

# Package ‘CINOEDV’

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**Type** Package

**Title** Co-Information based N-Order Epistasis Detector and Visualizer

**Version** 1.0

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**Description** A package for detecting and visualizing high-order epistatic interactions

**License** GPL-2

**LazyLoad** yes

**Depends** R.matlab, igraph, ggplot2, reshape2

**NeedsCompilation** no

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CINOEDV-package	<i>Co-Information based N-Order Epistasis Detector and Visualizer</i>
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## Description

A package for detecting and visualizing high-order epistatic interactions.

## Details

```
Package: CINOEDV
Type: Package
Version: 1.0
Date: 2014-05-02
License: GPL-2
```

```
##### ## Normal Using type ## #####
result <- CINOEDV_Main()
#### Please input the file name with its format (.mat) that saves SNP data. # test.mat
#### Please input the maximum order (1/2/3/4/5), and 3 is the Recommendation Option. # 3
#### Please input the 1 ratio threshold. # 1
```

```
##### Please input the 2 ratio threshold. # 0.5
##### Please input the 3 ratio threshold. # 0.8
##### Please input the 1 number threshold. # 10
##### Please input the 2 number threshold. # 20
##### Please input the 3 number threshold. # 8
##### Please select the evaluation measure (1/2/3), and 1 is the Recommendation Option. # 1
##### Please input the name of such file with (.mat) format. # NA
```

### Author(s)

Junliang Shang <shangjunliang110@163.com>

### Examples

```
rm(list=ls())

File1 <- system.file("extdata","test.mat",package="CINOEDV")
File2 <- system.file("extdata","test1.mat",package="CINOEDV")
File3 <- system.file("extdata","test_Name.mat",package="CINOEDV")
File4 <- system.file("extdata","test1_Name.mat",package="CINOEDV")

FileName <- c(File1,File2)
MaxOrder <- 2
RatioThreshold <- c(1,1)
NumberThreshold <- c(10,10)
measure <- 1
SNPNameFileName <- c(File3,File4)

BatCINOEDV(FileName, MaxOrder, RatioThreshold, NumberThreshold, measure, SNPNameFileName)

#####
##      Second      ##
#####

# Install Packages
# InstallPackage()

# Check SNP data
FileName <- system.file("extdata","test.mat",package="CINOEDV")
Data <- InputData(FileName)
pts <- Data$pts
class <- Data$class

# Check MaxOrder
MaxOrder <- 2
TestMaxOrder(as.character(MaxOrder))
MaxOrder <- as.numeric(MaxOrder)
```

```

# Check RatioThreshold
RatioThreshold <- c(1,1)
TestRatioThreshold(MaxOrder,as.character(RatioThreshold))
RatioThreshold <- as.numeric(RatioThreshold)

# Check NumberThreshold
NumberThreshold <- c(10,10)
TestNumberThreshold(MaxOrder,as.character(NumberThreshold))
NumberThreshold <- as.numeric(NumberThreshold)

# Check measure
measure <- 1

# Check SNPNameFileName
SNPNameFileName <- system.file("extdata","test_Name.mat",package="CINOEDV")
SNPNames <- TestSNPNameFile(ncol(pts),as.character(SNPNameFileName))
SNPNames <- SNPNames$SNPNames

# Define file name which is used for saving results.
SaveFileName <- "TEST_RESULT_"

# Search Strategies
Effect <- ExhaustiveSearch(pts,class,MaxOrder,measure,0)
SingleEffect <- Effect$SingleEffect
TwoEffect <- Effect$TwoEffect
ThreeEffect <- Effect$ThreeEffect
FourEffect <- Effect$FourEffect
FiveEffect <- Effect$FiveEffect

# Normalization
Effect <- NormalizationEffect(MaxOrder,SingleEffect,TwoEffect,ThreeEffect,FourEffect
                              ,FiveEffect,SaveFileName)

SingleEffect <- Effect$SingleEffect
TwoEffect <- Effect$TwoEffect
ThreeEffect <- Effect$ThreeEffect
FourEffect <- Effect$FourEffect
FiveEffect <- Effect$FiveEffect

# SNP Name Notation
Effect <- NotationName(MaxOrder,SingleEffect,TwoEffect,ThreeEffect,FourEffect
                      ,FiveEffect,SNPNames)

SingleEffect <- Effect$SingleEffect
TwoEffect <- Effect$TwoEffect
ThreeEffect <- Effect$ThreeEffect
FourEffect <- Effect$FourEffect
FiveEffect <- Effect$FiveEffect

# Collect Vertices and Edges
GraphData <- NetworkData(SingleEffect,TwoEffect,ThreeEffect,FourEffect,
                        FiveEffect,RatioThreshold,NumberThreshold)
Edges <- GraphData$edges

