

Package ‘PRP’

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Title Bayesian Prior and Posterior Predictive Replication Assessment

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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](#)>.

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LazyData true

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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>
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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>
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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>
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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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