Package 'flowUtils'

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Type Package

Title Utilities for flow cytometry

Version 1.18.0

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Description Provides utilities for flow cytometry data.

Depends R (>= 2.2.0), flowCore (>= 1.2.0)

Imports Biobase, flowCore, graph, methods, RUnit, stats, utils, XML,flowViz

Suggests gatingMLData

Collate AllClasses.R gatingML.R helperFunctions.R gate-methods.R
transforms.R parameter-methods.R compensation.R workflow2FlowJo.R zzz.R

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biocViews Infrastructure, FlowCytometry, CellBasedAssays

R topics documented:

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flowUtils-package   *Utilities for flow cytometry data*

Description

This package includes functions to import Gates,transformations and compensations defined in
compliance with Gating-ML Candidate recommendation for Gating Description.(Version V 1.5)
This package depends on the flowCore package for methods to evaluate the gatingML files read
into the workspace.

Details

Package:	flowUtils
Type:	Package
Version:	0.2.1
Date:	2006-11-16
License:	Artistic

The main features of this package provide compatability to the data standards defined by Gating-ML candidate recommendation for gating description in flow cytometry (Version 1.5).

The package also includes a Test Suite, which allows the user to test whether the implmentation of gates, trasnformations are in compliance with the Gating-ML standard.

Author(s)

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See Also

flowCore

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read.gatingML	*Function to parse an XML gating File into objects in the R enviroment*

Description

This function parses an XML file defined in compliance with the Gating-ML candidate recommendation into objects in the R environment, which can then be evaluated using functions provided by the flowCore package.

Usage

```
read.gatingML(file,flowEnv,...)
```

Arguments

file	XML file describing gates,transformations or compensations
flowEnv	environment into which the R objects created from the XML file are to be stored
...	additional arguments that are passed to the methods

Details

The Gating-ML specification has been developed as an interchange format for the description of gates relevant to a flow cytometry experiment. Presently, we can read version 1.5 of the specification, which was the most recent at the time of this writing.

Author(s)

Gopalakrishnan N

References

Gating-ML Candidate Recommendation for Gating Description in Flow Cytometry V 1.5

Examples

```
flowEnv=new.env()

fcsFile<-system.file("extdata/List-modeDataFiles","fcs2_int16_13367ev_8par_GvHD.fcs",package="gatingMLData
fcs <- read.FCS(fcsFile,transformation=FALSE)

gateFile <- system.file("extdata/Gating-MLFiles","02CtSRectangular.xml",package="gatingMLData")
read.gatingML(gateFile,flowEnv)

ls(flowEnv)

result=filter(fcs,flowEnv$CtSR_03)
summary(result)
```

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testGatingCompliance   *Function to perfom all the gating-ML Compliance tests*

Description

This funtion performs all the gating-ML compliance tests. The XML files, data files and the Expected results provided by the gatingMLData are utilized in performing the compliance tests. The results obtained are compared with the expected results and a summary html report is generated.

Usage

```
testGatingCompliance(file)
```

Arguments

file   name of the file in which the report generated is to be saved

Details

The testGatingCompliance depends on the data package gatingMLData for performing the compliance tests

Author(s)

Gopalakrishnan N

References

Gating-ML Candidate Recommendation for Gating Description in Flow Cytometry V 1.5

Examples

```
## Not run:
### performs all the Gating compliance tests  and writes the results to mytest.html
testGatingCompliance("mytest")

## End(Not run)
```

Index