

Package ‘GExMap’

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Title R functions for analysis genomic distribution of genes lists produced by transcriptomic studies

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Depends R (>= 2.0.1),multtest

Description - Perform statistical tests to unveil genomic clusters - Produces garphical interpretations of the statistical results in pdf files - Perform a Gene Ontology analysis and produces graphic results in pdf files

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`corr`*Correlation file to be used for example by GExMap*

Description

Correlation between ensembl ID and microarray ID.

Details

This dat set included in the GExMap package as an example.

Author(s)

Nicolas Cagnard <nicolas.cagnard@inserm.fr>

See Also

GExMap

`data`*Genomic data set to be used for example by GExMap*

Description

Text file tab separated with two columns. The first columns is for the probes identifiers and the second for the variation code (1 or -1). The title of the first column must be formatted as follow: [type of microarray], [microarray name]. The title of the second column must be "expression".

Details

This dat set included in the GExMap package as an example.

Author(s)

Nicolas Cagnard <nicolas.cagnard@inserm.fr>

See Also

GExMap

gex.mapping	<i>Function from the GExMap package which format the genome to be used by GExMap</i>
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Description

Format the genome according to the scale and the genomic distribution of the user gene list.

Usage

```
gex.mapping(data, list.chr, scale, I, list.ENS)
```

Arguments

data	Matrix of the data.data file
list.chr	Data about the analyzed chromosome
scale	Scale to format the genome.
I	This function is performed chromosome by chromosome, I is the name of the analyzed chromosome
list.ENS	List of ENSEMBL genes produced by the load.corr() function.

Details

This function is included in the GExMap package and could not be used independently.

Author(s)

Nicolas Cagnard <nicolas.cagnard@inserm.fr>

See Also

GExMap

gexgo	<i>Perform a GO analysis of the tested gene list</i>
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Description

Search and analyze the GO identifiers for each identified gene from the tested gene list and produces 3 scored lists, one for each GO (Biological processes, Cellular component and Biological function.) This function is used or not by GExMap, called by the main function gexmap() if the variable isGO=TRUE (by default).

Usage

```
gexgo(list.ENS, source, res)
```

Arguments

<code>list.ENS</code>	List of all identified genes
<code>source</code>	Source data folder where is located the go.Rdata file
<code>res</code>	Results folder where will be saved all the data files produced by the function

Details

This function is included in the GExMap package and could not be used independently.

Value

A GO.results folder is created which contains 3 files for each GO:\

<code>detail. .txt</code>	Complete list of genes for each GO ID sorted by decreasing score
<code>GO. .txt</code>	List of scored GO id with scores and relative proportion of each ID
<code>GO_ .pdf</code>	Pie chart of the GO ID which score is > 1 percent

Author(s)

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See Also

GExMap

gexgraph

Produces graphics to illustrate genomic density and statistical test results

Description

Function of the GExMap package which produces graphics in pdf files with data produces by the `gexmap()` main function.

Usage

```
gexgraph(genome.test, scale, results.graph, W)
```

Arguments

<code>genome.test</code>	Matrix of all data of genomic density, localizations and tests results to be graphically reported.
<code>scale</code>	The variable <code>scale</code> is the scale used to produce the graphics and to perform the statistical tests. Customizable in input in the <code>gexmap(scale="")</code> main function, the scale is set to 1 000 000 bp by default.
<code>results.graph</code>	Folder path where will be saved all the graphics pdf files.
<code>W</code>	<code>W</code> is the variable which permit to produce graphics for each of the two methods of hazard estimation. 1 for the specific method, 2 for the global method.

Details

This function is included in the GExMap package and could not be used independently.

Value

This function produces on pdf file by chromosom statistically validated.

Author(s)

Nicolas Cagnard <nicolas.cagnard@inserm.fr>

See Also

GExMap

`gexload.corr` *Function from the GExMap package which annotates identifier list*

Description

Creates a list of ENSEMBL id from the user gene list which contains microarray id

Usage

```
gexload.corr(data, list, scale, source, res)
```

Arguments

<code>data</code>	The ENSEMBL genome reference data.
<code>list</code>	The user gene list to be tested and which contains all id which are to be annotated.
<code>scale</code>	Scale to format the genome.
<code>source</code>	The source folder where would be placed all the Rdata files.
<code>res</code>	The results folder where would be saved all the result files.

Details

This function is included in the GExMap package and could not be used independently.

