# Package 'HW.pval'

February 19, 2015

Type Package

Title Testing Hardy-Weinberg Equilibrium for Multiallelic Genes

Version 1.0

Date 2012-06-22

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**Description** HW.pval calculates plain and fully conditional root-mean-square, chi-square, and log likelihood-ratio P-values for the user-provided genotypic counts to be consistent with the Hardy-Weinberg equilibrium model. For further information on the Hardy-Weinberg equilibrium model and the pseudocode, refer to the paper ``Testing Hardy-Weinberg equilibrium with a simple root-mean-square statistic" by Rachel Ward.

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**Repository** CRAN

Date/Publication 2012-07-11 12:43:08

NeedsCompilation no

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HW.pval-package

#### Description

Tests Hardy-Weinberg equilibrium for a multiallelic gene by displaying plain and/or fully conditional P-values.

#### Details

| Package: | HW.pval    |
|----------|------------|
| Type:    | Package    |
| Version: | 1.0        |
| Date:    | 2012-06-22 |
| License: | GPL-3      |

Tests a matrix of observed genotype counts for a multiallelic gene and returns plain and/or fully conditional P-values. The P-values are found by running the function HW.pval(). The P-values for the following test statistics are returned: Root Mean Square, Chi Square, and the Log Likelihood Ratio.

The matrix of observed genotype counts is a matrix of dimension r by r, where r is the number of alleles A\_1, A\_2,...,A\_r. The (j,k)-th entry of the matrix is the observed number of genotypes  $(A_j,A_k)$ .

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#### References

"Testing Hardy-Weinberg equilibrium with a simple root-mean-square statistic" by Rachel Ward.

#### See Also

HW.pval

create.model Creating the Hardy-Weinberg model distribution from a given lowertriangular array of genotype counts

### HW.cond

#### Description

Creates maximum-likelihood Hardy-Weinberg equilibrium model distribution from the observed genotype count matrix.

# Usage

```
create.model(observed, n)
```

#### Arguments

| observed | The genotype count matrix from which the Hardy-Weinberg equilibrium model distribution is created |
|----------|---|
| n        | Total number of genotypes.  |

#### Details

This function is called by HW.pval() and HW.plain() to create a model distribution.

#### Author(s)

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#### References

"Testing Hardy-Weinberg equilibrium with a simple root-mean-square statistic," by Rachel Ward

#### See Also

HW.pval, HW.plain

HW.cond

Computing the fully conditional P-value for a given lower-triangular array of genotype counts

# Description

Computes the fully conditional P-Value associated to the provided lower-triangular array of genotype counts to be consistent with the Hardy-Weinberg equilibrium model

#### Usage

```
HW.cond(obs_dist, model_dist, rms, chisq, gsq, T, n)
```

#### Arguments

| obs_dist   | Observed genotype count matrix   |
|------------|--|
| model_dist | Hardy-Weinberg equilibrium model distribution for the observed genotype count matrix determined in HW.pval(). Calculated via the function create.model() |
| rms        | Root-Mean-Square test statistic determined in HW.pval()  |
| chisq      | Chi-Square test statistic determined in HW.pval()  |
| gsq        | Log Likelihood-Ratio test statistic determined in HW.pval()  |
| т          | Number of Monte-Carlo simulations desired  |
| n          | Total number of observed genotypes   |

# Details

Determines the fully-conditional P-value via Monte-Carlo simulation as described in Algorithm 5.2 of the referenced paper

Returns fully conditional P-values associated to the root-mean-square, chi-square, and log likelihoodratio statistics.

### Author(s)

Shuhodeep Mukherji <deep.mukherji@utexas.edu>

#### References

"Testing Hardy-Weinberg equilibrium with a simple root-mean-square statistic" by Rachel Ward.

#### See Also

HW.pval, create.model, test.rms, test.chisq, and test.gsq

HW.plain

Computing the plain P-Value for a given lower-triangular array of genotype counts

# Description

Computes the plain P-Value associated to the provided lower-triangular array of genotype counts to be consistent with the Hardy-Weinberg equilibrium model

# Usage

HW.plain(model\_dist, rms, chisq, gsq, T, n)

# HW.pval

#### Arguments

| model_dist | Model distribution for the input genotype count matrix determined in HW.pval(). Calculated via the function create.model() |
|------------|--|
| rms        | Root Mean Square test statistic determined in HW.pval()  |
| chisq      | Chi-Square test statistic determined in HW.pval()  |
| gsq        | Log Likelihood-Ratio test statistic determined in HW.pval()  |
| Т          | Number of Monte-Carlo simulations desired.   |
| n          | Total count of observed genotypes  |

#### Details

Determines the plain P-value via Monte-Carlo simulation as described in Algorithm 5.1 of the referenced paper

Returns plain P-values associated to the root-mean-square, chi-square, and log likelihood-ratio statistics.

