

Package ‘iFlow’

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Type Package

Title GUI based visualization for flow cytometry

Version 2.13.0

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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

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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>

Author(s)

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References

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

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
```

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>).

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Examples

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

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