

Package ‘harmonicmeanp’

July 19, 2017

Type Package

Title Harmonic Mean p-Values and Model Averaging by Mean Maximum Likelihood

Version 1.0

Date 2017-07-19

Author Daniel J. Wilson

Maintainer Daniel Wilson <hmp.R.package@gmail.com>

Depends FMStable

Description The harmonic mean p-value (HMP) test simply and instantly combines p-values and corrects for multiple testing while controlling the family-wise error rate in a way that is more powerful than common alternatives including Bonferroni and Simes procedures, more stringent than controlling the false discovery rate, and is robust to positive correlations between tests and unequal weights. It is a multi-level test in the sense that a superset of one or more significant tests is almost certain to be significant and conversely when the superset is non-significant, the constituent tests are almost certain to be non-significant. It is based on MAMML (model averaging by mean maximum likelihood), a frequentist analogue to Bayesian model averaging, and is theoretically grounded in generalized central limit theorem.

License Unlimited

NeedsCompilation no

Repository CRAN

Date/Publication 2017-07-19 16:45:06 UTC

R topics documented:

| | |
|-----------------------|---|
| hmp-package | 2 |
| hmp.stat | 3 |
| mamml.stat | 4 |
| p.hmp | 5 |
| p.mamml | 6 |

| | |
|--------------|----------|
| Index | 8 |
|--------------|----------|

hmp-package

Harmonic mean p -values and model averaging by mean maximum likelihood

Description

The harmonic mean p -value (HMP) test simply and instantly combines p -values and corrects for multiple testing while controlling the family-wise error rate in a way that is more powerful than common alternatives including Bonferroni and Simes procedures, more stringent than controlling the false discovery rate, and is robust to positive correlations between tests and unequal weights. It is a multi-level test in the sense that a superset of one or more significant tests is almost certain to be significant and conversely when the superset is non-significant, the constituent tests are almost certain to be non-significant. It is based on MAMML (model averaging by mean maximum likelihood), a frequentist analogue to Bayesian model averaging, and is theoretically grounded in generalized central limit theorem.

Details

Package: hmp
Type: Package
Version: 1.0
Date: 2017-07-19
License: What license is it under?

The key function is `p.hmp` for combining p -values using the HMP

Author(s)

Daniel J. Wilson

Maintainer: Daniel Wilson <hmp.R.package@gmail.com>

References

Daniel J. Wilson (2017) The harmonic mean p -value and model averaging by mean maximum likelihood. In preparation.

See Also

Package FMStable

Examples

```
# Example: simulate from a non-uniform distribution mildly enriched for small  $p$ -values.  
# Compare the significance of the combined  $p$ -value for Bonferroni, Benjamini-Hochberg (i.e. Simes),  
# HMP and (equivalently) MAMML with 2 degrees of freedom.  
p = rbeta(1000,1/1.5,1)
```

```
min(p.adjust(p,"bonferroni"))
min(p.adjust(p,"BH"))
p.hmp(p)
p.mamml(1/p,2)
```

hmp.stat

Compute the harmonic mean p-value

Description

The harmonic mean p -value (HMP) is defined as the inverse of the (possibly weighted) arithmetic mean of the inverse p -values. When the HMP is small (e.g. less than 0.05), it is approximately well-calibrated, meaning that it can be directly interpreted. However, the function `p.hmp` calculates an exact p -value from the HMP and is preferred.

Usage

```
hmp.stat(p, w = NULL)
```

Arguments

| | |
|----------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>p</code> | A numeric vector of one or more p -values. Missing values (NAs) will cause a missing value to be returned. |
| <code>w</code> | An optional numeric vector of weights that can be interpreted as prior model probabilities for each of the alternative hypotheses represented by the individual p -values. If specified, it should sum to one. |

Value

The harmonic mean p -value is returned.

Author(s)

Daniel J. Wilson

References

Daniel J. Wilson (2017) The harmonic mean p -value and model averaging by mean maximum likelihood. In preparation.

See Also

`p.hmp`

Examples

```
p = rbeta(1000,1/1.5,1)
hmp.stat(p)
p.hmp(p)
```

`mamml.stat`*Compute the model-averaged mean maximized likelihood*

Description

The model-averaged mean maximized likelihood (MAMML) is defined as the (possibly weighted) arithmetic mean of the maximized likelihood ratios from a series of likelihood ratio tests comparing mutually exclusive alternative hypotheses with the same nested null hypothesis based on the exact same data.

