

Package ‘SpectralGEM’

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Title Discovering Genetic Ancestry Using Spectral Graph Theory

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Description Discovering Genetic Ancestry Using Spectral Graph Theory

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full_matching	<i>Matching case and control</i>
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Description

The function matches case and control based on distances as measured by the significant eigenvectors. Internal function.

Usage

```
full_matching(ext)
```

Arguments

ext	the file extension of the distance matrix
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Details

The function calls the full matching program in optmatch library.

Value

ma	A matrix that consists of sampleId, matched strata, and case/control status.
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getExcludeFile	<i>getExcludeFile</i>
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Description

Internal function

Usage

```
getExcludeFile(InputFile)
```

Arguments

InputFile	Input file name
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getRecord	<i>getRecord</i>
-----------	------------------

Description

Internal function

Usage

getRecord(ext)

Arguments

ext	file extension
-----	----------------

getVersion	<i>getVersion</i>
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Description

Internal function.

Usage

getVersion(InputFile)

Arguments

InputFile	Input file name.
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H	<i>Matrix example</i>
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Description

A matrix that can be used to match individuals into homogeneous strata.

Usage

data(H)

Format

The format is: num [1:345, 1:345] 2.941 0.048 -0.047 0.023 0.055 ... - attr(*, "dimnames")=List of 2 ..\$: chr [1:345] "1" "2" "3" "4"\$: chr [1:345] "V5" "V6" "V7" "V8" ...

id.info	<i>Sample information matrix</i>
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Description

A four-column matrix.

Usage

```
data(id.info)
```

Format

A data frame with 345 observations on the following 4 variables.

sampleId a numeric or string vector

sex a numeric vector

case.1/control.2 a numeric vector

groupId a numeric vector

InFile	<i>Generate a text file</i>
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Description

The function generates a text file that contains the parameters needed in the main fortran program and saves it in the current directory.

Usage

```
InFile(identifier="smal", stage="1", directory=".",
        MMfile="MMprime.txt", excludefile="exclude.txt",
        idlength=8, mincluster=10, logtype=0,
        mdim=-1, msnp=-1,
        outfile="matching_input.txt")
```

Arguments

identifier	Must be 4-letters long.
stage	Must be 1-letter long.
directory	The directory where the files will be generated.
MMfile	The MMprime matrix file name.
excludefile	The name of the file where the outliers have been or will be written.

idlength	The number of letters the longest sample name has.
mincluster	The smallest cluster required when do clustering, must be at least 5.
logtype	The type of log information output to the log file: 0=limited, 2=lots.
mdim	The maximum number of eigenvalues to print to the output file. The default is set at -1, which prints out every eigenvalues.
msnp	The number of SNPs to be used in determine the threshold for the significant eigenvalues. The default is set at -1, which the program estimates the value.
outfile	The name of the output file.

Details

The function generates a text file with one column which contains all the parameters needed. The parameters need to be in the right order in order for the main fortran program to use.

Value

A text file is saved in the current directory.

Author(s)

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References

<http://wpcr.wpic.pitt.edu/WPICCompGen/Spectral-GEM/GEM+.htm>

See Also

http://wpcr.wpic.pitt.edu/WPICCompGen/Spectral-GEM/matching_input.txt

loadInputFile	<i>Load the input file</i>
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Description

Internal function.

Usage

```
loadInputFile(InputFile)
```

Arguments

InputFile file name

MMfile

Produce a .txt file that contains the MM prime matrix.

Description

The function produces a .txt file of the proper format that contains the input data and the adjacency matrix. Because a common choice for the latter is MM' , this is called the MM prime matrix by default. This file is loaded to the main fortran program to do eigenvalue decomposition. Alternatively, the output file can be created from an input file containing M by the fortran program located at http://wpicr.wpic.pitt.edu/WPICCompGen/MMp/MMp_page.htm.

Usage

```
MMfile(H = H, sampleInfo = id.info, n=dim(H)[1], ntag=ntag, outfile = "MMprime.txt")
```

Arguments

H	A square symmetric matrix.
sampleInfo	A 4-column matrix containing sample_id, sex, case_control status, and group_id
n	Number of individual in the H matrix
ntag	Number of tag SNPs used to generate the H matrix.
outfile	The text file to write to. The default is set as MMprime.txt.

Details

The first two lines in the output file contains the information about the square matrix. The first line is the number of individuals in the matrix. The second line is the number of tag SNPs. The rest of the file is a table. Each line in the table contains the sample ID, gender, case/control status, group ID, and the square matrix.

Value

A text file is produced in the current directory.

Author(s)

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References

<http://wpicr.wpic.pitt.edu/WPICCompGen/Spectral-GEM/directions.pdf>

See Also

http://wpicr.wpic.pitt.edu/WPICCompGen/MMp/MMp_page.htm

pc_graphs_GEMp	<i>Plot ancestral structures</i>
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Description

The function makes .pdf and .ps plots based on the significant eigenvectors from the SpectralGEM function.

Usage

```
pc_graphs_GEMp(ext)
```

Arguments

`ext` the file extension generated by the identifier and the stage. The values are printed out in the R console after running SpectralGEM().