### Author(s)

Shubhodeep Mukherji <deep.mukherji@utexas.edu>

#### References

"Testing Hardy-Weinberg equilibrium with a simple root-mean-square statistic" by Rachel Ward.

#### See Also

HW.pval, create.model, test.rms, test.chisq, and test.gsq

HW.pval

Testing Hardy-Weinberg Equilibrium for Multiallelic Genes

#### Description

Tests Hardy-Weinberg equilibrium for a multiallelic gene by displaying plain and/or fully conditional P-values.

#### Usage

```
HW.pval(genotype_count, num_simulations = 10000, type = "both")
```

#### Arguments

| genotype_count  | A lower triangular matrix of observed genotype counts.                        |
|-----------------|---|
| num_simulations | 3   |
|                 | Number of Monte-Carlo simulations desired. The default is 10,000.             |
| type            | Determines type of p-value returned. Choices are "plain", "cond", and "both". |

#### Details

The observed genotype counts matrix does not have to be lower triangular, but the code is designed to only read the lower triangle. Thus, the entries in the upper triangle are irrelevant.

Determines the model distribution for the matrix of observed genotype counts by calling the function create.model() and calculates the empirical test statistics between the observed counts and the model counts. The test statistics are determined by calling the functions test.rms(), test.chisq(), and test.gsq(). Then, depending on the type of P-value requested, this function calls on HW.plain() and/or HW.cond() to return the requested P-values, which are calculated by Monte-Carlo simulations.

#### Value

Returns plain and/or fully conditional P-values associated to the Root Mean Square, Chi-Square, and Log Likelihood-Ratio statistics.

#### Note

Currently, this function will work properly only if the input genotype\_count is a matrix or array.

#### Author(s)

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#### References

"Testing Hardy-Weinberg equilibrium with a simple root-mean-square statistic" by Rachel Ward.

#### See Also

HW.pval-package, HW.plain, HW.cond, create.model, test.rms, test.chisq, and test.gsq.

#### Examples

```
gen <- cbind(c(0,3,5,3),c(0,1,18,7),c(0,0,1,5),c(0,0,0,2))
print(gen)</pre>
```

#The upper triangle is unimportant so it is filled with 0's in this case

HW.pval(gen,num\_simulations=10000,type="both")

test.chisq

#### Description

Calculates the Chi-Square test statistic between a lower-triangular matrix of genotypic counts and associated Hardy-Weinberg equilibrium model counts

#### Usage

test.chisq(observed, expected)

# Arguments

| observed | Matrix of observed genotypic counts |
|----------|-------------------------------------|
| expected | Matrix of model genotypic counts    |

#### Details

Called on by HW.pval(), HW.plain(), and HW.cond().

#### Author(s)

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#### References

"Testing Hardy-Weinberg equilibrium with a simple root-mean-square statistic," by Rachel Ward

# See Also

HW.pval, HW.plain, and HW.cond.

test.gsq

Computing the log likelihood-ratio test statistic

# Description

Calculates the Log Likelihood-Ratio test statistic between a lower-triangular matrix of genotypic counts and associated Hardy-Weinberg equilibrium model counts

#### Usage

test.gsq(observed, expected)

#### test.rms

#### Arguments

| observed | Matrix of observed genotypic counts |
|----------|-------------------------------------|
| expected | Matrix of model genotypic counts    |

### Details

Called on by HW.pval(), HW.plain(), and HW.cond().

#### Author(s)

Shubhodeep Mukherji <deep.mukherji@utexas.edu>

#### References

"Testing Hardy-Weinberg equilibrium with a simple root-mean-square statistic," by Rachel Ward

#### See Also

HW.pval, HW.plain, and HW.cond.

test.rms

Computing the root-mean-square test statistic

#### Description

Calculates the Root Mean Square test statistic between a lower-triangular matrix of genotypic counts and associated Hardy-Weinberg equilibrium model counts

# Usage

```
test.rms(observed, expected)
```

# Arguments

| observed | Matrix of observed genotypic counts |
|----------|-------------------------------------|
| expected | Matrix of model genotypic counts    |

# Details

Called on by HW.pval(), HW.plain(), and HW.cond().

#### Author(s)

Shubhodeep Mukherji <deep.mukherji@utexas.edu>

# References

"Testing Hardy-Weinberg equilibrium with a simple root-mean-square statistic," by Rachel Ward

test.rms

# See Also

HW.pval, HW.plain, and HW.cond.

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