```

```

Vertices <- GraphData$vertices

# Construct Complete Graph
ConstructCompleteGraph(Vertices,Edges,6,SaveFileName)

# Plot Top Effects
TpEffect <- PlotTopEffects(Vertices,20,SaveFileName)
TopEffect <- TpEffect$TopEffect
CombinationEffect <- TpEffect$CombinationEffect

# Degree Analysis
Degrees <- DegreeAnalysis(Vertices,Edges,SaveFileName)
Degrees <- Degrees$Degrees
print(Degrees)

# Split subgraphs
SubgraphSNPs <- SubgraphSplit(Vertices,Edges)
SubgraphSNPs <- SubgraphSNPs$SubgroupSNPs

# heatmap Factor
HeatMapFactors <- HeatMapFactor(pts,class,factor = c(5, 8),SaveFileName,Title = "")
HeatMapFactors <- HeatMapFactors$HeatMapFactors

```

---

BatCINOEDV

*Batch mode for using CINOEDV*


---

## Description

Batch mode for using CINOEDV function.

## Usage

```

BatCINOEDV(FileName, MaxOrder, RatioThreshold,
           NumberThreshold, measure, SNPNameFileName)

```

## Arguments

FileName	character. The file name with its format (.mat) that saves SNP data. It has two variables, i.e., pts and class. For pts, Row -> Sample, Column -> SNP, 1 -> AA, 2 -> Aa, 3 -> aa. For class, Row -> 1, Column -> class label, 1 -> case, 2-> control.
MaxOrder	numeric. The considered maximum order of epistatic interactions. It must be setted as 1, 2, 3, 4, or 5.
RatioThreshold	character. It controls the numbers of detected SNPs or SNP-combinations with the help of NumberThreshold. The length of RatioThreshold is equal to Max-Order. Each element is a decimal in [0,1].

NumberThreshold	character. It controls the numbers of detected SNPs or SNP-combinations with the help of RatioThreshold. The length of NumberThreshold is equal to MaxOrder. Each element is an integer.
measure	numeric. The used evaluation measure. 1 -> the classic co-information measure; 2 -> the normalized co-information measure; 3 -> TingHu's co-informationn measure.
SNPNameFileName	character. The file name with its format (.mat) that saves the names of SNPs. The file has only one variable, i.e., Name. In Name, Row -> 1, Column -> SNP Name, and the length is equal to RowNum. If not exist such file (default), SNPNameFileName <- NA.

**Value**

None

**Note**

The returned values save in files with (.mat) or (.RData) formats respectively.

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
File1 <- system.file("extdata","test.mat",package="CINOEDV")
File2 <- system.file("extdata","test1.mat",package="CINOEDV")
File3 <- system.file("extdata","test1_Name.mat",package="CINOEDV")
FileName <- c(File1,File2)
SNFName <- c(NA,File3)
MaxOrder <- 2
RThreshold <- c(1, 1)
NThreshold <- c(10, 10)
measure <- 1
BatCINOEDV(FileName, MaxOrder, RThreshold, NThreshold, measure, SNFName)
```

---

CheckVerticeType	<i>Test Vertice Type</i>
------------------	--------------------------

---

**Description**

This function check a vertice whether belongs to a real vertice or a virtual one.

**Usage**

```
CheckVerticeType(Vertice)
```

**Arguments**

Vertice            character. A vertice in the network, namely, the graph.

**Value**

Whether: logical. Whether the checked vertice belongs to a real vertice or a virtual one.

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
Vertice <- "rs1366208"  
Whether <- CheckVerticeType(Vertice)  
Whether <- Whether$Whether  
Vertice <- "rs2801008:rs4763023"  
Whether <- CheckVerticeType(Vertice)  
Whether <- Whether$Whether
```

---

CINOEDV_Main	<i>Co-Information based N-Order Epistasis Detector and Visualizer</i>
--------------	---

---

**Description**

This function integrates almost all functions of the package for providing one stop service.

**Usage**

```
CINOEDV_Main()
```

**Details**

No input parameters

**Value**

parameters	list. It returns six parameters, including FileName, MaxOrder, RatioThreshold, NumberThreshold, SNPNameFileName, and measure. FileName: character. The file name with its format (.mat) that saves SNP data. MaxOrder: numeric. The considered maximum order of epistatic interactions. RatioThreshold: numeric. It controls the numbers of detected SNPs or SNP-combinations with the help of NumberThreshold. NumberThreshold: numeric. It controls the numbers of detected SNPs or SNP-combinations with the help of RatioThreshold. SNPNameFileName: character or logical (NA). The file name with its format (.mat) that saves the names of SNPs. measure: numeric. The used evaluation measure.
data	list. It returns used data, including pts, class, and SNPNames. pts: matrix. SNP data. class: matrix. Class labels of samples. SNPNames: character or logical (NA). Names of SNPs.
results	list. It returns detected results, including SingleEffect, TwoEffect, ThreeEffect, FourEffect, and FiveEffect. SingleEffect: matrix. main Effects of SNPs. TwoEffect: matrix. interaction Effects of two-SNP combinations. ThreeEffect: matrix. interaction Effects of three-SNP combinations. FourEffect: matrix. interaction Effects of four-SNP combinations. FiveEffect: matrix. interaction Effects of five-SNP combinations.
graphs	list. It returns observed results from the constructed graph, including Edges, Vertices, TopEffect, Degrees, SubgraphSNPs, CombinationEffect and HeatMapFactors. Edges: matrix. Edges of constructed graphs. Vertices: matrix. Vertices of constructed graphs, including real vertices and virtual vertices. TopEffect: numeric. Top independent effects of SNPs or SNP-combinations. Degrees: matrix. Degrees of real vertices. SubgraphSNPs: list. SNPs in each subgraph of the graph. CombinationEffect: numeric. Top combination effects of SNPs or SNP-combinations. HeatMapFactors: data.frame. The heatmap data for observing how a SNP or a SNP-combination influencing the phenotype.

