IsoGeneGUI Package Vignette

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1 Introduction

The IsoGene Graphical User Interface (IsoGeneGUI) is a user friendly interface of the IsoGene package which is aimed to perform analysis of dose-response studies in microarray experiments. The IsoGeneGUI is developed for the user with no or limited knowledge about R programming so he/she can perform the analysis of dose-response in microarray setting easily. This GUI was developed using tcl/tk package. The statistical methodologies (test statistics, etc) used in this package are discussed by Lin et.al (2007 and 2008).

2 Usage

To run the package

```
> library(IsoGeneGUI)
> IsoGeneGUI()
```

3 Menus

The package has four main menus: File, Analysis, Plots and Help.

1. File:
   (a) Open Data
      i. R workspace (*.RData files)
      ii. Excel or text file (*.xls or *.txt files)
   (b) Show Data
   (c) Exit
2. Analysis:
   (a) Set seed
   (b) Likelihood Ratio Test E2 Analysis
   (c) Permutation Analysis
   (d) Significant Analysis of Microarrays (SAM)
      i. SAM Permutation

ii. SAM Analysis

3. Plot:
   (a) IsoPlot
   (b) Permutation Plot
   (c) SAM Plot
      i. Plot of FDR vs. Delta
      ii. Plot of number of significant genes vs. Delta
      iii. Plot of number of False Positive vs. Delta
   (d) User defined scatter plot
4. Help:
   (a) IsoGene Help
   (b) IsoGeneGUI Help
   (c) About

User can follow the links of the IsoGeneGUI package help to obtain more detail about the package. A full reference manual can be obtained from internet: `http://www.censtat.uhasselt.be/software/`

References

1. Lin, D., Shkedy, Z., Yekutieli, D., Burzykowski, T., Gĺohlmann, H., De Bondt, A., Perera, T., Geerts, T. and Bijnens, L. (2007) Testing for trends in dose-response microarray experiments: A comparison of several testing procedures, multiplicity and resamplingbased inference. *Statistical Applications in Genetics and Molecular Biology*, **6(1)**, Article 26.

2. Lin, D., Shkedy, Z., Burzykowki, R., Ion, T., Göhlmann, H.W.H., De Bondt, A., Perera, T., Geerts, T., Bijnens, L. (2008) An investigation on performance of Significance Analysis of Microarray (SAM) for the comparisons of several treatments with one control in the presence of small variance genes. *Biometrical Journal*, Multiple Comparison Problem, Special Issue, **50(5)**, 801–823.