Details

The function plots pairs of principle componets corresponding to the significant eigenvectors.

Value

The plots are in .pdf form and .ps form under the current directory.

Author(s)

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References

<http://wpicr.wpic.pitt.edu/WPICCompGen/Spectral-GEM/GEM+.htm>

Examples

```
# pc_graphs_GEMp("small")
```

pc_graphs_GEMpClusters

Plot ancestral structures with cluster id

Description

The function generates ancestral plots in .pdf and .ps form.

Usage

```
pc_graphs_GEMpClusters(ext)
```

Arguments

ext the identifier and stage concatenated

Details

The function plots pairs of principle componets corresponding to the significant eigenvectors. Use only after the clustering step.

Value

The plots are put in the current folder.

Author(s)

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References

<http://wpicr.wpic.pitt.edu/WPICCompGen/Spectral-GEM/GEM+.htm>

Examples

```
# pc_graphs_GEMpClusters("smal1")
```

plotLam

Plot the eigenvalues

Description

The function plots the eigenvalues the main fortran program produces. It helps user to determine the number of dimensions (mdim) to be used in the program.

Usage

plotLam(ext)

Arguments

ext The identifier

Details

The function generates a plot of all the eigenvalues.

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References

<http://wpicr.wpic.pitt.edu/WPICCompGen/Spectral-GEM/GEM+.htm>

SpectralGEM

Software for Matching

Description

SpectralGEM is designed to find the ancestry vectors and match cases and controls for association analysis.

Usage

SpectralGEM(InputFile = "matching_input.txt",CM="CM",outlier=TRUE)

Arguments

InputFile	The name of the file that contains the input parameters.
CM	options are C, M, and CM. C: for clustering only with removing outliers. M: for matching only without examining the outliers. CM: for clustering, removing outliers, and matching.
outlier	An option to remove outliers by checking the distributions of the distances between cases and contrls. Only applicable when CM="C"

Value

c1	a two column matrix: the first column is the sample ID, the second column is the cluster id
U	a matrix, the first column is the sample ID, the second columns is group id, the third column is the trivial eigenvector U0, and rest are the significant eigenvectors
lambda	eigenvalues corresponding to the eigenvectors
d	the distance between case and control

The program performs clustering and matching or matching only. The c1 values are generated at the clustering stage. The significant eigenvectors are generated at the matching stage.

A series of files are produced in the current directory.

Note

The function depends on the local fortran executable. The function asks whether the user would like to download the executable before it automatically downloads the executable from the reference website.

Author(s)

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References

<http://wpicr.wpicr.pitt.edu/WPICCompGen/Spectral-GEM/GEM+.htm>

Examples

```
data(H)
data(id.info)
MMfile(H=H,sampleInfo=id.info,ntag=1000,outfile="MMprime.txt")
InFile(identifier="smal",stage=1,directory=".",
        MMfile="MMprime.txt",excludefile="exclude.txt",
        idlength=8,mincluster=10,logtype=0,
        outfile="matching_input.txt")
```

#not run#

```

#out=SpectralGEM() #first do clustering and remove outliers
                    #then do matching
#out=SpectralGEM(CM="C") # do clustering and remove
                    #outliers
#out=SpectralGEM(CM="M") # do matching without removing
                    #outliers

# For continuous response, create new id.info for the H matrix
data(H)
n=345
y=sample(c(rnorm(mean=0,172),rnorm(mean=1,173)))
cc=rep(1,345)
cc[y>median(y)]=2 #create case control
newid.info=cbind(c(1:n),rep(1,n),cc,cc)
MMfile(H=H,sampleInfo=newid.info,ntag=1000,outfile="MMprime1.txt")
InFile(identifier="smal",stage=1,directory="./",
       MMfile="MMprime1.txt",excludefile="exclude.txt",
       idlength=8,mincluster=10,logtype=0,
       outfile="input.txt")

#not run#
#out=SpectralGEM(InputFile="input.txt",CM="C")

# buildin ancestry plots
#Current version: ext= smal1 ;
#not run
#pc_graphs_GEMpClusters("smal1")
#pc_graphs_GEMp("smal1")

#plot from the SpectralGEM output,
#significant eigenvectors start from out$U[,4] with
#significant eigenvalues start from from out$lambda[2]
#not run
#plot(sqrt(out$lambda[2])*out$U[,4],sqrt(out$lambda[3])*out$U[,5],
#col=out$U[,2],xlab="PC 1",ylab="PC 2") #for PC plots

```

updateExcludeFileDstr *Exclude outlier*

Description

Exclude outlier by examing the distribution of case/control distances. Internal functon.

Usage

```
updateExcludeFileDstr(excludeFile, ext)
```

Arguments

excludeFile	the text file that the outliers will be recorded to
ext	the file extension used in runing the program

Value

The outliers are recorded in the `excludeFile` in the current folder.

<code>updateInputFile</code>	<i>Update input file</i>
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Description

Internal function.

Usage

```
updateInputFile(oldInputFile, newInputFile, excludeFile)
```

Arguments

<code>oldInputFile</code>	old input file name
<code>newInputFile</code>	new input file name
<code>excludeFile</code>	exclude file name

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