

# Package ‘OLINgui’

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**Version** 1.76.0

**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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**Repository** Bioconductor 3.18

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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 an 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>

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**See Also**

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