Package ‘flowWorkspace’

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Type Package

Title Infrastructure for representing and interacting with gated and ungated cytometry data sets.

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Description This package is designed to facilitate comparison of automated gating methods against manual gating done in flowJo. This package allows you to import basic flowJo workspaces into BioConductor and replicate the gating from flowJo using the flowCore functionality. Gating hierarchies, groups of samples, compensation, and transformation are performed so that the output matches the flowJo analysis.

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LazyLoad yes

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flowWorkspace-package

Import and replicate flowJo workspaces and gating schemes using flowCore.

Description

Import flowJo workspaces into R. Generate the flowJo gating hierarchy and gates using flowCore functionality. Transform and compensate data in accordance with flowJo settings. Plot gates, gating hierarchies, population statistics, and compare flowJo vs flowCore population summaries.

Details

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Author(s)

Greg Finak, Mike Jiang

References

http://www.rglab.org/

add,GatingSet,list-method

Create a GatingSet and add/remove the flowCore gate(or population) to/from a GatingHierarchy/GatingSet.

Description

GatingSet method creates a gatingset from a flowSet with the ungated data as the root node. add method add the flowCore gate to a GatingHierarchy/GatingSet. setGate method update the gate of one population node in GatingHierarchy/GatingSet. Rm method Remove the population node from a GatingHierarchy/GatingSet. They are equivalent to the workFlow.add and Rm methods in flowCore package. recompute method does the actual gating after the gate is added, i.e. calculating the event indices according to the gate definition.
## Usage

```r
## S4 method for signature 'GatingSet,list'
add(wf, action, ...)

## S4 method for signature 'GatingSetList,list'
add(wf, action, ...)

## S4 method for signature 'GatingSet,filtersList'
add(wf, action, ...)

## S4 method for signature 'GatingSet,filterList'
add(wf, action, validityCheck = TRUE, ...)

## S4 method for signature 'GatingSetList,filterList'
add(wf, action, ...)

## S4 method for signature 'GatingSetList,filtersList'
add(wf, action, ...)

## S4 method for signature 'GatingSet,filter'
add(wf, action, ...)

## S4 method for signature 'GatingSet,filters'
add(wf, action, ...)

## S4 method for signature 'GatingSetList,filter'
add(wf, action, ...)

## S4 method for signature 'GatingSetList,filters'
add(wf, action, ...)

## S4 method for signature 'GatingHierarchy,filter'
add(wf, action, ...)

## S4 method for signature 'GatingHierarchy,filters'
add(wf, action, names = NULL, ...)

## S4 method for signature 'GatingHierarchy,quadGate'
add(wf, action, names = NULL, ...)

## S4 method for signature 'GatingHierarchy,logical'
add(wf, action, parent, name,
    recompute, cluster_method_name = NULL, ...)

## S4 method for signature 'GatingHierarchy(factor'
add(wf, action, name = NULL, ...)

## S4 method for signature 'GatingHierarchy,logicalFilterResult'
add(wf, action, ...)

## S4 method for signature 'GatingHierarchy,multipleFilterResult'
add(wf, action, ...)
```
add(wf, action,
   name = NULL, ...)

## S4 method for signature 'character,GatingSet,character'
Rm(symbol, envir, subSymbol, ...)

## S4 method for signature 'character,GatingSetList,character'
Rm(symbol, envir, subSymbol, ...)

## S4 method for signature 'character,GatingHierarchy,character'
Rm(symbol, envir,
   subSymbol, ...)

### Arguments

- **wf** | A GatingHierarchy or GatingSet
- **action** | A filter or a list of filters to be added to the GatingHierarchy or GatingSet. some other arguments to specify how the gates are added to the gating tree. • negated: a logical scalar to specify whether the gate is negated, which means the the population outside of the gate will be kept as the result population. It is FALSE by default.
- **validityCheck** | logical whether to check the consistency of tree structure across samples. default is TRUE. Can be turned off when speed is prefered to the robustness.
- **names** | a character vector of length four, which specifies the population names resulted by adding a quadGate.
- **parent** | a character scalar to specify the parent node name where the new gate to be added to, by default it is NULL, which indicates the root node
- **name** | a character scalar to specify the node name of population that is generated by the gate to be added.
- **recompute** | a logical flag The order of the names is clock-wise starting from the top left quadrant population.
- **symbol** | A character identifies the population node in a GatingHierarchy or GatingSet to remove
- **envir** | A GatingHierarchy or GatingSet
- **subSymbol** | Not used.

