Package ‘GWASExactHW’

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Title 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).
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GWASExactHW-package

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

Author(s)
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References

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


Examples

```r
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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