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 convient 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.bioligie.hu-berlin.de/~futschik/software/R/OLIN).

Author(s)

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References

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.bioligie.hu-berlin.de/~futschik/software/R/OLIN

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