Package ‘SEA’

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Title Segregation Analysis
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Description A few major genes and a series of polygene are responsive for each quantitative trait. Major genes are individually identified while polygene is collectively detected. This is mixed major genes plus polygene inheritance analysis or segregation analysis (SEA). In the SEA, phenotypes from a single or multiple bi-parental segregation populations along with their parents are used to fit all the possible models and the best model of the trait for population phenotypic distributions is viewed as the model of the trait. There are fourteen types of population combinations available. Zhang Yuan-Ming, Gai Jun-Yi, Yang Yong-Hua (2003, <doi:10.1017/S0016672303006141>).
Depends shiny,MASS,doParallel,foreach,methods
Imports KScorrect,utils,stats,grDevices,graphics,data.table
License GPL (>= 2)
NeedsCompilation no
Repository CRAN
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R topics documented:

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### Description

A few major genes and a series of polygene are responsive for each quantitative trait. Major genes are individually identified while polygene is collectively detected. This is mixed major genes plus polygene inheritance analysis or segregation analysis (SEA). In the SEA, phenotypes from a single or multiple bi-parental segregation populations along with their parents are used to fit all the possible models and the best model for population phenotypic distributions is viewed as the model of the trait. There are fourteen types of population combinations available. Zhang Yuan-Ming, Gai Jun-Yi, Yang Yong-Hua (2003, <doi:10.1017/S0016672303006141>), and Wang Jing-Tian, Zhang Ya-Wen, Du Ying-Wen, Ren Wen-Long, Li Hong-Fu, Sun Wen-Xian, Ge Chao, and Zhang Yuan-Ming (2022, <doi:10.3724/SP.J.1006.2022.14088>)
Details

Package: SEA
Type: Package
Version: 2.0.1
Date: 2022-03-28
Depends: shiny, MASS, doParallel, foreach
Imports: KScorrect, kolmim, utils, stats, grDevices, graphics, data.table
License: GPL(>=2)
LazyLoad: yes

Users can use 'SEA()' start the GUI.

Author(s)

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

References


Examples

```r
## Not run: SEA()
```

BCexdata

```r
BC population dataset
```

Description

The phenotype of BC population.

Usage

```r
data(BCexdata)
```

Details

Dataset input of BCFun function.

Author(s)

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>
BCFxdata \hspace{1cm} BCF population dataset

Description

The phenotype of BCF population.

Usage

data(BCFxdata)

Details

Dataset input of BCFFun function.

Author(s)

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

BCFFun \hspace{1cm} segregation analysis of BCF population

Description

Phenotypic observations in BCF population have often been used to identify mixed major-gene plus polygene inheritance model for quantitative traits in plants.

Usage

BCFFun(df,model,BCFtext2)

Arguments

df \hspace{1cm} phenotype matrix.
model \hspace{1cm} genetic model.
BCFtext2 \hspace{1cm} number of plants measured in each family.

Author(s)

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

Examples

BCF=data(BCFxdata)
BCFFun(BCFxdata,"0MG",1)
**BCFun**

*segregation analysis of BC population*

---

**Description**

Phenotypic observations in BC population have often been used to identify mixed major-gene plus polygene inheritance model for quantitative traits in plants.

**Usage**

```r
BCFun(df, model)
```

**Arguments**

- `df`: phenotype matrix.
- `model`: genetic model.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

**Examples**

```r
BC = data(BCexdata)
BCFun(BCexdata, "0MG")
```

---

**BILexdata**

*BIL population dataset*

---

**Description**

The phenotype of BIL population.

**Usage**

```r
data(BILexdata)
```

**Details**

Dataset input of BILFun function.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>
**BILFun**  
*segregation analysis of BIL population*

**Description**
Phenotypic observations in BIL population have often been used to identify mixed major-gene plus polygene inheritance model for quantitative traits in plants.

