Package 'gLRTH'

October 13, 2022

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

Date/Publication 2018-01-22 13:34:44 UTC

R topics documented:

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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*

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 $i = j$. θ_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)
```

| gLRTH_L | *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 $i = j$. θ_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)
```

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