Author(s)

Nicolas Cagnard <nicolas.cagnard@inserm.fr>

See Also

GExMap

gexload.data	<i>Function from the GExMap package which upload data files to be used by GExMap</i>
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Description

Upload automatically (or ask to the user) the data.Rdata file and the *.Rdata file specific to the user identifier type.

Usage

```
gexload.data(source, genome)
```

Arguments

source	The source folder where would be placed all the Rdata files.
genome	ENSEMBL genome whith all genomic informations

Details

This function is included in the GExMap package and could not be used independently.

Author(s)

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See Also

GExMap

gexmap

*Main function of the GExMap package***Description**

GExMap analyze genomic distribution and GO of genes lists produced by transcriptomic studies.

Usage

```
gexmap(genome = "homosapiens", scale = "", source = "", res = "", isGO = TRUE, isMAP = FALSE, lim_chi = 1, global_test_choice = 4, pcorr = "fdr", pcorr_v = "fdr")
```

Arguments

genome	~~Describe genome here~~
scale	The variable <code>scale</code> is the scale used to produce the graphics and to perform the statistical tests. Customizable in input in the <code>gexmap(scale="")</code> main function, the scale is set to 1 000 000 bp by default.
source	Folder which would contain all data source as *.Rdata files.
res	Folder which will contain the results data files and folders.
isGO	TRUE/FALSE, customizable input variable to perform or no the Gene Ontology analysis of the tested gene list.
isMAP	TRUE/FALSE, customizable input variable to perform or no the graphical reports of genomic analysis in pdf files.
lim_chi	Limit number of gene necessary to perform the CHI squared global test to statistically select the chromosomes. (used in the <code>gestest()</code> function).
global_test_choice	Choice of chromosomes selection according to the results of the global statistical tests (see <code>gextest()</code> function).\ 1- At least CHI is OK\ 2- At least Wilcoxon is OK\ 3- CHI & Wilcoxon are OK\ 4- CHI OR Wilcoxon is OK\ Default value is set at 4.
pcorrd	Choice of pvalue correction method for the global tests (see <code>gextest()</code> function).
pcorr_v	Choice of pvalue correction method for the local tests (see <code>gextest()</code> function).

Author(s)

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References

<http://gexmap.site.voila.fr/>

Examples

```
gexmap(genome="homosapiens", scale="", source="test", res="", isGO=TRUE, isMAP=TRUE, lim_chi=1, global_test_choice=4, pcorr="fdr", pcorr_v="fdr")
```

gextest

Perform the statistical analysis step

Description

This function selects the chromosomes by two global tests comparing an estimated hazard genomic distribution to the real distribution extracted from the user list. If the chromosome is selected, a local analysis is performed to localize and test regions of interest .

Usage

```
gextest(genome.test, nhazard, results.graph, lim_chi, global_test_choice, pcorrd, p
```

Arguments

genome.test	All genomic data to be tested.
nhazard	Total number of genes of the hazard distribution.
results.graph	Data necessary to produces the graphic files.
lim_chi	Limit of genes to perform the CHI squared global test (set to 5 by default).
global_test_choice	Choice of chromosomes selection according to the results of the global statistical tests (see <code>gextest()</code> function).\ 1- At least CHI is OK\ 2- At least Wilcoxon is OK\ 3- CHI & Wilcoxon are OK\ 4- CHI OR Wilcoxon is OK\ Default value is set at 4.
pcorrd	Choice of pvalue correction method for the global tests:\ 1- "Bonferroni" 2- "Holm" 3- "Hochberg" 4- "SidakSS" 5- "SidakSD" 6- "BH" 7- "BY"
pcorrv	Choice of pvalue correction method for the local tests:\ 1- "Bonferroni" 2- "Holm" 3- "Hochberg" 4- "SidakSS" 5- "SidakSD" 6- "BH" 7- "BY"

Details

This function is included in the GExMap package and could not be used independently.

Author(s)

Nicolas Cagnard <nicolas.cagnard@inserm.fr>

See Also

GExMap

go

GO data file

Description

List of GO ID and descriptions.

Details

This dat set included in the GExMap package as an example.

Author(s)

Nicolas Cagnard <nicolas.cagnard@inserm.fr>

See Also

GExMap

list

Gene list to be used for example by GExMap

Description

Text file tab separated with two columns. The first columns is for the probes identifiers and the second for the variation code (1 or -1). The title of the first column must be formatted as follow: [type of microarray], [microarray name]. The title of the second column must be "expression".

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See Also

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