

# Package ‘prome’

February 24, 2022

**Title** Patient-Reported Outcome Data Analysis with Stan

**Version** 0.0.0.8

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

**License** MIT + file LICENSE

**Encoding** UTF-8

**RoxygenNote** 7.1.2

**Biarch** true

**Depends** R (>= 3.5.0)

**Imports** methods, Rcpp (>= 0.12.0), RcppParallel (>= 5.0.1), rstan (>= 2.18.1), rstantools (>= 2.1.1)

**LinkingTo** BH (>= 1.66.0), Rcpp (>= 0.12.0), RcppEigen (>= 0.3.3.3.0), RcppParallel (>= 5.0.1), rstan (>= 2.18.1), StanHeaders (>= 2.18.0)

**SystemRequirements** GNU make

**NeedsCompilation** yes

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promem-package      *The 'promem' package.*

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### 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.

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ex100x3      *Sample PRO Data With Repeated Measures*

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### 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

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MeanHM      *Bayesian Hierarchical Model for Information Borrowing for Means*

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### 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**

```
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)
```

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 memixed

*Bayesian Hierarchical Model for RPO data with repeated measures*


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**Description**

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

**Usage**

```
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

**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 <- memixed(x0=ex100x3$w0,x1=ex100x3$w1,group=ex100x3$group,method="att")
out1
ResponderAnalysis(out1,mcid=1,type="abs")
out2 <- memixed(x0=ex100x3$w0,x1=ex100x3$w1,group=ex100x3$group,method="ate")
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")

```

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 PropHM

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*Bayesian Hierarchical Model for Information Borrowing for Proportions*


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**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**

```
PropHM(x, n, weights)
```

**Arguments**

x	Numeric vector of events.
n	Numeric vector of group sample sizes.
weights	Numeric vector of weights (for the power prior method).

**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))
```

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