# Package 'SEA'

October 12, 2022

Type Package

Title Segregation Analysis
Version 2.0.1
<b>Date</b> 2022-3-28
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Description A few major genes and a series of polygene are responsive for each quantitative trait. Ma jor 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="">).</doi:10.1017>
<b>Depends</b> shiny,MASS,doParallel,foreach,methods
Imports KScorrect,utils,stats,grDevices,graphics,data.table
License GPL (>= 2)
NeedsCompilation no
Repository CRAN
<b>Date/Publication</b> 2022-03-30 07:30:12 UTC
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R topics documented:
SEA-package BCexdata BCFexdata BCFFun BCFun

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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>)

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# **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<a href="mailto:yuanming.com/soyzhang@mail.hzau.edu.cn">yuanming.com/soyzhang@mail.hzau.edu.cn</a>

#### References

The EIM algorithm in the joint segregation analysis of quantitative traits. Zhang Yuan-Ming\*, Gai Junyi, Yang Yonghua (2003).

# **Examples**

## Not run: SEA()

**BCexdata** 

BC population dataset

# Description

The phenotype of BC population .

# Usage

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>

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**BCFexdata** 

BCF population dataset

### **Description**

The phenotype of BCF population.

### Usage

```
data(BCFexdata)
```

#### **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** 

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 phenotype matrix. model genetic model.

BCFtext2 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(BCFexdata)
BCFFun(BCFexdata, "0MG",1)
```

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**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

```
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<a href="mailto:yaunding-mail.hzau.edu.cn">yaunding-Maintainer</a>: Yuanming Zhang<a href="mailto:yaunding-mail.hzau.edu.cn">yaunding-mail.hzau.edu.cn</a>

# **Examples**

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

BILexdata

BIL population dataset

# **Description**

The phenotype of BIL population.

### Usage

```
data(BILexdata)
```

### **Details**

Dataset input of BILFun function.

# Author(s)

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming Maintainer: Yuanming Zhang<a href="mailto:yuanming.com/ya-wen/">yuan-Ming Zhang</a> @mail.hzau.edu.cn>

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**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.
BIL fr 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, "OMG", "BIL1(F1xP1)")
```

DHexdata

DH population dataset

### **Description**

The phenotype of DH population .

### Usage

```
data(DHexdata)
```

### **Details**

Dataset input of DHFun function.

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

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**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

```
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**

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

F23exdata

F23 population dataset

# **Description**

The phenotype of F23 population.

### Usage

```
data(F23exdata)
```

### **Details**

Dataset input of F23Fun function.

# Author(s)

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming Maintainer: Yuanming Zhang<a href="mailto:yuanming.com/ya-wen/">yuan-Ming Zhang</a> @mail.hzau.edu.cn>

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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.

```
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```

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F2Fun

segregation analysis of F2 population

# **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

```
F2Fun(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**

```
F2=data(F2exdata)
F2Fun(F2exdata, "0MG")
```

G3DHexdata

G3DH population dataset

# **Description**

The phenotype of G3DH population.

### Usage

```
data(G3DHexdata)
```

# **Details**

Dataset input of G3DHFun function.

# Author(s)

Wang Jing-Tian, Zhang Ya-Wen, and Zhang Yuan-Ming Maintainer: Yuanming Zhang<a href="mailto:yuanming.com/ya-wen/">yuan-Ming Zhang</a> @mail.hzau.edu.cn>

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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.

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

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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>

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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

```
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**

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

G5BCexdata

G5BC population dataset

### **Description**

The phenotype of G5BC population .

### Usage

```
data(G5BCexdata)
```

### **Details**

Dataset input of G5BCFun function.

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

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**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)
```

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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)

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# **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.

```
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```

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G5Fun

segregation analysis of G5 population

### **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

G6 population dataset

### **Description**

The phenotype of G6 population .

### Usage

```
data(G6exdata)
```

### **Details**

Dataset input of G6Fun function.

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

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G6Fexdata

G6F population dataset

#### **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

segregation analysis of G6F population

# **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)
```

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G6Fun

segregation analysis of G6 population

# Description

Phenotypic observations in G6 population have often been used to identify mixed major-gene plus polygene 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

Posterior Probability

# 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.

PosPro

# 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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