Package ‘GWASExactHW’

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Type Package

Title Exact Hardy-Weinburg Testing for Genome Wide Association Studies

Version 1.2

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Description Exact Hardy-Weinburg testing (using Fisher's test) for SNP genotypes
as typically obtained in a Genome Wide Association Study (GWAS).

License GPL-3

LazyLoad yes

Repository CRAN

NeedsCompilation yes

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Contents

`GWASExactHW-package` *Exact Hardy-Weinburg testing for Genome Wide Association Studies*

Description

This package contains a function to do exact Hardy-Weinburg testing (using Fisher’s test) over all or a selection of SNP genotypes as typically obtained in a Genome Wide Association Study (GWAS).

Details

Package:	GWASExactHW
Type:	Package
Version:	1.01
Date:	2013-01-04
License:	GNU
LazyLoad:	yes

The function HWExact runs fast Hardy-Weinburg testing for a set of bi-alleleic genotypes.

Author(s)

Ian Painter, University of Washington

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References

Wigginton, JE, Cutler, DJ, and Abecasis, GR (2005) A Note on Exact Tests of Hardy-Weinberg Equilibrium. American Journal of Human Genetics. 76

`HWExact` *Function to calculate Hardy-Weinburg exact p-values*

Description

This function calculates Hardy-Weinburg (Fisher's) exact p-values for GWAS SNP data.

Usage

```
HWExact(GenotypeCounts)
```

Arguments

`GenotypeCounts`	A dataframe of genotype counts, with columns called `nAA`, `nAa` and `naa`, one row for each SNP.

Value

A vector of exact p-values.

Note

This function uses a C function `SNPHWE.c` written by Jan Wigginton as described in the above reference.

Author(s)

Ian Painter

References

Wigginton, JE, Cutler, DJ, and Abecasis, GR (2005) A Note on Exact Tests of Hardy-Weinberg Equilibrium. American Journal of Human Genetics. 76

Examples

```
pA<- runif(1)
pAA<- pA^2
pAa<- 2*pA*(1-pA)
paa<- (1-pA)^2

counts<- rmultinom(1000, 3000, c(pAA, pAa, paa) )
genotypes<- data.frame(nAA = counts[1,], nAa = counts[2,], naa = counts[3,])
hwPvalues<- HWExact(genotypes)
```

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