Package ‘gLRTH’

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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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R topics documented:

gLRTH_A ................................................................. 2
gLRTH_L ................................................................. 3

Index 5
The function for the likelihood ratio test for genome-wide association under genetic heterogeneity with genotype frequencies as input values

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

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

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


Examples

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

gLRTH_A, 2

gLRTH_L, 3