

# Package ‘GWASExactHW’

January 20, 2025

**Type** Package

**Title** Exact Hardy-Weinburg Testing for Genome Wide Association Studies

**Version** 1.2

**Date** 2024-03-11

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**Maintainer** Stephanie Gogarten <sdmorris@uw.edu>

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

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## 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-Weinberg testing for a set of bi-allelic 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

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HWExact

*Function to calculate Hardy-Weinberg exact p-values*

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**Description**

This function calculates Hardy-Weinberg (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<- HWEexact(genotypes)
```

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