Package 'SEA'

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Type Package

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:

SEA-package   *Segregation Analysis*

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

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>

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)
```

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<soyzhang@mail.hzau.edu.cn>

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<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

```
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<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   *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<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

```
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
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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.

Author(s)

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

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   *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.

Author(s)

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

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)
```

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.

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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