**Usage**
BILFun(df, model, BILfr)

**Arguments**
- `df`: phenotype matrix.
- `model`: genetic model.
- `BILfr`: BIL type.

**Author(s)**
Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

**Examples**
```
BIL=data(BILexdata)
BILFun(BILexdata,"0MG","BIL1(F1xP1)")
```

---

**DHexdata**  
*DH population dataset*

**Description**
The phenotype of DH population.

**Usage**
data(DHexdata)

**Details**
Dataset input of DHFun function.

**Author(s)**
Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>
DHFun

*segregation analysis of DH population*

**Description**

Phenotypic observations in DH population have often been used to identify mixed major-gene plus polygene inheritance model for quantitative traits in plants.

**Usage**

```r
DHFun(df, model)
```

**Arguments**

- `df`: phenotype matrix.
- `model`: genetic model.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming

Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

**Examples**

```r
DH=data(DHexdata)
DHFun(DHexdata,"0MG")
```

---

**F23exdata**

*F23 population dataset*

**Description**

The phenotype of F23 population.

**Usage**

```r
data(F23exdata)
```

**Details**

Dataset input of F23Fun function.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming

Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>
F23Fun  

*segregation analysis of F23 population*

**Description**
Phenotypic observations in F23 population have often been used to identify mixed major-gene plus polygene inheritance model for quantitative traits in plants.

**Usage**

F23Fun(df,model,m_nf)

**Arguments**

- df: phenotype matrix.
- model: genetic model.
- m_nf: number of plants measured in each family.

**Author(s)**
Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

**Examples**

F23=data(F23exdata)
F23Fun(F23exdata,"0MG",1)

---

F2exdata  

*F2 population dataset*

**Description**
The phenotype of F2 population.

**Usage**

data(F2exdata)

**Details**
Dataset input of F2Fun function.

**Author(s)**
Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>
F2Fun

**Description**

Phenotypic observations in F2 population have often been used to identify mixed major-gene plus polygene inheritance model for quantitative traits in plants.

**Usage**

\[
\text{F2Fun}(\text{df}, \text{model})
\]

**Arguments**

- **df**: phenotype matrix.
- **model**: genetic model.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

**Examples**

\[
\text{F2=\text{data(F2exdata)}} \quad \text{F2Fun(F2exdata,"0MG")}
\]

---

G3DHexdata

**Description**

The phenotype of G3DH population.

**Usage**

\[
\text{data(G3DHexdata)}
\]

**Details**

Dataset input of G3DHFun function.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>
G3DHFun

*segregation analysis of G3DH population*

**Description**

Phenotypic observations in G3DH population have often been used to identify mixed major-gene plus polygene inheritance model for quantitative traits in plants.

**Usage**

G3DHFun(df,model,G3DHtext2)

**Arguments**

- df: phenotype matrix.
- model: genetic model.
- G3DHtext2: number of plants measured in each family.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

**Examples**

G3DH=data(G3DHexdata)
G3DHFun(G3DHexdata,"0MG",1)

---

G4F2exdata

*G4F2 population dataset*

**Description**

The phenotype of G4F2 population.

**Usage**

data(G4F2exdata)

**Details**

Dataset input of G4F2Fun function.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>
**G4F2Fun**

*segregation analysis of G4F2 population*

---

**Description**

Phenotypic observations in G4F2 population have often been used to identify mixed major-gene plus polygene inheritance model for quantitative traits in plants.

**Usage**

```
G4F2Fun(df,model)
```

**Arguments**

- `df` : phenotype matrix.
- `model` : genetic model.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming

Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

**Examples**

```
G4F2=data(G4F2exdata)
G4F2Fun(G4F2exdata,"PG-AD")
```

---

**G4F3exdata**

*G4F3 population dataset*

---

**Description**

The phenotype of G4F3 population.

**Usage**

```
data(G4F3exdata)
```

**Details**

Dataset input of G4F3Fun function.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming

Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>
**G4F3Fun**  
*segregation analysis of G4F3 population*

**Description**

Phenotypic observations in G4F3 population have often been used to identify mixed major-gene plus polygene inheritance model for quantitative traits in plants.

