

Package ‘GExMap’

January 2, 2012

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 Biobase, multtest

Date 2011-11-19

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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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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)

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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

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 formatted as follow: [type of microarray], [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 = 5,
```

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 <code>gexmap(scale="")</code> 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 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).
pcorrv	Choice of pvalue correction method for the local tests (see <code>gextest()</code> function).

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References

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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 formatted as follow: [type of mocoarray], [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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