# Package: gLRTH (via r-universe)

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**Type** Package

**Title** Genome-Wide Association and Linkage Analysis under Heterogeneity

**Version** 0.2.0

**Description** Likelihood ratio tests for genome-wide association and genome-wide linkage analysis under heterogeneity.

**Depends** R (>= 3.4.0)

**License** GPL-3

**LazyData** true

**Suggests** knitr, rmarkdown

**RoxygenNote** 6.0.1

**NeedsCompilation** no

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**Repository** CRAN

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## Contents

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| gLRTH_A | *The function for the likelihood ratio test for genome-wide association under genetic heterogeneity with genotype frequencies as input values* |
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### Description

We consider a binary trait and focus on detecting association with disease at a single locus with two alleles $A$ and $a$. The likelihood ratio test is based on a binomial mixture model of $J$ components $(J \geq 2)$ for diseased cases:

$$P_\eta(X_D = g) = \sum_{j=1}^{J} \alpha_j B_2(g, \theta_j), \ g = 0, 1, 2, \ J \geq 2, \ \sum_{j=1}^{J} \alpha_j = 1, \ \theta_j, \alpha_j \in (0, 1),$$

where $\eta = (\eta_j)_{j \leq J}, \eta_j = (\theta_j, \alpha_j)^T, j = 1, \ldots, J, B_2(g, \theta_j)$ is the probability mass function for a binomial distribution $X \sim Bin(2, \theta_j)$, and $\theta_i = \theta_j$ if and only if $i = j$. $\theta_j$ is the probability of having the allele of interest on one chromosome for a subgroup of case $j$. In particular, $J$ is likely to be quite large for many of the complex disease with genetic heterogeneity. Note that the LRT-H can be applied to association studies without the need to know the exact value of $J$ while allowing $J \geq 2$.

### Usage

```
gLRTH_A(n0, n1, n2, m0, m1, m2)
```

### Arguments

| | |
|---|---|
| n0 | AA genotype frequency in case |
| n1 | Aa genotype frequency in case |
| n2 | aa genotype frequency in case |
| m0 | AA genotype frequency in control |
| m1 | Aa genotype frequency in control |
| m2 | aa genotype frequency in control |

### Value

The test statistic and asymptotic p-value for the likelihood ratio test for GWAS under genetic heterogeneity

### Author(s)

Xiaoxia Han and Yongzhao Shao

### 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.

### Examples

```
gLRTH_A(n0=2940, n1=738, n2=53, m0=3601, m1=1173, m2=117)
```

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| gLRTH_L | *The function for the likelihood ratio test for genetic linkage under transmission heterogeneity* |

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### Description

We consider a binary trait and focus on detecting a transmission heterogeneity at a single locus with two alleles $A$ and $a$. We consider independent families each with one marker homozygous ($AA$) parent, one marker heterozygous parent ($Aa$) and two diseased children. This likelihood ratio test is to test transmission heterogeneity of preferential transmission of marker allele "a" to an affected child based on a binomial mixture model with $J$ components ($J \geq 2$),

$$P_\eta(X_D = g) = \sum_{j=1}^{J} \alpha_j B_2(g, \theta_j), \ g = 0, 1, 2, \ J \geq 2, \ \sum_{j=1}^{J} \alpha_j = 1, \ \theta_j, \alpha_j \in (0, 1),$$

where $\eta = (\eta_j)_{j \leq J}, \eta_j = (\theta_j, \alpha_j)^T, j = 1, \ldots, J, B_2(g, \theta_j)$ is the probability mass function for a binomial distribution $X \sim Bin(2, \theta_j)$, and $\theta_i = \theta_j$ if and only if $i = j$. $\theta_j$ is the probability of transmission of the allele of interest in a subgroup of families $j$. In particular, $J$ is likely to be quite large for many of the complex disease under transmission heterogeneity. Note that this LRT can be applied to genome-wide linkage analysis without the need to know the exact value of $J$ while allowing $J \geq 2$.

### Usage

```
gLRTH_L(n0, n1, n2)
```

### Arguments

| | |
|---|---|
| n0 | Number of affected sibling pairs both of which inherited A from their heterozygous parent Aa |
| n1 | Number of affected sibling pairs which one inherited A and the other inherited a from their heterozygous parent Aa |
| n2 | Number of affected sibling pairs both of which inherited a from their heterozygous parent Aa |

### Value

The test statistic and asymptotic p-value for the likelihood ratio test for linkage analysis under genetic heterogeneity

### Author(s)

Xiaoxia Han and Yongzhao Shao

## References

Shao Y. (2014) Linkage analysis, originally published in Encyclopedia of Quantitative Risk Analysis and Assessment, John Wiley & Sons, Ltd, USA, 2008, and republished in Wiley StatsRef: Statistics Reference Online 2014.

## Examples

```
gLRTH_L(n0=100, n1=70, n2=30)
```

# Index