Package 'flowUtils'

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Type Package

Title Utilities for flow cytometry

Version 1.22.0

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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 specification version 1.5 and 2.0. This package depends on the flow-Core package for methods to evaluate the gatingML files read into the workspace. Note: Gating-ML 2.0 support in progress.

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 the Gating-ML specification version 1.5 and 2.0.

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 1.5 standard. (At this point, Gating-ML 2.0 does not come with a similar test suite).

Author(s)

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See Also

flowCore

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read.gatingML   *Function to parse a Gating-ML XML file into objects in the R enviro-ment*

Description

This function parses a Gating-ML XML file defined in compliance with the Gating-ML recommen-dation 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`	Gating-ML XML file describing gates, transformations and/or compensations
`flowEnv`	environment into which the R objects created from the Gating-ML 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 Gating-ML versions 1.5 and 2.0 of the specification. Version 2.0 is the most recent at the time of this writing. Note: Gating-ML 2.0 support in progress.

Author(s)

N. Gopalakrishnan, J. Spidlen

References

Spidlen J, Leif RC, Moore W, Roederer M, ISAC DSTF, Brinkman RR. 2008. Gating-ML: XML-based gating descriptions in flow cytometry. Cytometry A. 73A(12):1151–7.

Spidlen J, ISAC DSTF, Brinkman RR. 2008. Gating-ML Candidate Recommendation for Gating Description in Flow Cytometry version 1.5. http://flowcyt.sf.net/gating/Gating-ML.v1.5.081030.pdf http://flowcyt.sf.net/gating/Gating-ML.v1.5.081030.full.zip http://flowcyt.sf.net/gating/Gating-ML.v1.5.081030.Compliance-tests.081030.zip

Spidlen J, ISAC DSTF, Brinkman RR. 2013. Gating-ML 2.0. http://flowcyt.sf.net/gating/20130122.pdf http://flowcyt.sf.net/gating/20130122.full.zip

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)

#TODO Add Gating-ML 2.0 examples
```

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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)
```

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