

# Package ‘rmtQTL’

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**Type** Package  
**Title** Multi-trait QTL analysis using robust multivariate techniques  
**Version** 0.01  
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**Description** Multi-trait QTL analysis.  
**Depends** R (>= 4.0)  
**Imports** qtl (>= 1.39-5)  
**License** GPL (>= 2.10)  
**Encoding** UTF-8  
**LazyData** true  
**NeedsCompilation** no

## R topics documented:

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bcMVNmtQTL	<i>Multivariate normal (MVN) distribution based multi-trait QTL analysis.</i>
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## Description

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

## Usage

```
bcMVNmtQTL(inData, phenoCols=1, Chrs)
```

**Arguments**

inData	Input data set along with genotype probabilities 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.

**Value**

It will return a dataframe with the values of chromosome number, marker position (in cM) and LOD statistic for multi-trait QTL mapping.

**Author(s)**

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**Examples**

```
library(qtl)
library(rmtQTL)
data(bcSimData)
multGenoProb <- calc.genoprob(bcSimData, step=1, stepwidth="max")
LODstat<-bcMVNmtQTL(inData=multGenoProb, phenoCols=c(1:3), Chrs=c(1:13))
```

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bcRobMVNmtQTL	<i>Multivariate normal (MVN) distribution based multi-trait QTL analysis.</i>
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**Description**

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

**Usage**

```
bcRobMVNmtQTL(inData, phenoCols=1, Chrs, Beta=0)
```

**Arguments**

inData	Input data set for multi-trait QTL analysis.
phenoCols	A numeric value of column number or a vector of column numbers in the phenotype matrix which should be used in the analysis. Default value is phenoCols=1
Chrs	Vector of chromosome number(s) for which LOD scores should be calculated.
Beta	Tuning parameter. Default value is 0 for which the estimates reduce to the classical estimates.

**Value**

It will return a dataframe with the values of chromosome number, marker position (in cM) and robust LOD statistic for multi-trait QTL mapping.

**Author(s)**

Md. Jahangir Alam <jahangir\_statru63@yahoo.com>

**Examples**

```
library(qtl)
library(rmtQTL)
data(bcSimData)
multGenoProb <- calc.genoprob(bcSimData, step=1, stepwidth="max")
LODstat<-bcRobMVNmtQTL(inData=multGenoProb, phenoCols=c(1:3), Chrs=c(1:13), Beta=0.001)
```

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bcSimData

*Simulated multi-trait QTL dataset*

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**Description**

A Simulated dataset of a QTL experiment with multiple traits for backcross (BC) population.

**Usage**

```
data(bcSimData)
```

**Examples**

```
data(bcSimData)
summary(bcSimData)
```

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