Package ‘prome’

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MeanHM

**Description**

Algorithms to implement the Bayesian methods to denoise the measurement errors in patient-reported outcome data with repeated measures. Also, two algorithms are included to discount the subgroup means or proportions for clinical studies with multiple subgroups.

**MeanHM**

Bayesian Hierarchical Model for Information Borrowing for Means

**Description**

To compute the mean values of subgroups based on a Bayesian hierarchical model.

**Usage**

MeanHM(x, group, sigma)

**Arguments**

- **x**
  - Numeric vector of observations for the subgroups.
- **group**
  - Group ID.
- **sigma**
  - Hyper-parameter. to be estimated or can be given.
Value

- `data`: data with estimates.
- `theta`: population mean.
- `sigma`: population standard deviation.

Examples

```r
x1 <- rnorm(100,2,1)
x2 <- rnorm(100,3,1.5)
x3 <- rnorm(100,4,1.9)
x <- c(x1,x2,x3)
group <- c(rep("grp1",length(x1)),
            rep("grp2",length(x2)),
            rep("grp3",length(x3)))
MeanHM(x,group,sigma=0.5)
```

memixed

Bayesian Hierarchical Model for RPO data with repeated measures

Description

A Bayesian hierarchical model to denoise PRO data using repeated measures.

Usage

```r
memixed(x0,x1,group,method="ATT")
ResponderAnalysis(x,mcid,type="absolute",conf.level=0.95)
```

Arguments

- `x0,x1`: Numeric vector/matrix of observations at T0 (baseline) and T1 (end point) of a study.
- `group`: group assignments. Current version support one or two groups only
- `method`: ATT: average treatment effect on treated; ATE: average treatment effect.
- `x`: An R object generated by memixed
- `mcid`: A threshold to define 'responder'
- `type`: Type of metric used for effectiveness evaluation. Can be 'absolute' changes, or 'relative' changes from baseline.
- `conf.level`: Confidence level of the credible interval
PropHM

Bayesian Hierarchical Model for Information Borrowing for Proportions

Description

To compute the proportions of the subgroups assuming the subgroups follow the same binomial distribution with parameter \( p \). A beta prior with parameters \( \alpha \) and \( \beta \) are used (\( \alpha + \beta = 2 \)).

Usage

\[
\text{PropHM}(x, n, \text{weights})
\]

Arguments

\begin{itemize}
\item \( x \) Numeric vector of events.
\item \( n \) Numberic vector of group sample sizes.
\item \( \text{weights} \) Numeric vector of weights (for the power prior method).
\end{itemize}
PropHM

Value

- 'data': data with estimates.
- 'alpha': parameter of the beta distribution.
- 'beta': parameter of the beta distribution.

Examples

```r
out <- PropHM(x=c(5,10,2),n=c(20,50,30))
```
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