**Note**

The returned values also save in files with (.mat) or (.RData) formats respectively.

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None



**Examples**

```
# See details of package CINOEDV
```

---

class	<i>Class labels of samples</i>
-------	--------------------------------

---

**Description**

Class labels of samples

**Usage**

```
data(class)
```

**Format**

The format is: num [1, 1:4000] 2 1 1 2 1 1 1 1 1 ... - attr(\*, "dimnames")=List of 2 ..\$ : NULL ..\$ : chr [1:4000] "Sample1" "Sample2" "Sample3" "Sample4" ...

**References**

None

**Examples**

```
data(class)
```

---

CoInformation	<i>Co-Information Computation</i>
---------------	-----------------------------------

---

**Description**

This function compute co-information value of a given SNP combination.

**Usage**

```
CoInformation(pts, class, factor)
```

**Arguments**

pts	matrix. SNP data. Each row represents a sample. Each column represents a SNP. For the element, 1 -> AA, 2 -> Aa, 3 -> aa.
class	matrix. Class labels of samples. It only has one row. Each column represents a class label. For the element, 1 -> case, 2-> control.
factor	numeric. The considered SNP or SNP-combination. For example, factor <- 5, or factor <- c(2,5)

**Value**

Co\_Information\_Value: matrix. co-information value of a give SNP combination.

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
data(pts)
data(class)
factor <- c(2,5)
V <- CoInformation(pts, class, factor)
Co_Information_Value <- V$Co_Information_Value
```

---

CombinationEntropy      *Combination Entropy Computation*

---

**Description**

This function compute combination entropy of given variables. These variables can be one SNP, the class label, SNP-combination, or SNP-combination-class label.

**Usage**

```
CombinationEntropy(data)
```

**Arguments**

data                    matrix. The given variables, for example, data <- cbind(pts[,factor],t(class))

**Value**

Combination\_Entropy\_Value: matrix. combination entropy value.

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
data(pts)
data(class)
factor <- c(2, 5)
data <- cbind(pts[, factor], t(class))
V <- CombinationEntropy(data)
Combination_Entropy_Value <- V$Combination_Entropy_Value
```

---

ConstructCompleteGraph

*Construct complete graph*

---

**Description**

This function construct complete graph by using all vertices and edges.

**Usage**

```
ConstructCompleteGraph(Vertices, Edges, BaseSize = 6, SaveFileName = "")
```

**Arguments**

Vertices	matrix. Vertices of constructed graphs, including real vertices and virtual vertices. The first column represents SNP ID or SNP-combination ID. The second column represents effect value. The third column represents the class of vertices, "1" -> real vertice, others -> virtual vertice.
Edges	matrix. Edges of constructed graphs.
BaseSize	numeric. Basic size of vertices in the graph. By default, BaseSize <- 6.
SaveFileName	character. Basic file name for saving figure. By default, SaveFileName <- "".

**Value**

None

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
data(Vertices)
data(Edges)
ConstructCompleteGraph(Vertices, Edges, BaseSize = 6, SaveFileName = "")
```

---

DegreeAnalysis	<i>Degree analysis of real vertices</i>
----------------	---

---

**Description**

Degree analysis of real vertices.

**Usage**

```
DegreeAnalysis(Vertices, Edges, SaveFileName = "")
```

**Arguments**

Vertices	matrix. Vertices of constructed graphs, including real vertices and virtual vertices. The first column represents SNP ID or SNP-combination ID. The second column represents effect value. The third column represents the class of vertices, "1" -> real vertice, others -> virtual vertice.
Edges	matrix. Edges of constructed graphs.
SaveFileName	character. Basic file name for saving figure. By default, SaveFileName <- "".

**Value**

Degrees: matrix. Degrees of real vertices.

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
data(Vertices)
data(Edges)
Degrees <- DegreeAnalysis(Vertices, Edges, SaveFileName = "")
Degrees <- Degrees$Degrees
```

---

Edges	<i>Edges of constructed graphs</i>
-------	------------------------------------

---

**Description**

Edges of constructed graphs

**Usage**

```
data(Edges)
```

**Format**

The format is: chr [1:45, 1:2] "rs00008:rs00019" "rs00005:rs00017" ... - attr(\*, "dimnames")=List of 2 ..\$ : NULL ..\$ : chr [1:2] "From" "To"

**References**

None

**Examples**

```
data(Edges)
```

---

EvaluationMeasure	<i>Evaluation Measure</i>
-------------------	---------------------------

---

**Description**

This function provides several co-information based measures for measuring main or interaction effect of a SNP or SNP-combination.

