

iFlow

October 5, 2010

guiEnv

Accessor to the internal GUI environment

Description

All state information for the GUI is stored in an internal environment. This function can be used to access this environment.

Usage

```
guiEnv()
```

Value

The internal gui environment.

Author(s)

Florian Hahne

Examples

```
guiEnv()
```

iFlow-package

iFlow

Description

GUI based visualization for preprocessing of analyzing Flow Cytometry data.

Details

Package:

Type:

Version:

Date:

License:

LazyLoad:

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The tutorial video can be downloaded from <http://bioconductor.fhcrc.org/docs/workflows/flowcyt>

Author(s)

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References

<http://www.hindawi.com/journals/abi/2009/103839.html>

<code>iflow</code>	<i>Main function for iFlow</i>
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Description

Main function for iFlow. It calls up the main graphical user interface (GUI) of the iFlow package.

Usage

```
iflow()
```

Details

The GUI Pull-Down Menu consists of "File", "Data", "Graphics", "Gate", "ProbBin", and "Help" selections. The user can start with "File" Pull-Down menu to load data files of interest. The data file can be in either rda or FCS format. Please see the vignette or tutorial video for more detail (<http://bioconductor.fhcrc.org/docs/workflows/flowcytometry/tutorial.mpeg>).

Author(s)

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Examples

```
## on R console  
iflow()  
data(ITN)
```

<code>initializeEnv</code>	<i>initialize global variables</i>
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Description

It defined global variables.

Author(s)

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