Package ‘iFlow’

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Type Package

Title GUI based visualization for flow cytometry

Version 2.10.0

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Description Tool to explore and visualize flow cytometry

License Artistic-2.0

Depends R (>= 2.13.0), flowCore, flowViz, flowStats (>= 1.3.20)

Imports
Biobase, RGtk2, cairoDevice, flowCore, flowStats, flowViz,grDevices, graphics, methods, utils

biocViews FlowCytometry, Bioinformatics, GUI

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

LazyLoad yes

R topics documented:

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iFlow-package *iFlow*

Description

GUI based visualization for preprocessing of analyzing Flow Cytometry data.

Details

Package:
Type:
Version:
Date:
License:
LazyLoad:
The tutorial video can be downloaded from http://bioconductor.fhcrc.org/docs/workflows/flowcytometry/tutorial.n

Author(s)

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References

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

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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$list name such as Gate.list, workflowlist
```

Value

The internal gui environment.

Author(s)

Kyongryun Lee

Examples

```
## 1. Run iFlow
## Not run: iflow()
## 2. Load data
## Not run: data(GvHD)
## 3. Activate data by clicking a data name on Data panel
## 4. Create a gate
## 5. It is able to access created gate objects or workflow of the data on the command lines as follows.
## The workflow is automatically created whenever the operations of the data are run.

## wf.list <- .guiEnv$workflow.list
## wf.list
```

```
## gt.list <-.guiEnv$Gate.list
## gt.list

## Not run: iFlow:::guiEnv$Gatelist
```

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iflow *Main function for iFlow*

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)
```

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