Package ‘GExMap’

February 19, 2015

Type Package

Title A visual, intuitive, easy to use software giving access to a new type of information buried into your microarray data.

Version 1.1.3

Depends R (>= 2.10), Biobase, multtest

Date 2011-11-19

Author Nicolas Cagnard

Maintainer Nicolas Cagnard <`nicolas.cagnard@gmail.com`>

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

License GPL

LazyLoad yes

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R topics documented:

`GExMap-package` *GExMap: A visual, intuitive, easy to use software giving access to a new type of information buried into your microarray data.*

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\

Details

Package:	GExMap
Type:	Package
Version:	1.1.3
Date:	2011-11-18
License:	GPL version 2 or newer
Depends:	multtest
LazyLoad:	yes

Author(s)

Nicolas Cagnard

Maintainer: Nicolas Cagnard <nicolas.cagnard@gmail.com>

References

http://gexmap.voila.net/index.html Research Article JPB/Vol.2.1 051- 059(2009)/January 2009 doi:10.4172/jpb.1000060 GExMap: An Intuitive Visual Tool to Detect and Analyze Genomic Distribution in Microarray-generated Lists of Differentially Expressed Genes Nicolas Cagnard, Carlo Lucchesi, Gilles Chiocchia

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`corr` *Correspondence file used as an example by GExMap*

Description

Correspondence between ensembl ID and microarray ID.

Usage

```
data(corr)
```

Details

The data set included in the GExMap package as an example.

Source

http://gexmap.voila.net/index.html

`data` *Genomic data set used as an 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 formated as follow: [type of mocroarray], [microarray name]. The title of the second column must be "expression".

Usage

```
data(data)
```

Details

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

Source

http://gexmap.voila.net/index.html

`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 = FALSE, isMAP = TRUE, lim_chi =
```

Arguments

`genome`	Annotation data and genomic localizations for all genes of a specific genome
`scale`	The variable `scale` is the scale used to produce the graphics and to perform the statistical tests. Customizable in input in the gexmap(scale="") main function, the scale is set to 1 000 000 bp by default.
`source`	Folder which would contain alla 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 reoprts 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 `gestest()` function).
`global_test_choice`	Choice of chromosomes selection according to the results of the global statistical tests (see `gextest()` 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 `gextest()` function).
`pcorrv`	Choice of pvalue correction method for the local tests (see `gextest()` function).

Author(s)

Nicolas Cagnard <nicolas.cagnard@gmail.com>

References

http://gexmap.voila.net/index.html Research Article JPB/Vol.2.1 051- 059(2009)/January 2009 doi:10.4172/jpb.1000060 GExMap: An Intuitive Visual Tool to Detect and Analyze Genomic Distribution in Microarray-generated Lists of Differentially Expressed Genes Nicolas Cagnard, Carlo Lucchesi, Gilles Chiocchia

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`go` *GO data file*

Description

List of GO ID and descriptions.

Usage

```
data(go)
```

Details

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

Source

http://gexmap.voila.net/index.html Research Article JPB/Vol.2.1 051- 059(2009)/January 2009 doi:10.4172/jpb.1000060 GExMap: An Intuitive Visual Tool to Detect and Analyze Genomic Distribution in Microarray-generated Lists of Differentially Expressed Genes Nicolas Cagnard, Carlo Lucchesi, Gilles Chiocchia

References

http://gexmap.voila.net/index.html

`list` *Gene list used as an 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 formated as follow: [type of mocroarray], [microarray name]. The title of the second column must be "expression".

Usage

```
data(list)
```

Format

A data frame with 3856 observations on the following variable.

`V2` a factor with levels `-1` `1` `expression`

Details

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

Source

http://gexmap.voila.net/index.html

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