

# 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

**License** Artistic-2.0

**biocViews** Infrastructure, FlowCytometry, CellBasedAssays

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flowUtils-package      *Utilities for flow cytometry data*

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### 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 flowCore 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 compatibility 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 implementation of gates, transformations 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)

Maintainer: Nishant Gopalakrishnan <ngopalak@fhcrc.org> Authors: N. Gopalakrishnan, F. Hahne, B. Ellis, R. Gentleman, M. Dalphin, N. Le Meur, B. Purcell, J. Spidlen

### See Also

[flowCore](#)

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

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### 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. 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 perform all the gating-ML Compliance tests*

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**Description**

This function 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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