Usage

```
mamml.stat(R, w = NULL)
```

Arguments

| | |
|---|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| R | A numeric vector of one or more maximized likelihood ratios. Missing values (NAs) will cause a missing value to be returned. |
| w | An optional numeric vector of weights that can be interpreted as prior model probabilities for each of the alternative hypotheses represented by the individual p -values. If specified, it should sum to one. |

Value

The model-averaged mean maximized likelihood ratio is returned.

Author(s)

Daniel J. Wilson

References

Daniel J. Wilson (2017) The harmonic mean p -value and model averaging by mean maximum likelihood. In preparation.

See Also

`p.mamml`

Examples

```
nu = 3
R = exp(0.5*rchisq(1000,nu))
mamml.stat(R)
p.mamml(R,nu)
```

p.hmp

Compute a combined p-value via the harmonic mean p-value

Description

The harmonic mean p -value (HMP) test combines p -values and corrects for multiple testing while controlling the family-wise error rate in a way that is more powerful than common alternatives including Bonferroni and Simes procedures, more stringent than controlling the false discovery rate, and is robust to positive correlations between tests and unequal weights. It is a multi-level test in the sense that a superset of one or more significant tests is almost certain to be significant and conversely when the superset is non-significant, the constituent tests are almost certain to be non-significant. It is based on MAMML (model averaging by mean maximum likelihood), a frequentist analogue to Bayesian model averaging, and is theoretically grounded in generalized central limit theorem.

Usage

```
p.hmp(p, w = NULL)
```

Arguments

| | |
|---|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| p | A numeric vector of one or more p -values. Missing values (NAs) will cause a missing value to be returned. |
| w | An optional numeric vector of weights that can be interpreted as prior model probabilities for each of the alternative hypotheses represented by the individual p -values. If specified, it should sum to one. |

Value

A combined p -value is returned.

Author(s)

Daniel J. Wilson

References

Daniel J. Wilson (2017) The harmonic mean p -value and model averaging by mean maximum likelihood. In preparation.

See Also

hmp.stat

Examples

```
# Example: simulate from a non-uniform distribution mildly enriched for small  $p$ -values.
# Compare the significance of the combined  $p$ -value for Bonferroni, Benjamini-Hochberg (i.e. Simes),
# HMP and (equivalently) MAMML with 2 degrees of freedom.
p = rbeta(1000, 1/1.5, 1)
min(p.adjust(p, "bonferroni"))
min(p.adjust(p, "BH"))
p.hmp(p)
p.mamml(1/p, 2)
```

| | |
|---------|-------------------------------------------------------------------------------------------------------|
| p.mamml | <i>Compute a combined p-value via the model-averaged mean maximized likelihood ratio</i> |
|---------|-------------------------------------------------------------------------------------------------------|

Description

The model averaging by mean maximum likelihood (MAMML) test combines likelihood ratio tests and corrects for multiple testing while controlling the family-wise error rate in a way that is more powerful than common alternatives including Bonferroni and Simes procedures, more stringent than controlling the false discovery rate, and is robust to positive correlations between tests and unequal weights. It is a frequentist analogue to Bayesian model averaging, is theoretically grounded in generalized central limit theorem, and motivates the simpler and better-calibrated harmonic mean p -value (HMP) test. The model-averaged mean maximized likelihood (MAMML) is defined as the (possibly weighted) arithmetic mean of the maximized likelihood ratios from a series of likelihood ratio tests comparing mutually exclusive alternative hypotheses with the same nested null hypothesis based on the exact same data.

Usage

```
p.mamml(R, nu, w = NULL)
```

Arguments

| | |
|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| R | A numeric vector of one or more maximized likelihood ratios. Missing values (NAs) will cause a missing value to be returned. |
| nu | A numeric scalar or vector for the degrees of freedom corresponding to all or each of the maximized likelihood ratios respectively. |
| w | An optional numeric vector of weights that can be interpreted as prior model probabilities for each of the alternative hypotheses represented by the individual p -values. If specified, it should sum to one. |

Value

The model-averaged mean maximized likelihood ratio is returned.

Author(s)

Daniel J. Wilson

References

Daniel J. Wilson (2017) The harmonic mean p -value and model averaging by mean maximum likelihood. In preparation.

See Also

mamml.stat, hmp.stat, p.hmp

Examples

```
nu = 3
R = exp(0.5*rchisq(1000,nu))
mamml.stat(R)
p.mamml(R,nu)
```

Index

*Topic `\textasciitildeMAMML`

`mamml.stat`, 4

`p.mamml`, 6

*Topic `\textasciitildehmp`

`hmp.stat`, 3

`p.hmp`, 5

`hmp (hmp-package)`, 2

`hmp-package`, 2

`hmp.stat`, 3

`mamml.stat`, 4

`p.hmp`, 5

`p.mamml`, 6