Package ‘LRTH’

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LRTH-package

A Likelihood Ratio Test Accounting for Genetic Heterogeneity

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

Author(s)
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### LRT_H

The Function for Likelihood Ratio Test Accounting for Genetic Heterogeneity

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**Description**

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

**Usage**

\[ \text{LRT}_H(x, y) \]

**Arguments**

- \( x \) a \( n \times 1 \) 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 \( n \times 1 \) vector of disease status; case/control: 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**


Examples

```r
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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