

OLINgui

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OLINgui

Graphical user interface for OLIN package

Description

The function `OLINgui` provides a graphical user interface for visualisation, normalisation and quality testing of two-channel microarray data. It is based on the functions of the OLIN package.

Usage

`OLINgui ()`

Details

The function `OLINgui` launches a graphical user interface for the OLIN package. It is based on Tk widgets using the R TclTk interface by Peter Dalgaard. It also employs some pre-made widgets from the `tkWidgets` Bioconductor-package by Jianhua Zhang for the selection of objects/files to be loaded.

`OLINgui` provides a convenient interface to most functionalities of the OLIN package without restriction of options. An exception is the visualisation, where default arguments for plotting are used. To fine-tune plots, the underlying plotting functions in the OLIN package can be applied.

The usage of `OLINgui` assumes existing marray objects for the batch of arrays to be analysed and normalised. To construct marray objects using a graphical interface, refer to `read.marrayRaw`. Some underlying functions (e.g. `mxy2.plot` and optionally `olin`) require an additional list of X- and Y-coordinates of spots. This has to be done “by hand” yet. However, most functions do not need this list.

For a overview of the functionality of `OLINgui`, please refer to the package documentation.

Value

`OLINgui` returns a `tclObj` object.

Note

The newest versions of `OLINgui` can be found at the OLIN webpage (<http://itb.biologie.hu-berlin.de/~futschik/software/R/OLIN>).

Author(s)

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References

1. M.Futschik and T.Crompton (2004) *Model selection and efficiency testing for normalization of cDNA microarray data*, **Genome Biology**, 5:R60
2. M.Futschik and T.Crompton (2005), Optimized normalization, visualization and quality testing for two-channel microarray data, *Bioinformatics*, 21(8):1724-6
3. OLIN web-page: <http://itb.biologie.hu-berlin.de/~futschik/software/R/OLIN>

See Also

[olin](#)

Index

*Topic **misc**

OLINgui, 1

*Topic **multivariate**

OLINgui, 1

*Topic **nonlinear**

OLINgui, 1

mxy2.plot, 1

olin, 1, 2

OLINgui, 1

read.marrayRaw, 1