Package 'flowUtils'

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Type Package

Title Utilities for flow cytometry

Version 1.28.0

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Description Provides utilities for flow cytometry data.

Depends R (>= 2.2.0), flowCore (>= 1.29.20)

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

Suggests gatingMLData

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

License Artistic-2.0

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 Gating-ML 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 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

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

Description

This function parses a Gating-ML XML file defined in compliance with the Gating-ML 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`	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.

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. International Society for Advancement of Cytometry (ISAC) standard for representing gating descriptions in flow cytometry. http://flowcyt.sf.net/gating/20130122.pdf http://flowcyt.sf.net/gating/20130122.full.zip

See Also

write.gatingML

Examples

```
#######################
# Gating-ML 2.0 example
#######################
flowEnv <- new.env()

fcsFile <- system.file("extdata/Gml2/FCSFiles",
  "data1.fcs", package="gatingMLData")
fcs <- read.FCS(fcsFile,
  transformation="linearize-with-PnG-scaling")
```

```
gateFile <- system.file("extdata/Gml2/Gating-MLFiles",
  "gates1.xml", package="gatingMLData")
read.gatingML(gateFile, flowEnv)
ls(flowEnv)

result = filter(fcs, flowEnv$Polygon1)
summary(result)

########################
# Gating-ML 1.5 example
########################
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)
```

---

testGatingMLCompliance

Function to perform all the Gating-ML compliance tests

Description

This function performs the Gating-ML compliance tests. Either Gating-ML 1.5 or Gating-ML 2.0 compatibility may be checked. The Gating-ML XML files, FCS 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

```
testGatingMLCompliance(file = "GatingMLComplianceReport", version = 2.0)
```

Arguments

file	Name of the file in which the generated Gating-ML compliance report is to be saved. The .html extension will be added.
version	The Gating-ML version that is supposed to be checked. Currently, versions 1.5 and 2.0 are supported.

Details

The testGatingMLCompliance function depends on the gatingMLData data package for performing the compliance tests.

Author(s)

Spidlen J., Gopalakrishnan N.

References

Gating-ML 2.0: International Society for Advancement of Cytometry (ISAC) standard for representing gating descriptions in flow cytometry. http://flowcyt.sourceforge.net/gating/20130122.pdf

Spidlen J, Leif RC, Moore W, Roederer M; International Society for the Advancement of Cytometry Data Standards Task Force, Brinkman RR. Gating-ML: XML-based gating descriptions in flow cytometry. Cytometry A. 2008 Dec; 73A(12):1151-7. doi: 10.1002/cyto.a.20637.

Examples

```
## Not run:
### Performs Gating-ML 1.5 compliance tests and
### writes the results to Gating-ML_1.5_Compliance_Report.html
testGatingMLCompliance("Gating-ML_1.5_Compliance_Report", version = 1.5)

### Performs Gating-ML 2.0 compliance tests and
### writes the results to Gating-ML_2.0_Compliance_Report.html
testGatingMLCompliance("Gating-ML_2.0_Compliance_Report", version = 2.0)

## End(Not run)
```

---

write.gatingML	*UNDER DEVELOPMENT (DO NOT USE). Function to write a Gating-ML XML file based on gating and transformation objects stored in an R environment.*

Description

This function saves gating and transformation objects stored in an R environment to a Gating-ML 2.0 XML file. The objects expected and supported in the R environment are those that can normally be created by the read.gatingML function when a Gating-ML 2.0 XML file is read.

Usage

```
write.gatingML(flowEnv, file = NULL)
```

Arguments

`flowEnv`	The R environment that is being searched for gating objects and transformations
`file`	The name of the output Gating-ML XML file. The standard output will be used if file is NULL.

Details

The Gating-ML specification has been developed as an interchange format for the description of gates relevant to a flow cytometry experiment. Presently, flowUtils can read Gating-ML versions 1.5 and 2.0 of the specification (see `read.gatingML`). Gating-ML version 2.0 only is being used when saving Gating-ML.

Author(s)

Spidlen, J.

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. International Society for Advancement of Cytometry (ISAC) standard for representing gating descriptions in flow cytometry. `http://flowcyt.sf.net/gating/20130122.pdf` `http://flowcyt.sf.net/gating/20130122.full.zip`

See Also

`read.gatingML`

Examples

```
#######################
# TODO
#######################
```

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