Package 'FastMtQTL'

August 24, 2020

Type Package

Title Regression based fast multi-trait genome-wide QTL analysis using
the properties of multivariate normal distribution

Version 0.01

Date 2020-08-24

Author Md. Jahangir Alam and Md. Nurul Haque Mollah

Maintainer Md. Jahangir Alam <jahangir_statru63@yahoo.com>

Description Multi-trait QTL analysis using the properties of multivariate normal distribution.

Depends R (>= 3.5)

Imports qtl (>= 1.39-5)

License GPL (>= 2.10)

Encoding UTF-8

LazyData true

NeedsCompilation no

R topics documented:

---

bcMVNmtQTL   *Regression based fast multi-trait genome-wide QTL analysis using the*
                       properties of multivariate normal (MVN) distribution.

Description

This function calculates the LOD (log of odds) for multi-trait QTL analysis using the properties of multivariate normal distribution.

Usage

```
bcMVNmtQTL(inData, phenoCols, Chrs, markerInterval=1.01)
```

Arguments

`inData`	Input data set for multi-trait QTL analysis.
`phenoCols`	Column numbers in the phenotype matrix which should be used in the analysis.
`Chrs`	Vector of chromosome number(s) for which LOD scores should be calculated.
`markerInterval`	Maximum distance (in cM) between positions at which the genotype probabilities are calculated, though for step = 0, probabilities are calculated only at the marker locations.

Value

It will return a dataframe with the values of log of odds (LOD) statistic for multi-trait QTL mapping.

Author(s)

Md. Jahangir Alam <jahangir_statru63@yahoo.com>

Examples

```
#bcMVNmtQTL(inData=SimData,phenoCols=c(1:5),Chrs=Chrs=c(1:13))
```

Index