### Value

- **GatingSet method** returns a GatingSet object with just root node.
- **add method** returns a population node ID (or four population node IDs when adding a quadGate) that uniquely identify the population node within a GatingHierarchy.

### See Also

- **GatingSet-class**
## Examples

```r
## Not run:

data(GvHD)
#select raw flow data
fs<-GvHD[1:3]

#transform the raw data
tf <- transformList(colnames(fs[[1]])[3:6], asinh, transformationId="asinh")
fs_trans<-transform(fs,tf)

#add transformed data to a gatingset
gs <- GatingSet(fs_trans)
gs
getNodes(gs[[1]]) #only contains root node

#add one gate
rg <- rectangleGate("FSC-H"=c(200,400), "SSC-H"=c(250, 400),
                   filterId="rectangle")

nodeID<-add(gs, rg)#it is added to root node by default if parent is not specified
nodeID
getNodes(gs[[1]]) #the second population is named after filterId of the gate

#add a quadGate
qg <- quadGate("FL1-H"=2, "FL2-H"=4)
nodeIDs<-add(gs,qg,parent="rectangle")
nodeIDs #quadGate produces four population nodes
getNodes(gs[[1]]) #population names are named after dimensions of gate if not specified

#add a boolean Gate
bg<-booleanFilter("CD15 FITC-CD45 PE+",
                  "CD15 FITC+CD45 PE-")
bg
nodeID2<-add(gs,bg,parent="rectangle")
nodeID2
getNodes(gs[[1]])

#do the actual gating
recompute(gs)

#plot one gate for one sample
plotGate(gs[[1]],"rectangle")
plotGate(gs[[1]],nodeIDs) #may be smoothed automatically if there are not enough events after gating

#plot gates across samples using lattice plot
plotGate(gs,nodeID)

#plot all gates for one sample
plotGate(gs[[1]])#boolean gate is skipped by default
plotGate(gs[[1]],bool=TRUE)

#plot the gating hierarchy
require(Rgraphviz)
plot(gs[[1]])

#remove one node causing the removal of all the descendants
Rm('rectangle', gs)
getNodes(gs[[1]])

## End(Not run)
```
asinh_Gml2

Inverse hyperbolic sine transformation.

Description

Used to construct inverse hyperbolic sine transform object.

Usage

asinh_Gml2_trans(..., n = 6, equal.space = FALSE)

Arguments

... parameters passed to asinh_Gml2
n desired number of breaks (the actual number will be different depending on the data range)
equal.space whether breaks at equal-spaced intervals

Value

asinhGml2 transformation object

Examples

trans.obj <- asinhGml2_trans(equal.space = TRUE)
data <- 1:1e3
brks.func <- trans.obj["breaks"]
brks <- brks.func(data)
brks # fasinh space displayed at raw data scale
#transform it to verify it is equal-spaced at transformed scale
trans.func <- trans.obj["transform"]
brks.trans <- trans.func(brks)
brks.trans

asinh_Gml2

inverse hyperbolic sine transform function generator (GatingML 2.0 version)

Description

hyperbolic sine/inverse hyperbolic sine transform function constructor. It is simply a special form of flowJo.fasinh with length set to 1 and different default values for parameters t,m,a.

Usage

asinh_Gml2(T = 262144, M = 4.5, A = 0, inverse = FALSE)
booleanFilter-class

A class describing logical operation (& or |) of the reference populations

Description

booleanFilter class inherits class expressionFilter and exists for the purpose of methods dispatching.

