IsoGeneGUI: a graphical user interface for analyzing dose-response studies in microarray experiments

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The main objectives in drug-discovery studies in the pharmaceutical industry are to find a safe and efficacious dose or a dose range, and to establish a dose response relationship. The emerging of biomedical technologies leads to an integration of dose-response studies with microarray technologies. In this setting, the response are gene-expressions measured at a set of increasing dose levels. The aim of such a study is to identify a set of genes with monotonic increasing/decreasing mean expressions at increasing doses. Lin et al. (2010) discussed several testing procedures for dose-response studies of microarray experiments. These testing procedures which take into account the order restriction of means with respect to increasing doses, are Williams (Williams, 1971 and 1972), Marcus (Marcus, 1976), the likelihood ratio test (Barlow et al. 1972, and Robertson et al. 1988), the M statistic (Hu et al., 2005), and the modified M statistic (Lin et al., 2007).

The aforementioned methods are implemented in an R package called **IsoGene** (Pramana et al., 2010). The **IsoGene** package requires the user to have basic knowledge of R. To overcome this limitation, a user friendly interface called **IsoGeneGUI** is developed. It is a menu driven package and data analysis can be perform simply by selecting options from the menus of the package. The **IsoGeneGUI** is developed by using the R-Tcl/Tk interface implemented in the **tcltk** package (Dalgaard, 2001).

The inference is based on resampling methods to obtain the p-values (Ge et al., 2003). The multiplicity adjustment includes: Bonferroni, Holm (1979), Hochberg (1988), and Sidak procedures for controlling the family-wise Type I error rate (FWER), and the Benjamini-Hochberg (BH-FDR, Benjamini and Hochberg, 1995) and Benjamini-Yekutieli (BY-FDR, Benjamini and Yekutieli, 2001) procedures for controlling the False Discovery Rate (FDR), and the Significance Analysis of Microarrays (SAM, Tusher et al., 2001).

The package provides three options in its Analysis menu (1) Likelihood ratio test statistic, (2) Permutations, and (3) Significance Analysis of Microarrays (SAM). The package produces some default graphical displays as well as user-defined graphical output which can be save as different image types. The analysis results can be saved in R workspaces and/or excel files. The IsoGeneGUI package can be obtained from:

- R-forge site: https://r-forge.r-project.org/projects/isogenegui/,
- **IsoGene** project site: http://www.ibiostat.be/software/IsoGeneGUI/index.html.

At the **IsoGene** project site, users manuals and example data sets can be downloaded. Moreover, illustrative examples are provided at the site as well.

References

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