**Usage**

```r
G4F3Fun(df,model,G4F3text2)
```

**Arguments**

- `df`: phenotype matrix.
- `model`: genetic model.
- `G4F3text2`: number of plants measured in each family.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

**Examples**

```r
G4F3=data(G4F3exdata)
G4F3Fun(G4F3exdata,"PG-AD",1)
```

---

**G5BCexdata**  
*G5BC population dataset*

**Description**

The phenotype of G5BC population.

**Usage**

```r
data(G5BCexdata)
```

**Details**

Dataset input of G5BCFun function.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>
G5BCFexdata

G5BCFexdata  G5BCF population dataset

Description
The phenotype of G5BCF population.

Usage
data(G5BCFexdata)

Details
Dataset input of G5BCFFun function.

Author(s)
Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

G5BCFFun  segregation analysis of G5BCF population

Description
Phenotypic observations in G5BCF population have often been used to identify mixed major-gene plus polygene inheritance model for quantitative traits in plants.

Usage
G5BCFFun(df,model,G5BCFtext2)

Arguments
df  phenotype matrix.
model  genetic model.
G5BCFtext2  number of plants measured in each family.

Author(s)
Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

Examples
G5BCF=data(G5BCFexdata)
G5BCFFun(G5BCFexdata,"1MG-AD",1)
G5BCFun

*segregation analysis of G5BC population*

**Description**

Phenotypic observations in G5BC population have often been used to identify mixed major-gene plus polygene inheritance model for quantitative traits in plants.

**Usage**

G5BCFun(df, model)

**Arguments**

- *df*  phenotype matrix.
- *model*  genetic model.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming

Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

**Examples**

G5BC=data(G5BCexdata)
G5BCFun(G5BCexdata,"1MG-AD")

---

G5exdata  *G5 population dataset*

**Description**

The phenotype of G5 population.

**Usage**

data(G5exdata)

**Details**

Dataset input of G5Fun function.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming

Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>
G5Fun

**Description**

Phenotypic observations in G5 population have often been used to identify mixed major-gene plus polygene inheritance model for quantitative traits in plants.

**Usage**

G5Fun(df,model,G5text2)

**Arguments**

- df: phenotype matrix.
- model: genetic model.
- G5text2: number of plants measured in each family.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming

Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

**Examples**

G5=data(G5exdata)
G5Fun(G5exdata,"PG-AD",1)

G6exdata

**Description**

The phenotype of G6 population.

**Usage**

data(G6exdata)

**Details**

Dataset input of G6Fun function.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming

Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>
G6Fexdata

**Description**

The phenotype of G6F population.

**Usage**

data(G6Fexdata)

**Details**

Dataset input of G6FFun function.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

---

G6FFun

**Description**

Phenotypic observations in G6F population have often been used to identify mixed major-gene plus polygene inheritance model for quantitative traits in plants.

**Usage**

G6FFun(df,model,G6Ftext2)

**Arguments**

- **df**: phenotype matrix.
- **model**: genetic model.
- **G6Ftext2**: number of plants measured in each family.

**Author(s)**

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

**Examples**

G6F=data(G6Fexdata)
G6FFun(G6Fexdata,"PG-AD",1)
G6Fun

Description
Phenotypic observations in G6 population have often been used to identify mixed major-gene plus
dyogene inheritance model for quantitative traits in plants.

Usage
G6Fun(df,model)

Arguments
- df: phenotype matrix.
- model: genetic model.

Author(s)
Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

Examples
G6=data(G6exdata)
G6Fun(G6exdata,"PG-AD")

PosPro

Description
calculate posterior probability of the optimal model

Usage
PosPro(Population,result,data)

Arguments
- Population: which Population to analysis.
- result: result of calculation used corresponding population function.
- data: phenotype matrix.
Author(s)
Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming
Maintainer: Yuanming Zhang<soyzhang@mail.hzau.edu.cn>

Examples
F23=data(F23exdata)
result<-F23Fun(F23exdata,"1MG-AD",1)
PosPro("F2:3",result,F23exdata)
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