

Package ‘PRP’

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Title Bayesian Prior and Posterior Predictive Replication Assessment

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Author Yi Zhao [aut, cre],
Xiaoquan Wen [aut]

Maintainer Yi Zhao <zhayi@umich.edu>

Description Utilize the Bayesian prior and posterior predictive checking approach to provide a statistical assessment of replication success and failure. The package is based on the methods proposed in Zhao, Y., Wen X.(2021) <[arXiv:2105.03993](#)>.

License GPL-2

Encoding UTF-8

Imports mvtnorm, stats, graphics

LazyData true

RoxygenNote 7.1.1

Depends R (>= 2.10)

NeedsCompilation no

Repository CRAN

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mortality

Cardiovascular disease impact on the mortality of COVID-19

Description

This is a dataset containing several effect estimates and their standard errors for the impact of cardiovascular disease on the mortality of COVID-19 in the literature.

Usage

```
data("mortality")
```

Format

An object of class `data.frame` with 6 rows and 3 columns.

Examples

```
data("mortality")
```

posterior_prp

Posterior Predictive Replication p-value Calculation

Description

Posterior Predictive Replication p-value Calculation

Usage

```
posterior_prp(
  beta,
  se,
  L = 1000,
  r_vec = c(0, 8e-04, 0.006, 0.024),
  test = Q,
  print_test_dist = FALSE
)
```

Arguments

`beta` A vector, containing the estimates in the original study and the replication study.

`se` A vector, containing the standard errors of the estimates in the original study and the replication study.

`L` A value, determining the times of repeating simulation.

| | |
|-----------------|---|
| r_vec | A vector, defining the prior reproducible model. Each r value corresponds to a probability of sign consistency. |
| test | A function designed to calculate the test quantity, the default one is the Cochran's Q test statistics. |
| print_test_dist | A boolean, determining whether the simulated test statistics value difference will be plot as a histogram or not. Default is False. |

Value

A list with the following components:

| | |
|-----------------|---|
| grid | Detailed grid values for the hyperparameters. |
| test_statistics | The test statistics used in calculating the replication p-value. |
| n_sim | The L value. |
| test_stats_dif | The difference between the simulated test statistics quantity and the original value. |
| pvalue | The resulting posterior predictive replication p-value. |

Examples

```
data("mortality")
res = posterior_prp(beta = mortality$beta, se = mortality$se, test=Q)
names(res)
print(res$pvalue)
```

prior_prp

Prior Predictive Replication p-value Calculation

Description

Assessing the prior predictive distribution and calculating the replication p-value based on it.

Usage

```
prior_prp(
  beta,
  se,
  r_vec = c(0, 8e-04, 0.006, 0.024),
  test = "two_sided",
  report_PI = FALSE
)
```

Arguments

| | |
|-----------|--|
| beta | A 2-D vector, containing the estimates in the original study and the replication study. |
| se | A 2-D vector, containing the standard errors of the estimates in the original study and the replication study. |
| r_vec | A vector, defining the prior reproducible model. Each r value corresponds to a probability of sign consistency. |
| test | A string, determining which test statistics to utilize. If not specified, the default two-sided one will be used. |
| report_PI | A boolean, denoting whether the 95% predictive interval for the estimates be reported or not. This option is only valid for two-sided test statistics. The default is FALSE. |

Value

A list with the following components:

| | |
|---------------------|--|
| grid | The detailed grid values for the hyperparameters. |
| test_statistics | The test statistics used in calculating the replication p-value. |
| pvalue | The resulting prior predictive replicaition p-value. |
| predictive_interval | The 95% predictive interval if required. |

Examples

```
data("RPP_filtered")
attach(RPP_filtered)
rpp_pval<-sapply(1:nrow(RPP_filtered),function(x)
  prior_prp(beta=c(beta_orig[x], beta_rep[x]),se=c(se_orig[x], se_rep[x]))$pvalue)
```

| | |
|-----------|--|
| prob_to_r | <i>Sign consistency probability and the value for r parameter 1-1 transformation</i> |
|-----------|--|

Description

This function transforms the probability of simulated β_j having the same sign with the underlying true effect β_j to the corresponding heterogeneity r parameter value.

Usage

```
prob_to_r(p)
```

Arguments

`p` A value, the required probability of sign consistency.

Value

The corresponding heterogeneity parameter value.

| | |
|--------------|--------------------------|
| RPP_filtered | <i>Filtered RPP data</i> |
|--------------|--------------------------|

Description

This contains the RP:P data from the Open Science Collaboration project after filtering.

Usage

```
data("RPP_filtered")
```

Format

An object of class `data.frame` with 73 rows and 5 columns.

Examples

```
data("RPP_filtered")
```

| | |
|----------|--|
| severity | <i>Cardiovascular disease impact on the severe case rate of COVID-19</i> |
|----------|--|

Description

This is a dataset containing several effect estimates and their standard errors for the impact of cardiovascular disease on the severe case rate of COVID-19 in the literature.

Usage

```
data("severity")
```

Format

An object of class `data.frame` with 6 rows and 3 columns.

Examples

```
data("severity")
```

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