions for a range of weights on the informative component of the robust MAP prior*

Description

Returns a data frame containing the default quantiles of posterior mixture distributions generated with varying weights on the informative component of the MAP prior.

Usage

```
createPosteriorData(mapPrior, newTrialData, sigma, nullTreatmentEffect = 0)
```

Arguments

mapPrior
: A MAP prior containing information about the trial(s) in the source population, created using RBesT.

newTrialData
: A vector containing information about the new trial. See createNewTrialData().

sigma
: Standard deviation to be used for the weakly informative component of the MAP prior, recommended to be the unit-information standard deviation.

nullTreatmentEffect
: The mean of the robust component of the MAP prior. Defaults to 0.

Value

A data frame containing posterior distributions for varying weights

References

Best, N., Price, R. G., Pouliquen, I. J., & Keene, O. N. (2021). Assessing efficacy in important subgroups in confirmatory trials: An example using Bayesian dynamic borrowing. Pharm Stat, 20(3), 551–562. https://doi.org/10.1002/pst.2093

See Also

createNewTrialData, createPriorData, RBesT::automixfit

Examples

```
# create vector for new observations
newTrialData <- createNewTrialData(
  nTotal = 30, treatmentEffectEstimate = 1.27,
  standardError = 0.95
)

# read MAP prior created by RBesT
mapPrior <- loadTipmapData("tipmapPrior.rds")
```

```
# create posterior data
posteriorData <- createPosteriorData(
  mapPrior = mapPrior,
  newTrialData = newTrialData, sigma = 12
)
```

createPriorData   *Creates input data frame for construction of MAP prior*

Description

Assembling information from trials in the source population in a structured way (required as a pre-processing step for MAP prior creation).

Usage

```
createPriorData(
  studyLabel = NULL,
  nTotal,
  treatmentEffectEstimate,
  standardError
)
```

Arguments

studyLabel   An optional vector containing trial labels.

nTotal   A vector containing total sample sizes.

treatmentEffectEstimate

                    A vector containing treatment effect estimates.

standardError   A vector containing standard errors of the effect estimates.

Value

A data frame containing data on the trials in the source population.

See Also

[RBesT::gMAP](), [RBesT::automixfit]()

Examples

```
priorData <- createPriorData(
  nTotal = c(160, 240, 320),
  treatmentEffectEstimate = c(1.23, 1.40, 1.51),
  standardError = c(0.4, 0.36, 0.31)
)
```

---

createTippingPointData

Create data frame ready to use for tipping point analysis

Description

Combines new trial data created by `createTargetData()`, a posterior distribution created by `createPosteriorData()` and a robust MAP prior using `RBesT::automixfit()` and an optional meta-analysis created using the `meta` package into a data frame needed for the functions `tippingPointPlot()` and `getTippingPoint()`.

Usage

```
createTippingPointData(newTrialData, posterior, mapPrior, metaAnalysis = NULL)
```

Arguments

newTrialData	A data frame containing information about the target population. See `createNewTrialData()`.
posterior	A mixture combining MAP prior and target population. See `createPosteriorData()`.
mapPrior	A robust MAP prior created by `RBesT::automixfit()`.
metaAnalysis	A data frame containing a meta-analysis of trial(s) to be borrowed from. See `createPriorData()`.

Value

A data frame ready to be used for `tippingPointPlot()` and `getTippingPoint()`

See Also

[createNewTrialData](#), [createPosteriorData](#), [RBesT::automixfit](#), [tippingPointPlot](#), [getTippingPoint](#)

Examples

```
# specify new trial data
newTrialData <- createNewTrialData(nTotal = 30, treatmentEffectEstimate = 1.5, standardError = 2.1)

# read MAP prior
mapPrior <- loadTipmapData("tipmapPrior.rds")

# read posterior
posterior <- loadTipmapData("tipPost.rds")

tipdat <- createTippingPointData(
  newTrialData = newTrialData, posterior = posterior,
  mapPrior = mapPrior
)
```

---

defaultQuantiles   *Default quantiles*

Description

Default quantiles

Usage

defaultQuantiles

Format

An object of class numeric of length 13.

