Package 'SuperCurveGUI'

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Version 2.1.5

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Title 'SuperCurve' GUI Package

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Description Graphical User Interface for RPPA analysis using the 'SuperCurve' package.

Depends R (>= 2.15)

Imports methods, tcltk, SuperCurve (>= 1.5), tclish (>= 1.0)

SystemRequirements Tcl/Tk

NeedsCompilation no

URL http://supercurve.r-forge.r-project.org/#SuperCurveGUI

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LazyLoad yes

Repository R-Forge

Repository/R-Forge/Project supercurve

R topics documented:

SuperCurveGUI-package   *GUI for reverse phase protein lysate array analysis*

Description

A package for analyzing reverse phase protein lysate arrays (RPPA).

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Details

Package:	SuperCurveGUI
Type:	Package
Version:	2.1.5
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License:	Artistic-2.0

For a complete list of functions, use `library(help="SuperCurveGUI")`.
For a high-level summary of the changes for each revision, use
`file.show(system.file("NEWS", package="SuperCurveGUI"))`.

Author(s)

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supercurveGUI	*Graphical User Interface for the SuperCurve package*

Description

Graphical User Interface for the SuperCurve package.

Usage

```
supercurveGUI()
scui()
```

Details

The function `supercurveGUI` launches a Graphical User Interface for the **SuperCurve** package. The GUI uses Tk widgets (via the R-Tcl/Tk interface by Peter Dalgaard) in order to provide a simple interface to the SuperCurve functions for analyzing reverse phase protein lysate arrays.

The function `scui` is an alias for the aforementioned function.

If set, the environment variable `SC_DIR` will be used as the initial location for the directory containing quantification files.

Resources

The Tk options database is loaded from user-specific defaults files, such as '`.Xdefaults`', and resource databases loaded into the X server. The package will attempt to load its resources upon startup, following the X11R5 method of merging app-default files from multiple sources. The standard X11 paths are searched first, followed by paths specified by the environment variables `XFILESEARCHPATH`, `XAPPLRESDIR`, `XUSERFILESEARCHPATH`, respectively. Unlike X11, **ALL** matching files will be loaded, not just the first.

One way to make use of the options database is to create a file named '`supercurveGUI.ad`' in your home directory, specifying any desired resources. Set your `XUSERFILESEARCHPATH` environment variable within R with the command:
`Sys.setenv(XUSERFILESEARCHPATH=file.path(path.expand("~"), "%N.ad"))`

For example, to cause **SuperCurve** to convert each quantification file as it's read from a single subgrid physical layout into its actual logical one by default, add the following resource value to the app-defaults file mentioned above:
`*software: superslide`

Author(s)

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Examples

```
  ## Not run:
supercurveGUI()
# -or-
scui()

## End(Not run)
```

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