Package 'IsoCorrectoRGUI'

November 12, 2026

Title Graphical User Interface for IsoCorrectoR

Version 1.28.0

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, BiocStyle

VignetteBuilder knitr

git_url https://git.bioconductor.org/packages/IsoCorrectoRGUI

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`GetGUIstatus` *Function to get activation status of IsoCorrectoR GUI*

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()
```

`IsoCorrectionGUI` *Graphical User Interface for IsoCorrectoR*

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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