Package ‘IsoCorrectoRGUI’

May 21, 2024

Title  Graphical User Interface for IsoCorrectoR
Version  1.20.0
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
git_branch  RELEASE_3_19
git_last_commit  89b33d1
git_last_commit_date  2024-04-30
Repository  Bioconductor 3.19
Date/Publication  2024-05-21
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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

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

Description

Graphical User Interface for IsoCorrectoR

Usage

`IsoCorrectionGUI()`

Value

Calls internal function to display IsoCorrectoR’s Graphical User Interface
Examples

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