

# Package ‘IsoCorrectoRGUI’

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**Title** Graphical User Interface for IsoCorrectoR

**Version** 1.2.0

**Imports** IsoCorrectoR, readxl, tcltk2, tcltk, utils

**Description** IsoCorrectoRGUI is a Graphical User Interface for the IsoCorrectoR package. IsoCorrectoR performs the correction of mass spectrometry data from stable isotope labeling/tracing metabolomics experiments with regard to natural isotope abundance and tracer impurity. Data from both MS and MS/MS measurements can be corrected (with any tracer isotope: 13C, 15N, 18O...), as well as high resolution MS data from multiple-tracer experiments (e.g. 13C and 15N used simultaneously).

**Depends** R (>= 3.6)

**URL** <https://genomics.ur.de/files/IsoCorrectoRGUI>

**License** GPL-3

**LazyData** TRUE

**NeedsCompilation** no

**biocViews** Software, Metabolomics, MassSpectrometry, Preprocessing, GUI, ImmunoOncology

**RoxygenNote** 6.1.0

**Suggests** knitr, rmarkdown, testthat

**VignetteBuilder** knitr

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

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GetGUIstatus

*Function to get activation status of IsoCorrectoR GUI*

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**Description**

The function GetGUIstatus can be used in scripts to get the activation status of the IsoCorrectoR GUI (logical, FALSE for closed, TRUE for active). It is required if the GUI is to be started e.g. via a bash script without manually starting an R session.

**Usage**

```
GetGUIstatus()
```

**Value**

Returns the activation status of the IsoCorrectoR GUI. FALSE represents closed and TRUE represents active state. Returns NULL if GUI has not been started.

**Examples**

```
# this function is never called directly but BiocCheck() requires a runnable example.  
status<-GetGUIstatus()
```

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IsoCorrectionGUI*Graphical User Interface for IsoCorrectoR*

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**Description**

Graphical User Interface for IsoCorrectoR

**Usage**

```
IsoCorrectionGUI()
```

**Value**

Calls internal function to display IsoCorrectoR's Graphical User Interface

**Examples**

```
IsoCorrectionGUI()
```

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