**Usage**

```
EvaluationMeasure(factor, pts, class, measure = 1)
```

**Arguments**

pts	matrix. SNP data. Each row represents a sample. Each column represents a SNP. For the element, 1 -> AA, 2 -> Aa, 3 -> aa.
class	matrix. Class labels of samples. It only has one row. Each column represents a class label. For the element, 1 -> case, 2-> control.
factor	numeric. The considered SNP or SNP-combination. For example, factor <- 5, or factor <- c(2,5)
measure	numeric. The used evaluation measure. 1 -> the classic co-information measure; 2 -> the normalized co-information measure; 3 -> TingHu's co-informatiomm measure.

**Value**

Value: matrix. The main or interaction effect value corresponding to a sing SNP or a SNP combination.

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
factor <- c(2,5)
data(pts)
data(class)
V <- EvaluationMeasure(factor, pts, class, measure = 1)
Value <- V$Value
```

---

ExhaustiveSearch

*Exhaustive Search*

---

**Description**

This function exhaustively compute main effects of all SNPs and interaction effects of all SNP-combinations within the maximum order.

**Usage**

```
ExhaustiveSearch(pts, class, MaxOrder = 3, measure = 1, alpha = 0)
```

**Arguments**

pts	matrix. SNP data. Each row represents a sample. Each column represents a SNP. For the element, 1 -> AA, 2 -> Aa, 3 -> aa.
class	matrix. Class labels of samples. It only has one row. Each column represents a class label. For the element, 1 -> case, 2-> control.
MaxOrder	numeric. The considered maximum order of epistatic interactions. It must be setted as 1, 2, 3, 4, or 5.
measure	numeric. The used evaluation measure. 1 -> the classic co-information measure; 2 -> the normalized co-information measure; 3 -> TingHu's co-informationn measure.
alpha	numeric. The lower threshold of effects, either main effects or interaction effects, which must be higher or equal to 0, By default, alpha <- 0.

**Value**

SingleEffect	matrix. main Effects of SNPs. There are 2 columns. The first column saves all SNPs, and the second column saves their corresponding effects. Descending save according to their effects.
TwoEffect	matrix. interaction Effects of two-SNP combinations. There are three columns. The first two columns save all two-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
ThreeEffect	matrix. interaction Effects of three-SNP combinations. There are four columns. The first three columns save all three-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
FourEffect	matrix. interaction Effects of four-SNP combinations. There are five columns. The first four columns save all four-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
FiveEffect	matrix. interaction Effects of five-SNP combinations. There are six columns. The first five columns save all five-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
data(pts)
data(class)
Effect <- ExhaustiveSearch(pts, class, MaxOrder = 2, measure = 1, alpha = 0)
SingleEffect <- Effect$SingleEffect
TwoEffect <- Effect$TwoEffect
ThreeEffect <- Effect$ThreeEffect
FourEffect <- Effect$FourEffect
FiveEffect <- Effect$FiveEffect
```

---

FiveEffect

*Interaction Effects of five-SNP combinations*

---

**Description**

Interaction Effects of five-SNP combinations

**Usage**

```
data(FiveEffect)
```

**Format**

The format is: num [1, 1] 0

**References**

None

**Examples**

```
data(FiveEffect)
```

---

FourEffect

*Interaction Effects of four-SNP combinations*

---

**Description**

Interaction Effects of four-SNP combinations

**Usage**

```
data(FourEffect)
```

**Format**

The format is: num [1, 1] 0

**References**

None

**Examples**

```
data(FourEffect)
```



---

HeatMapFactor	<i>Heatmap function</i>
---------------	-------------------------

---

**Description**

This function create a heatmap figure for visualizing how a SNP or a SNP-combination influencing the phenotype.

**Usage**

```
HeatMapFactor(pts, class, factor, SaveFileName = "", Title = "")
```

**Arguments**

pts	matrix. SNP data. Each row represents a sample. Each column represents a SNP. For the element, 1 -> AA, 2 -> Aa, 3 -> aa.
class	matrix. Class labels of samples. It only has one row. Each column represents a class label. For the element, 1 -> case, 2-> control.
factor	numeric. The considered SNP or SNP-combination. For example, factor <- 5, or factor <- c(2,5)
SaveFileName	character. Basic file name for saving figure. By default, SaveFileName <- "".
Title	character. Title of the heatmap figure. By default, Title <- "".

**Value**

HeatMapFactors: data.frame. The heatmap data for observing how a SNP or a SNP-combination influencing the phenotype.

