Package 'IsoGeneGUI'

October 16, 2019

Type Package

Title A graphical user interface to conduct a dose-response analysis
of microarray data

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Description

The IsoGene Graphical User Interface (IsoGene-GUI) is a user friendly interface of the Iso-
Gene package which is aimed to identify for genes with a monotonic trend in the expression lev-
els with respect to the increasing doses. Additionally, GUI extension of original package con-
tains various tools to perform clustering of dose-response profiles. Testing is ad-
dressed through several test statistics: global likelihood ratio test (E2), Bartholomew 1961, Bar-
low et al. 1972 and Robertson et al. 1988), Williams (1971, 1972), Mar-
cus (1976), the M (Hu et al. 2005) and the modified M (Lin et al. 2007). The p-
values of the global likelihood ratio test (E2) are obtained using the exact distribution and permu-
tations. The other four test statistics are obtained using permutations. Several p-values adjust-
ment are provided: Bonferroni, Holm (1979), Hochberg (1988), and Sidak procedures for con-
trolling the family-wise Type I error rate (FWER), and BH (Ben-
jamini and Hochberg 1995) and BY (Benjamini and Yekutieli 2001) procedures are used for con-
trolling the FDR. The inference is based on resampling methods, which control the False Discov-
ery Rate (FDR), for both permutations (Ge et al., 2003) and the Significance Analysis of Mi-
croarrays (SAM, Tusher et al., 2001). Clustering methods are outsourced from CRAN pack-
ages ORCME, ORIClust. The package ORCME is based on delta-
clustering method (Cheng and Church, 2000) and ORIClust on Order Restricted Information Cri-
terion (Liu et al., 2009), both perform same task but from different perspective and their out-
puts are clusters of genes. Additionally, profile selection for given gene based on General-
ized ORIC (Kuiper et al., 2014) from package goric and permutation test for E2 based on pack-
age orQA are included in IsoGene-GUI. None of these four packages has GUI.

Depends tcltk, xlsx

Imports Rcpp, tkrplot, multtest, relimp, geneplotter, RColorBrewer,
Iso, IsoGene, ORCME, ORIClust, orQA, goric, ff, Biobase, jpeg

Suggests RUnit

biocViews Microarray, DifferentialExpression, GUI

License GPL-2

LazyLoad yes

Collate about.R adjustment.R browse.R browse2.R CalcStat.R
ChooseStat.R CVPlot.R diginum.R doGORIC.R doORCME.R
doORIClust.R ExactE2.R ExactE2Val.R exit.R get.ResSAM.R
getDose.R IsofudgeMod.R IsofudgeMod2.R IsoGenemMod.R Isomean.R
Isoplot.R IsoPlot.mod.R IsoPlotSldr.R IsopvalPlot.R
IsopvaluePlot.R IsoqqstatMOD.R IsoRawpMod.R IsoGeneGUI.R
IsoStat.R IsoTest.R loadDataSet.R MeanDiff.R onHelpIsoGene.R
IsoGeneGUIHelp.R openFile.R orQAE2.R Permutation.R PermuteSAM.R
Plot2.R PlotFdrDlt.R PlotFPDlt.R plotORCME.R PlotSigDlt.R
printExact.R printOrQA.R printsummary.R PvalAdj.R samplot2.R
save.result.R save.result.mult.R save.result.ORCME.R
save.result.ORICC.R saveDir.R SaveGraph.R saveXls.R savingRwd.R
SEPlot.R Setseed.R showdata.R Signif.R summ.R UserPlot.R
UserPlotting.R xfudge.R IsoGeneGUIVignette.R

URL http:
//ibiostat.be/online-resources/online-resources/isogenegui/isogenegui-package

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git_branch RELEASE_3_9

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R topics documented:

IsoGeneGUI-package   *IsoGeneGUI Graphical User Interface for the IsoGene package*

Description

The IsoGene Graphical User Interface (IsoGene-GUI) is a user friendly interface of the IsoGene package which is aimed to identify for genes with a monotonic trend in the expression levels with respect to the increasing doses. Additionally, GUI extension of original package contains various tools to perform clustering of dose-response profiles. Testing is addressed through several test statistics: global likelihood ratio test (E2), Bartholomew 1961, Barlow et al. 1972 and Robertson et al. 1988), Williams (1971, 1972), Marcus (1976), the M (Hu et al. 2005) and the modified M (Lin et al. 2007).

The p-values of the global likelihood ratio test (E2) are obtained using the exact distribution and permutations. The other four test statistics are obtained using permutations. Several p-values adjustment are provided: Bonferroni, Holm (1979), Hochberg (1988), and Sidak procedures for controlling the family-wise Type I error rate (FWER), and BH (Benjamini and Hochberg 1995) and BY (Benjamini and Yekutieli 2001) procedures are used for controlling the FDR. The inference is based on resampling methods, which control the False Discovery Rate (FDR), for both permutations (Ge et al., 2003) and the Significance Analysis of Microarrays (SAM, Tusher et al., 2001).

Clustering methods are outsourced from CRAN packages ORCME, ORIClust. The package OR-CME is based on delta-clustering method (Cheng and Church, 2000) and ORIClust on Order Restricted Information Criterion (Liu et al., 2009), both perform same task but from different perspective and their outputs are clusters of genes. Additionally, profile selection for given gene based on Generalized ORIC (Kuiper et al., 2014) from package goric and permutation test for E2 based on package orQA are included in IsoGene-GUI. None of these four packages has GUI.

Details

The IsoGene Graphical User Interface (IsoGene-GUI) is a user friendly interface of the IsoGene package enriched by methods from packages ORIClust, ORCME, orQA and goric.

Author(s)

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References

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Examples

```
## Not run:
library(IsoGeneGUI)
IsoGeneGUI()

## End(Not run)
```

IsoGeneGUI   *IsoGeneGUI*

Description

This function will load the IsoGeneGUI package.

Usage

```
IsoGeneGUI()
```

Details

To run the package, we use the function: IsoGeneGUI().

Author(s)

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Examples

```
## Not run:
library(IsoGeneGUI)
IsoGeneGUI()

## End(Not run)
```

IsoGeneGUIHelp *IsoGeneGUI Help*

Description

Function to for opening the IsoGeneGUI help.

Usage

```
IsoGeneGUIHelp()
```

Details

To run the package, we use the function: IsoGeneGUI().

Author(s)

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Examples

```
## Not run:
library(IsoGeneGUI)
IsoGeneGUIHelp()

## End(Not run)
```

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