

# flowUtils

November 11, 2009

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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 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, tranformations are in compliance with the Gating-ML standard.

## Author(s)

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**See Also**[flowCore](#)

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read.gatingML	<i>Function to parse an XML gating File into objects in the R environment</i>
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**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="flowCore")
fcs <- read.FCS(fcsFile,transformation=FALSE)

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

ls(flowEnv)

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

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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**

<code>file</code>	name of the file in which the report generated is to be saved
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**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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