

Package: GSMX (via r-universe)

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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

Repository CRAN

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GSMX-package

Multivariate Genomic Selection

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)

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References

Control overfitting heritability in genomic selection through cross validation

Examples

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

gsm	<i>Estimate genetic variance-covariances and calculate heritability and predictability using cross validation</i>
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Description

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

Usage

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

Arguments

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

Value

res	Results
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Examples

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

pseudo.data	<i>Pseudo dataset</i>
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Description

Simulated dataset

Examples

```
library(GSMX)
data(pseudo.data)
length(pseudo.data)
```

`pseudo.kin`*Pseudo kinship matrix*

Description

Simulated kinship matrix

Examples

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

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