Package ‘prome’

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Title Patient-Reported Outcome Data Analysis with Stan

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Description Algorithms and subroutines for patient-reported outcome data analysis.

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R topics documented:

<table>
<thead>
<tr>
<th>Topic</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>prome-package</td>
<td>2</td>
</tr>
<tr>
<td>bate</td>
<td>2</td>
</tr>
<tr>
<td>ex100x3</td>
<td>3</td>
</tr>
<tr>
<td>MeanHM</td>
<td>3</td>
</tr>
<tr>
<td>PropHM</td>
<td>4</td>
</tr>
</tbody>
</table>

Index 5
The 'prome' package.

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.

Bayesian Hierarchical Model for RPO data with repeated measures

Description

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

Usage

bate(x0,x1,group,z,x.range,...)
ResponderAnalysis(x,mcid,type="absolute",conf.level=0.95,show=TRUE)

Arguments

- x0, x1: Numeric vector/matrix of observations at T0 (baseline) and T1 (end point) of a study.
- z: covariates
- group: group assignments. Current version supports one or two groups only
- x.range: range of data 'x0' and 'x1'
- x: An R object generated by memixed
- mcid: A threshold to define 'responder'
- type: The type of responder analysis: absolute or relative changes
- conf.level: Confidence level of the credible interval
- show: control whether results should be displayed
- ...: Parameters ("adapt_delta","stepsize","max_treedepth") to improve model fitting/convergence.

Value

- 'xfit': fitted results using stan.
- 'mu.t0': baseline mean.
- 'sig.t0': baseline SD.
- 'sig.me': SD of measurement errors.
- 'mu.active': mean effect size of active treatment.
- 'sig.active': sd of effect size of active treatment.
- 'mu.sham': mean effect size of sham treatment.
- 'sig.sham': sd of effect size of sham treatment.
MeanHM

Examples

data(n100x3)
out1 <- bate(x0=ex100x3$w0,x1=ex100x3$w1,group=ex100x3$group)
out1
ResponderAnalysis(out1,mcid=1,type="abs")
out2 <- bate(x0=ex100x3$w0,x1=ex100x3$w1,group=ex100x3$group,
    control = list(adapt_delta = 0.8,
        stepsize = 5,
        max_treedepth = 10)
)
out2
ResponderAnalysis(out2,mcid=1,type="abs")
out <- out2
ResponderAnalysis(out,mcid=0.5,type="abs")
ResponderAnalysis(out,mcid=1,type="abs")
ResponderAnalysis(out,mcid=1.5,type="abs")
ResponderAnalysis(out,mcid=0.3,type="relative")
ResponderAnalysis(out,mcid=0.2,type="relative")
ResponderAnalysis(out,mcid=0.1,type="relative")

ex100x3  Sample PRO Data With Repeated Measures

Description

A simulated data set of patient-reported outcomes with repeated measures.

Format

A data frame with observations at baseline and at a follow-up time.

| w0       | matrix | measures at baseline |
| w1       | matrix | measures at follow-up time |
| group    | character | group assignment |

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,sigma)
Arguments

- **x**: Numeric vector of observations for the subgroups.
- **sigma**: Hyper-parameter. To be estimated or can be given.

Value

- '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 <- cbind(x1,x2,x3)
MeanHM(x, sigma=0.5)
```

---

**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*. The approach on partial pooling by Bob Carpenter has been used – "Hierarchical Partial Pooling for Repeated Binary Trials" [https://mc-stan.org/users/documentation/case-studies/pool-binary-trials.html](https://mc-stan.org/users/documentation/case-studies/pool-binary-trials.html)

Usage

```r
PropHM(x, n, kappa)
```

Arguments

- **x**: Numeric vector of events.
- **n**: Numeric vector of group sample sizes.
- **kappa**: \( \alpha + \beta > 1 \). Must be given if the number of subgroups is 2.

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))
```
Index

* datasets
  ex100x3, 3
bate, 2
ex100x3, 3
MeanHM, 3
n100x3 (ex100x3), 3
plot.memix (bate), 2
pratio (bate), 2
print.memix (bate), 2
prome (prome-package), 2
prome-package, 2
ProphM, 4
ResponderAnalysis (bate), 2