

Package ‘prome’

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Title Patient-Reported Outcome Data Analysis with Stan

Version 1.9.1.0

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

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prome-package *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.

bate *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

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

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

```
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	<i>Bayesian Hierarchical Model for Information Borrowing for Proportions</i>
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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>

Usage

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

Arguments

x Numeric vector of events.
 n Numeric vector of group sample sizes.
 kappa $kappa = \alpha + \beta > 1$. 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

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

`xover`*Bayesian analysis of 2x2 crossover trial data*

Description

A Bayesian hierarchical model to analysis data from 2x2 (AB/BA) crossover trials.

Usage

```
xover(group, y1, y2, y0, ...)
```

Arguments

<code>y0, y1, y2</code>	vectors of data from baseline, period 1, and period 2, respectively.
<code>group</code>	group or treatment sequence.
<code>...</code>	other parameters, i.e. 'control' for model fitting.

Value

- 'stat': summary statistics.
- 'best': estimates using Bayesian analysis.

Examples

```
xover(y0=rnorm(20, 34, 1.5), y1=rnorm(20, 30, 2),  
      y2=rnorm(20, 25, 1.5), group=round(runif(20)<0.5))
```

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