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
data(pts)
data(class)
factor <- c(2,5)
H <- HeatMapFactor(pts, class, factor, SaveFileName = "", Title = "")
HeatMapFactors <- H$HeatMapFactors
```

---

**InputData***Input data*

---

**Description**

Input SNP data from a file with (.mat) format.

**Usage**

```
InputData(FileName)
```

**Arguments**

**FileName** character. The file name with its format (.mat) that saves SNP data. It has two variables, i.e., pts and class. For pts, Row -> Sample, Column -> SNP, 1 -> AA, 2 -> Aa, 3 -> aa. For class, Row -> 1, Column -> class label, 1 -> case, 2-> control.

**Value**

**pts** matrix. Each row represents a sample. Each column represents a SNP. For the element, 1 -> AA, 2 -> Aa, 3 -> aa.

**class** matrix. It only has one row. Each column represents a class label. For the element, 1 -> case, 2-> control.

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
# The files (test.mat) should be downloaded from http://sourceforge.net/projects/cinoedv/files/.  
  
FileName <- system.file("extdata", "test.mat", package="CINOEDV")  
Data <- InputData(FileName)  
pts <- Data$pts  
class <- Data$class
```

---

InstallPackage	<i>Install CINOEDV used packages</i>
----------------	--------------------------------------

---

**Description**

Install CINOEDV used packages, including R.matlab, igraph, ggplot2, and reshape2.

**Usage**

```
InstallPackage()
```

**Value**

None

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
InstallPackage()
```

---

NetworkData	<i>Collect vertices and edges for network construction</i>
-------------	--

---

**Description**

Collect vertices and edges from effect data (SingleEffect, TwoEffect, ThreeEffect, FourEffect, FiveEffect) for network construction.

**Usage**

```
NetworkData(SingleEffect, TwoEffect, ThreeEffect,  
            FourEffect, FiveEffect, RatioThreshold, NumberThreshold)
```

**Arguments**

SingleEffect	matrix. main Effects of SNPs. There are 2 columns. The first column saves all SNPs, and the second column saves their corresponding effects. Descending save according to their effects.
TwoEffect	matrix. interaction Effects of two-SNP combinations. There are three columns. The first two columns save all two-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
ThreeEffect	matrix. interaction Effects of three-SNP combinations. There are four columns. The first three columns save all three-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
FourEffect	matrix. interaction Effects of four-SNP combinations. There are five columns. The first four columns save all four-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
FiveEffect	matrix. interaction Effects of five-SNP combinations. There are six columns. The first five columns save all five-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
RatioThreshold	character. It controls the numbers of detected SNPs or SNP-combinations with the help of NumberThreshold. The length of RatioThreshold is equal to Max-Order. Each element is a decimal in [0,1].
NumberThreshold	character. It controls the numbers of detected SNPs or SNP-combinations with the help of RatioThreshold. The length of NumberThreshold is equal to Max-Order. Each element is an integer.

**Details**

Parameters 'RatioThreshold' and 'NumberThreshold' are used together to control the numbers of vertices and edges. That is,  $\min(\text{NumberThreshold}[1], \text{RatioThreshold}[1] * \text{nrow}(\text{SingleEffect}))$ ,  $\min(\text{NumberThreshold}[2], \text{RatioThreshold}[2] * \text{nrow}(\text{TwoEffect}))$ ,  $\min(\text{NumberThreshold}[3], \text{RatioThreshold}[3] * \text{nrow}(\text{ThreeEffect}))$ ,  $\min(\text{NumberThreshold}[4], \text{RatioThreshold}[4] * \text{nrow}(\text{FourEffect}))$ ,  $\min(\text{NumberThreshold}[5], \text{RatioThreshold}[5] * \text{nrow}(\text{FiveEffect}))$ . Using above settings, the numbers of virtual vertexes denoting high order epistatic interactions in the graph are clear. Nevertheless, the number of Real Vertexes (i.e., the number of SNPs) is unclear, which is obviously more than the above set, since some of them must be included to connect virtual vertexes.

**Value**

Vertices	matrix. Vertices of constructed graphs, including real vertices and virtual vertices. The first column represents SNP ID or SNP-combination ID. The second column represents effect value. The third column represents the class of vertices, "1" -> real vertice, others -> virtual vertice.
Edges	matrix. Edges of constructed graphs.

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
data(SingleEffect)
data(TwoEffect)
data(ThreeEffect)
data(FourEffect)
data(FiveEffect)
RatioThreshold <- c(1,1,1,1,1)
NumberThreshold <- c(10,10,10,10,10)
Net <- NetworkData(SingleEffect, TwoEffect, ThreeEffect, FourEffect,
  FiveEffect, RatioThreshold, NumberThreshold)
Vertices <- Net$Vertices
Edges <- Net$Edges
```

---

NormalizationEffect    *Normalization Effect*

---

**Description**

Normalization of main effects, and n-order interaction effects in SingleEffect, TwoEffect, ThreeEffect, FourEffect and FiveEffect respectively.

