

# Package ‘IsoGeneGUI’

April 5, 2014

**Type** Package

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

**Version** 1.18.0

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**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 using 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 permutation. The other four test statistics are obtained using permutation. 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) (both permutations (Ge et al., 2003) and the Significance Analysis of Microarrays (SAM), Tusher et al., 2001).

**Depends** tcltk, tkrplot, IsoGene

**Imports** multtest, relimp, WriteXLS,gdata, RColorBrewer, geneplotter

**Suggests** RUnit

**biocViews** Microarray, DifferentialExpression, GUI

**References** Pramana S., Haldermans P., and Verbeke, T. (2012) A User Friendly Interface for Analyzing Dose-response Studies in Microarray Experiments: The IsoGeneGUI package. A Book Chapter in Lin, D., Shkedy, Z., Amaratunga, D., Yekutieli, D and Bijnens, L. (Editors), “Modeling of Dose-response Microarray Data in Early Drug Development Experiments Using R”, Springer.

**License** GPL-2

**LazyLoad** yes

**Collate** about.R adjustment.R browse.R browse2.R CalcStat.R  
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**URL** <http://www.ibiostat.be/software/IsoGeneGUI/index.html>

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### 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 using 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 permutation. The other four test statistics are obtained using permutation .

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.

### Details

The IsoGene Graphical User Interface (IsoGene-GUI) is a user friendly interface of the IsoGene package.

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**References**

Pramana S., Haldermans P., and Verbeke, T. (2012) A User Friendly Interface for Analyzing Dose-response Studies in Microarray Experiments: The IsoGeneGUI package. A Book Chapter in Lin, D., Shkedy, Z., Amaratunga, D., Yekutieli, D and Bijmens, L. (Editors), "Modeling of Dose-response Microarray Data in Early Drug Development Experiments Using R", Springer.

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Williams, D. (1972) The comparison of several dose levels with a zero dose control. *Bio- metrics*, 28, 519-531.

**Examples**

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

IsoGeneGUI

*IsoGeneGUI*

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**Description**

This function will load the IsoGeneGUI package.

**Usage**

```
IsoGeneGUI()
```

**Details**

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

**Author(s)**

Author: Setia Pramana

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**Examples**

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

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IsoGeneGUIHelp*IsoGeneGUI Help*

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**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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