Package: IsoCorrectoRGUI (via r-universe)

June 26, 2024

Title Graphical User Interface for IsoCorrectoR
Version 1.21.0
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)
<pre>URL https://genomics.ur.de/files/IsoCorrectoRGUI</pre>
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
Repository https://bioc.r-universe.dev
RemoteUrl https://github.com/bioc/IsoCorrectoRGUI
RemoteRef HEAD
RemoteSha cea3de7635238fa9482e387a55a20f304577be33
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GetGUIstatus

Function to get activation status of IsoCorrectoR GUI

Description

The function GetGUI status 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()</pre>
```

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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