

Package ‘shinyTANDEM’

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Type Package

Title Provides a GUI for rTANDEM

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Description

This package provides a GUI interface for rTANDEM. The GUI is primarily designed to visualize rTANDEM result object or result xml files. But it will also provides an interface for creating parameter objects, launching searches or performing conversions between R objects and xml files.

biocViews MassSpectrometry, Proteomics

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Depends rTANDEM (>= 1.3.5), shiny, mixtools, methods, xtable

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`shinyTANDEM`*Launch a shiny GUI for rTANDEM*

Description

The function `shinyTANDEM(dataset, port)` launch a shiny GUI running on the given port. The shiny GUI will use the default browser. A `rTANDEM` result object can be passed as an argument. In this case, the dataset will be loaded as the GUI opens. The dataset can be changed later on by loading another dataset either from an xml or an Rdata file. If a dataset is loaded from an Rda file that contains more than one object, the name of the object to be loaded must be specified.

Usage

```
shinyTANDEM(dataset=NULL, port=8100,...)
```

Arguments

<code>dataset</code>	An optional <code>rTANDEM</code> result object (class <code>rTResult</code>) that will be loaded as the GUI opens.
<code>port</code>	Shiny's default port is 8100. The port parameter lets you specify a different one.
<code>...</code>	Arguments can be passed to <code>shiny::runApp()</code> .

Value

This function does not return. Interrupt R to stop the GUI (usually by pressing `Ctrl+C` or `Esc`).

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Examples

```
# The package contains a RDS file with a rTResult object. Load it into
# memory and pass it to the call to shinyTANDEM.
# To exit the GUI, press your interupt command
# (usually Ctrl+C or Esc) in the R window.

my.result <- readRDS(system.file("extdata/result.RDS", package="shinyTANDEM"))
if(interactive()){ shinyTANDEM(dataset=my.result) }
```

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