**Usage**

```
NormalizationEffect(MaxOrder, SingleEffect, TwoEffect,
  ThreeEffect, FourEffect, FiveEffect, SaveFileName = "")
```

**Arguments**

MaxOrder	numeric. The considered maximum order of epistatic interactions. It must be setted as 1, 2, 3, 4, or 5.
SingleEffect	matrix. main Effects of SNPs. There are 2 columns. The first column saves all SNPs, and the second column saves their corresponding effects. Descending save according to their effects.
TwoEffect	matrix. interaction Effects of two-SNP combinations. There are three columns. The first two columns save all two-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.

ThreeEffect	matrix. interaction Effects of three-SNP combinations. There are four columns. The first three columns save all three-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
FourEffect	matrix. interaction Effects of four-SNP combinations. There are five columns. The first four columns save all four-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
FiveEffect	matrix. interaction Effects of five-SNP combinations. There are six columns. The first five columns save all five-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
SaveFileName	character. Basic file name for saving figure. By default, SaveFileName <- "".

**Value**

SingleEffect	matrix. main Effects of SNPs. There are 2 columns. The first column saves all SNPs, and the second column saves their corresponding effects. Descending save according to their effects.
TwoEffect	matrix. interaction Effects of two-SNP combinations. There are three columns. The first two columns save all two-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
ThreeEffect	matrix. interaction Effects of three-SNP combinations. There are four columns. The first three columns save all three-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
FourEffect	matrix. interaction Effects of four-SNP combinations. There are five columns. The first four columns save all four-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
FiveEffect	matrix. interaction Effects of five-SNP combinations. There are six columns. The first five columns save all five-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```

data(pts)
data(class)
MaxOrder <- 2
measure <- 1
SaveFileName <- ""

# Search Strategies
Effect <- ExhaustiveSearch(pts,class,MaxOrder,measure,0)
SingleEffect <- Effect$SingleEffect
TwoEffect <- Effect$TwoEffect
ThreeEffect <- Effect$ThreeEffect
FourEffect <- Effect$FourEffect
FiveEffect <- Effect$FiveEffect

# Normalization
Effect <- NormalizationEffect(MaxOrder,SingleEffect,TwoEffect,ThreeEffect,FourEffect
                              ,FiveEffect,SaveFileName)

SingleEffect <- Effect$SingleEffect
TwoEffect <- Effect$TwoEffect
ThreeEffect <- Effect$ThreeEffect
FourEffect <- Effect$FourEffect
FiveEffect <- Effect$FiveEffect

```

---

NotationName	<i>Notation of real SNP Name</i>
--------------	----------------------------------

---

**Description**

If there are real SNP names which will be used for constructing graphs and further analysis, this function then replaces SNP indexes by real SNP names.

**Usage**

```

NotationName(MaxOrder, SingleEffect, TwoEffect,
              ThreeEffect, FourEffect, FiveEffect, SNPNames = NA)

```

**Arguments**

MaxOrder	numeric. The considered maximum order of epistatic interactions. It must be setted as 1, 2, 3, 4, or 5.
SingleEffect	matrix. main Effects of SNPs. There are 2 columns. The first column saves all SNPs, and the second column saves their corresponding effects. Ddescending save according to their effects.

TwoEffect	matrix. interaction Effects of two-SNP combinations. There are three columns. The first two columns save all two-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
ThreeEffect	matrix. interaction Effects of three-SNP combinations. There are four columns. The first three columns save all three-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
FourEffect	matrix. interaction Effects of four-SNP combinations. There are five columns. The first four columns save all four-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
FiveEffect	matrix. interaction Effects of five-SNP combinations. There are six columns. The first five columns save all five-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
SNPNames	character or logical (NA). Names of SNPs. Row -> 1, Column -> SNP Name

**Value**

SingleEffect	matrix. main Effects of SNPs. There are 2 columns. The first column saves all SNPs, and the second column saves their corresponding effects. Ddescending save according to their effects.
TwoEffect	matrix. interaction Effects of two-SNP combinations. There are three columns. The first two columns save all two-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
ThreeEffect	matrix. interaction Effects of three-SNP combinations. There are four columns. The first three columns save all three-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
FourEffect	matrix. interaction Effects of four-SNP combinations. There are five columns. The first four columns save all four-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.
FiveEffect	matrix. interaction Effects of five-SNP combinations. There are six columns. The first five columns save all five-SNP combinations, and the last column saves their corresponding effects. Descending save according to their interaction effects.

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None



**Examples**

```

data(pts)
data(class)
MaxOrder <- 2
measure <- 1
SaveFileName <- ""
SNPNames <- c("rs1366208", "rs1950123", "rs10485136", "rs1484673",
              "rs1484433", "rs1795462", "rs10501558", "rs2018041",
              "rs10489495", "rs3846302", "rs2801008", "0", "rs1773409",
              "rs4786670", "rs2260614", "rs1326298", "rs9315726",
              "rs1582545", "rs10505084", "rs4763023")

