

Package ‘LRTH’

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Type Package

Title A Likelihood Ratio Test Accounting for Genetic Heterogeneity

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Description R code of a likelihood ratio test for genome-wide association under genetic heterogeneity.

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Description

R code of a likelihood ratio test for genome-wide association under genetic heterogeneity.

Author(s)

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References

Qian M., Shao Y., 2013. A Likelihood Ratio Test for Genome-Wide Association under Genetic Heterogeneity. *Annals of Human Genetics*, 77(2): 174-182.

Zhou H., Pan W., 2009. Binomial Mixture Model-based Association Tests under Genetic Heterogeneity. *Annals of Human Genetics*, 73(6): 614-630.

LRT_H

The Function for Likelihood Ratio Test Accounting for Genetic Heterogeneity

Description

It gives the asymptotic p-value of the LRT_H test.

Usage

LRT_H(x, y)

Arguments

x a n x 1 vector of genotypic score for SNP (i.e. 0, 1 or 2, the number of minor alleles of a SNP); n is the number of observations.

y a n x 1 vector of disease status; case/xcontrol: 1/0; ; n is the number of observations.

Details

Missing values in either x or y (i.e. genotype or disease status) will be removed.

Value

The asymptotic p-value of LRT_H test.

Author(s)

Zhiyuan (Jason) Xu and Wei Pan

References

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Examples

```
y = c(rep(1,500),rep(0,500))
x1 = sample(c(0,1,2),500,replace=TRUE,prob = c(0.64,0.32,0))
x2 = sample(c(0,1,2),500,replace=TRUE,prob = c(0.49,0.42,0))
x = c(x1,x2)
LRT_H(x,y)
```

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*Topic **Likelihood ratio test, genetic heterogeneity**

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