---

defaultWeights   *Default weights*

Description

Default weights

Usage

defaultWeights

Format

An object of class numeric of length 201.

---

getPosteriorByWeight   *Filter posterior by given weights*

Description

Returns quantiles for the given posterior filtered by specified weights.

Usage

getPosteriorByWeight(posterior, weight)

Arguments

posterior	The posterior to be filtered (see createPosteriorData()).
weight	The weight(s) to be filtered by.

Value

The filtered posterior values

See Also

[createPosteriorData](#)

Examples

```
getPosteriorByWeight(
  posterior = loadTipmapData("tipPost.rds"),
  weight = c(0.05, 0.1)
)
```

---

getTippingPoint	*Identify tipping point for a specific quantile.*

Description

Given a tipping point data frame, identifies the weight closest to tipping point for one or multiple specified quantiles.

Usage

```
getTippingPoint(tippingPointData, quantile, nullTreatmentEffect = 0)
```

Arguments

tippingPointData

  A data frame created by `createTippingPointData()`.

quantile   The quantile or quantiles of the tipping point. Possible values are 0.025, 0.05, 0.1, 0.2, 0.8, 0.9, 0.95 and 0.975.

nullTreatmentEffect

  The null treatment effect. Defaults to 0.

Value

The weight closest to the tipping point for the specified quantile

See Also

[createTippingPointData](#)

Examples

```
tipdat <- loadTipmapData("tipdat.rds")

getTippingPoint(tipdat, quantile = 0.025)
getTippingPoint(tipdat, quantile = c(0.025, 0.05, 0.1, 0.2), nullTreatmentEffect = 0.1)
```

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loadTipmapData   *Load pre-specified data sets for examples*

Description

Loads one of three pre-specified data sets ready to be used in functions

Usage

```
loadTipmapData(file)
```

Arguments

file   The dataset to be loaded

Value

A pre-saved dataset

Examples

```
loadTipmapData(file = "tipdat.rds")

loadTipmapData(file = "tipmapPrior.rds")

loadTipmapData(file = "tipPost.rds")
```

---

tipmapDarkBlue   *Custom dark blue*

Description

Custom dark blue

Usage

```
tipmapDarkBlue
```

Format

An object of class character of length 1.

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tipmapLightRed *Custom light red*

Description

Custom light red

Usage

```
tipmapLightRed
```

Format

An object of class `character` of length 1.

---

tippingPointPlot *Visualize tipping point analysis*

Description

Uses a data frame created by `createTippingPointData()` to visualize the tipping point analysis.

Usage

```
tippingPointPlot(
  tippingPointData,
  nullTreatmentEffect = 0,
  targetPopLabel = "Trial in target\n population",
  yRange = NULL,
  yBreaks = NULL,
  title = NULL,
  ylab = "Endpoint",
  xlab = "Weight on informative component",
  mapPriorLabel = "MAP \nprior",
  metaAnalysisLabel = "MA",
  legendLabel = "Posterior quantile"
)
```

Arguments

tippingPointData

A data frame containing tipping point data, generated by `createTippingPointData()`.

nullTreatmentEffect

The null treatment effect, determining where tipping points are calculated. Defaults to 0.

targetPopLabel   A label for the trial in the target population.

yRange   An optional argument specifying range of the y axis.

yBreaks   An optional vector specifying breaks on the y axis.

title   The plot title.

ylab   The label for the y axis. Defaults to "Endpoint".

xlab   The label for the x axis. Defaults to "Weight on informative component".

mapPriorLabel   The label for the MAP prior. Defaults to "MAP prior"

metaAnalysisLabel
                  An optional label for a meta-analysis (if included).

legendLabel   An optional label for the plot legend. Defaults to "Posterior quantile".

Value

A ggplot object of the tipping point plot

See Also

createTippingPointData

Examples

```
tipdat <- loadTipmapData("tipdat.rds")

tippingPointPlot(tipdat)
```

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