# Search Strategies
Effect <- ExhaustiveSearch(pts, class, MaxOrder, measure, 0)
SingleEffect <- Effect$SingleEffect
TwoEffect <- Effect$TwoEffect
ThreeEffect <- Effect$ThreeEffect
FourEffect <- Effect$FourEffect
FiveEffect <- Effect$FiveEffect

# Normalization
Effect <- NormalizationEffect(MaxOrder, SingleEffect, TwoEffect, ThreeEffect, FourEffect
                             , FiveEffect, SaveFileName)

SingleEffect <- Effect$SingleEffect
TwoEffect <- Effect$TwoEffect
ThreeEffect <- Effect$ThreeEffect
FourEffect <- Effect$FourEffect
FiveEffect <- Effect$FiveEffect

# SNP Name Notation
Effect <- NotationName(MaxOrder, SingleEffect, TwoEffect, ThreeEffect, FourEffect
                      , FiveEffect, SNPNames)

SingleEffect <- Effect$SingleEffect
TwoEffect <- Effect$TwoEffect
ThreeEffect <- Effect$ThreeEffect
FourEffect <- Effect$FourEffect
FiveEffect <- Effect$FiveEffect

```

---

PlotTopEffects

*Plot top n effects with their corresponding SNPs or SNP-combinations*


---

**Description**

Effects can be respectively considered as independent effects and combination effects. Independent Effect: Effect that only the SNP or SNP-combination has. Combination Effect: Effect is the addition of all effects of SNP-combination and its sub-combinations. This function plots top n

effects (including Independent Effect and Combination Effect) with their corresponding SNPs or SNP-combinations.

### Usage

```
PlotTopEffects(Vertices, Top = 20, SaveFileName = "")
```

### Arguments

Vertices	matrix. Vertices of constructed graphs, including real vertices and virtual vertices. The first column represents SNP ID or SNP-combination ID. The second column represents effect value. The third column represents the class of vertices, "1" -> real vertice, others -> virtual vertice.
Top	numeric. Top n Effects. By default, Top <- 20.
SaveFileName	character. Basic file name for saving figure. By default, SaveFileName <- "".

### Value

TopEffect	numeric. Top independent effects of SNPs or SNP-combinations.
CombinationEffect	numeric. Top combination effects of SNPs or SNP-combinations.

### Author(s)

Junliang Shang <shangjunliang110@163.com>

### References

None

### Examples

```
data(Vertices)
data(Edges)
TP <- PlotTopEffects(Vertices, Top = 20, SaveFileName = "")
TopEffect <- TP$TopEffect
CombinationEffect <- TP$CombinationEffect
```

---

pts

*SNP data*

---

### Description

SNP data

### Usage

```
data(pts)
```

**Format**

The format is: int [1:4000, 1:20] 1 2 1 3 1 2 2 1 1 1 ... - attr(\*, "dimnames")=List of 2 ..\$ : chr [1:4000] "Sample1" "Sample2" "Sample3" "Sample4" ... ..\$ : chr [1:20] "SNP1" "SNP2" "SNP3" "SNP4" ...

**References**

None

**Examples**

data(pts)

---

SingleEffect

*Main Effects of SNPs*

---

**Description**

Main Effects of SNPs

**Usage**

data(SingleEffect)

**Format**

The format is: chr [1:20, 1:2] "rs00013" "rs00010" "rs00006" "rs00001" ... - attr(\*, "dimnames")=List of 2 ..\$ : NULL ..\$ : chr [1:2] "SNP" "Value"

**References**

None

**Examples**

data(SingleEffect)

---

SubgraphSplit	<i>Split subgraphs</i>
---------------	------------------------

---

**Description**

Split subgraphs using walktrap.community algorithm

**Usage**

```
SubgraphSplit(Vertices, Edges)
```

**Arguments**

Vertices	matrix. Vertices of constructed graphs, including real vertices and virtual vertices. The first column represents SNP ID or SNP-combination ID. The second column represents effect value. The third column represents the class of vertices, "1" -> real vertice, others -> virtual vertice.
Edges	matrix. Edges of constructed graphs.

**Value**

SubgroupSNPs: list. SNPs in each subgraph of the graph.

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
data(Vertices)
data(Edges)
SubgroupSNPs <- SubgraphSplit(Vertices, Edges)
SubgroupSNPs <- SubgroupSNPs$SubgroupSNPs
```

---

TestMaxOrder	<i>Test the parameter MaxOrder</i>
--------------	------------------------------------

---

**Description**

This function check the parameter MaxOrder. MaxOrder is the maximum order of epistatic interactions that CINOEDV considered.

**Usage**

```
TestMaxOrder(MaxOrder)
```

**Arguments**

MaxOrder            character. It must be setted as "1", "2", "3", "4", or "5".

