

# Package ‘SEA’

February 27, 2021

**Type** Package

**Title** Segregation Analysis

**Version** 2.0

**Date** 2021-2-24

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

**Maintainer** Yuanming Zhang<soy Zhang@mail.hzau.edu.cn>

**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 YM, Gai JY, Yang YH (2003) <doi:10.1017/S0016672303006141>.

**Depends** shiny, MASS, doParallel, foreach, methods

**Imports** KSCorrect, kolmim, utils, stats, grDevices, graphics, data.table

**License** GPL (>= 2)

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2021-02-27 08:20:06 UTC

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SEA-package	<i>Segregation Analysis</i>
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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 YM, Gai JY, Yang YH (2003) <doi:10.1017/S0016672303006141>.

## Details

Package:	SEA
Type:	Package
Version:	2.0
Date:	2021-02-24
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<soy Zhang@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<soy Zhang@mail.hzau.edu.cn>

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BCFexdata	<i>BCF population dataset</i>
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**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<soy Zhang@mail.hzau.edu.cn>

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BCFFun	<i>segregation analysis of BCF population</i>
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**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<soy Zhang@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<soy Zhang@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<soy Zhang@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<soy Zhang@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<soy Zhang@mail.hzau.edu.cn>

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DHFun	<i>segregation analysis of DH population</i>
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**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<soy Zhang@mail.hzau.edu.cn>

**Examples**

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

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F23exdata	<i>F23 population dataset</i>
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**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<soy Zhang@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<soy Zhang@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<soy Zhang@mail.hzau.edu.cn>

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F2Fun	<i>segregation analysis of F2 population</i>
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**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<soy Zhang@mail.hzau.edu.cn>

**Examples**

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

---

G3DHexdata	<i>G3DH population dataset</i>
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**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<soy Zhang@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<soy Zhang@mail.hzau.edu.cn>

**Examples**

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

---

G4F2exdata

*G4F2 population dataset*


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**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<soy Zhang@mail.hzau.edu.cn>

---

G4F2Fun	<i>segregation analysis of G4F2 population</i>
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---

**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<soy Zhang@mail.hzau.edu.cn>

**Examples**

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

---

G4F3exdata	<i>G4F3 population dataset</i>
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---

**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<soy Zhang@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  
 Maintainer: Yuanming Zhang<soy Zhang@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.

**Author(s)**

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

---

G5BCFexdata	<i>G5BCF population dataset</i>
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---

**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<soy Zhang@mail.hzau.edu.cn>

---

G5BCFFun	<i>segregation analysis of G5BCF population</i>
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---

**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<soy Zhang@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<soy Zhang@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<soy Zhang@mail.hzau.edu.cn>

---

G5Fun	<i>segregation analysis of G5 population</i>
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---

**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<soy Zhang@mail.hzau.edu.cn>

**Examples**

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

---

G6exdata	<i>G6 population dataset</i>
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---

**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<soy Zhang@mail.hzau.edu.cn>

---

G6Fexdata	<i>G6F population dataset</i>
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---

**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<soy Zhang@mail.hzau.edu.cn>

---

G6FFun	<i>segregation analysis of G6F population</i>
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**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<soy Zhang@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<soy Zhang@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<soy Zhang@mail.hzau.edu.cn>

**Examples**

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

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