

# Package ‘OLINgui’

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**Version** 1.80.0

**Title** Graphical user interface for OLIN

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**Depends** R (>= 2.0.0), OLIN (>= 1.4.0)

**Imports** graphics, marray, OLIN, tcltk, tkWidgets, widgetTools

**Description** Graphical user interface for the OLIN package

**biocViews** Microarray, TwoChannel, QualityControl, Preprocessing, Visualization

**License** GPL-2

**URL** <http://olin.sysbiolab.eu>

**git\_url** <https://git.bioconductor.org/packages/OLINgui>

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OLINgui	<i>Graphical user interface for OLIN package</i>
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## 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)

Matthias E. Futschik (<http://itb.biologie.hu-berlin.de/~futschik>)

## 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`

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