**Value**

None

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
MaxOrder <- "1"  
TestMaxOrder(MaxOrder)
```

---

TestNumberThreshold	<i>Test the parameter NumberThreshold</i>
---------------------	---

---

**Description**

This function check the parameter NumberThreshold

**Usage**

```
TestNumberThreshold(MaxOrder, NumberThreshold)
```

**Arguments**

MaxOrder            numeric. The considered maximum order of epistatic interactions. It must be setted as 1, 2, 3, 4, or 5.

NumberThreshold    character. It controls the numbers of detected SNPs or SNP-combinations with the help of RatioThreshold. The length of NumberThreshold is equal to Max-Order. Each element is an integer with the character format.

**Value**

None

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
MaxOrder <- 3
NumberThreshold <- c("5", "20", "10")
TestNumberThreshold(MaxOrder, NumberThreshold)
```

---

TestRatioThreshold    *Test the parameter RatioThreshold*

---

**Description**

This function check the parameter RatioThreshold.

**Usage**

```
TestRatioThreshold(MaxOrder, RatioThreshold)
```

**Arguments**

MaxOrder            numeric. The considered maximum order of epistatic interactions. It must be setted as 1, 2, 3, 4, or 5.

RatioThreshold    character. It controls the numbers of detected SNPs or SNP-combinations with the help of NumberThreshold. The length of RatioThreshold is equal to Max-Order. Each element is a decimal in [0,1] with the character format.

**Value**

None

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
MaxOrder <- 3
RatioThreshold <- c("1.0", "0.5", "0.2")
TestRatioThreshold(MaxOrder, RatioThreshold)
```

---

TestSNPNameFile	<i>Test the parameter TestSNPNameFile</i>
-----------------	---

---

**Description**

This function check the parameter TestSNPNameFile. If there are real SNP names which will be used for constructing graphs and further analysis, the name of file that saves real SNP names should be provided.

**Usage**

```
TestSNPNameFile(RowNum, SNPNameFileName = NA)
```

**Arguments**

RowNum            numeric. It is the number of considered SNPs.  
SNPNameFileName    character or logical (NA). The file name with its format (.mat) that saves the names of SNPs. The file has only one variable, i.e., Name. In Name, Row -> 1, Column -> SNP Name, and the length is equal to RowNum. If not exist such file (default), SNPNameFileName <- NA.

**Value**

SNPNames: character or logical (NA). Names of SNPs.

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```

RowNum <- 10
SNPNameFileName <- NA
SNPNames <- TestSNPNameFile(RowNum, SNPNameFileName)
SNPNames <- SNPNames$SNPNames

```

---

ThreeEffect	<i>Interaction Effects of three-SNP combinations</i>
-------------	--

---

**Description**

Interaction Effects of three-SNP combinations

**Usage**

```
data(ThreeEffect)
```

**Format**

The format is: chr [1:1137, 1:4] "rs00002" "rs00008" "rs00004" "rs00001" ... - attr(\*, "dim-names")=List of 2 ..\$ : NULL ..\$ : chr [1:4] "SNP1" "SNP2" "SNP3" "Value"

**References**

None

**Examples**

```
data(ThreeEffect)
```

---

tic	<i>Start stopwatch timer</i>
-----	------------------------------

---

**Description**

tic starts a stopwatch timer to measure performance. The function records the internal time at execution of the tic command. Display the elapsed time with the toc function.

**Usage**

```
tic(gcFirst = TRUE, type = c("elapsed", "user.self", "sys.self"))
```

**Arguments**

gcFirst	gcFirst <- TRUE
type	type <- c("elapsed","user.self","sys.self")



**Value**

None

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
tic()
Sys.sleep(2)
toc()
```

---

toc

*Read elapsed time from stopwatch*

---

**Description**

toc reads the elapsed time from the stopwatch timer started by the tic function. The function reads the internal time at the execution of the toc command, and displays the elapsed time since the most recent call to the tic function that had no output, in seconds.

**Usage**

```
toc()
```

**Value**

None

**Author(s)**

Junliang Shang <shangjunliang110@163.com>

**References**

None

**Examples**

```
tic()
Sys.sleep(2)
toc()
```

---

TwoEffect	<i>Interaction Effects of two-SNP combinations</i>
-----------	--

---

**Description**

interaction Effects of two-SNP combinations

**Usage**

```
data(TwoEffect)
```

**Format**

The format is: chr [1:187, 1:3] "rs00008" "rs00005" "rs00013" "rs00005" ... - attr(\*, "dimnames")=List of 2 ..\$ : NULL ..\$ : chr [1:3] "SNP1" "SNP2" "Value"

**References**

None

**Examples**

```
data(TwoEffect)
```

---

Vertices	<i>Vertices of constructed graphs</i>
----------	---------------------------------------

---

**Description**

Vertices of constructed graphs, including real vertices and virtual vertices.

**Usage**

```
data(Vertices)
```

**Format**

The format is: chr [1:37, 1:3] "rs00002" "rs00008" "rs00004" "rs00001" ... - attr(\*, "dimnames")=List of 2 ..\$ : NULL ..\$ : chr [1:3] "id" "value" "label"

**References**

None

**Examples**

```
data(Vertices)
```

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