Package ‘GSMX’

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Type Package
Title Multivariate Genomic Selection
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Imports stats, MASS

Description Estimating trait heritability and handling overfitting. This package includes a collection of functions for (1) estimating genetic variance-covariances and calculate trait heritability; and (2) handling overfitting by calculating the variance components and the heritability through cross validation.

 Depends R (>= 3.0.0)
License GPL (>= 2)

LazyLoad no
NeedsCompilation no
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R topics documented:

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Description

The package GSMX consists of the functions to estimate genetic variance-covariances and calculate trait heritability, and handle overfitting by calculating the variance components and the heritability through cross validation.

Details

Package: GSMX
Type: GSMX
Version: 1.3
Date: 2017-10-16
License: GPL>=2

Control overfitting heritability in genomic selection through cross validation

Genomic selection (GS) is a form of marker-assisted selection (MAS) where markers across the entire genome are used such that all quantitative trait loci (QTL) are in linkage disequilibrium with at least one marker. Increased number of markers and their density along with increased sample size improve the resolution of QTL mapping, and therefore improve estimated breeding values and genetic gain. However, the genetic variance-covariances were estimated from training samples using a large number of markers including many trait-irrelevant markers, and then being used for calculating trait heritability, leading to severe overfitting. In this package, we developed an algorithm to handle such overfitting by calculating the variance components and the heritability through cross validation. This method provides an accurate estimation of trait heritability (equivalent to trait predictability), and objectively reflects the level of applicability of the GS models to other breeding materials.

Author(s)

Zhenyu Jia

References

Control overfitting heritability in genomic selection through cross validation

Examples

library(GSMX)
data(pseudo.kin)
gsm

```r
data(pseudo.data)
myfit=gsm(pseudo.data, pseudo.kin, nfold=5)
```

---

**gsm**

*Estimate genetic variance-covariances and calculate heritability and predictability using cross validation*

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**Description**

The function estimate genetic variance-covariances and calculate heritability and predictability for multivariate genetic selection using cross validation

**Usage**

```r
gsm(mydata, mykin, nfold)
```

**Arguments**

- **mydata**: dataset with two traits
- **mykin**: kinship matrix
- **nfold**: number of folds for cross validation

**Value**

- **res**: Results

**Examples**

```r
library(gsmX)
data(pseudo.kin)
data(pseudo.data)
myfit=gsm(pseudo.data, pseudo.kin, nfold=5)
```

---

**pseudo.data**

*Pseudo dataset*

---

**Description**

Simulated dataset

**Examples**

```r
library(gsmX)
data(pseudo.data)
length(pseudo.data)
```
Description

Simulated kinship matrix

Examples

library(GSMX)
data(pseudo.kin)
dim(pseudo.kin)
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