Usage

booleanFilter(expr, ..., filterId = "defaultBooleanFilter")

char2booleanFilter(expr, ..., filterId = "defaultBooleanFilter")

## S4 method for signature 'booleanFilter'

show(object)

Arguments

expr expression

... further arguments to the expression

filterId character identifier

object booleanFilter

See Also

add GatingHierarchy
Examples

# "4+/TNFa+" and "4+/IL2+" are two existing gates
# note: no spaces between node names and & , ! operators
booleanFilter("4+/TNFa+&!4+/IL2+")

# programmatically
n1 <- "4+/TNFa+"
n2 <- "4+/IL2+"
exprs <- paste0(n1, "&", n2)
call <- substitute(booleanFilter(v), list(v = as.symbol(exprs)))
eval(call)

checkRedundantNodes x try to determine the redundant terminal(or leaf) nodes that can be removed

Arguments

x GatingSet or list of groups(each group is a list of 'GatingSet'). When it is a list, it is usually the outcome from groupByTree.
path argumented passed to getNodes. The default value is "auto".
... other arguments passed to getNodes.

Value

a list of the character vectors indicating the nodes that are considered to be redundant for each group of GatingSets.

Examples

## Not run:
gslist <- list(gs1, gs2, gs3, gs4, gs5)
gs_groups <- groupByTree(gslist)
toRm <- checkRedundantNodes(gs_groups)

## End(Not run)
**clone**

**Description**

clone a GatingSet

**Usage**

```r
close(x, ...)
```

**Arguments**

- `x`: A GatingSet
- `...`: `ncdfFile = NULL`: see `clone.ncdfFlowSet`

**Details**

Note that the regular R assignment operation on a GatingSet object does not return the copy as one would normally expect because the GatingSet contains environment slots (and external pointer for GatingSet), which require deep-copying. So make sure to use this clone method in order to make a copy of existing object.

**Value**

A copy of a given GatingSet.

**Examples**

```r
## Not run:
#G is a GatingSet
G1<-clone(G)
## End(Not run)
```

**compensate, GatingSet, ANY-method**

*compensate the flow data associated with the GatingSet*

**Description**

The compensation is saved in the GatingSet and can be retrieved by `getCompensationMatrices`.

**Usage**

```r
## S4 method for signature 'GatingSet,ANY'
compensate(x, spillover)
```

```r
## S4 method for signature 'GatingSetList,ANY'
compensate(x, spillover)
```
compute_timestep

**Arguments**

- `x` GatingSet or GatingSetList
- `spillover` compensation object or a list of compensation objects

**Value**

a GatingSet or GatingSetList object with the underlying flow data compensated.

**Examples**

```r
## Not run:
cfile <- system.file("extdata","compdata","compmatrix", package="flowCore")
comp.mat <- read.table(cfile, header=TRUE, skip=2, check.names = FALSE)
## create a compensation object
comp <- compensation(comp.mat, compensationId="comp1")
# add it to GatingSet
gs <- compensate(gs, comp)

## End(Not run)
```

---

**compute_timestep**

**compute time step from fcs keyword**

**Description**

compute time step from fcs keyword

**Usage**

```r
compute_timestep(kw, unit.range, timestep.source = c("TIMESTEP", "BTIM"))
```

**Arguments**

- `kw` list of keywords
- `unit.range` the actual measured time unit range
- `timestep.source` either “TIMESTEP” or “BTIM”. Prefer to STIMESTEP keyword when it is non NULL
dropRedundantChannels  Remove the channels from flow data that are not used by gates

Description

Removing these redundant channels can help standardize the channels across different GatingSet objects and make them mergable.

Usage

dropRedundantChannels(gs, ...)

Arguments

- gs: a GatingSet
- ...: other arguments passed to getNodes method

Value

A new GatingSet object that has redundant channels removed. Please note that this new object shares the same reference (or external pointers) with the original GatingSets.

Examples

```r
## Not run:
gs_new <- dropRedundantChannels(gs)
## End(Not run)
```

dropRedundantNodes  Remove the terminal leaf nodes that make the gating trees to be different from one another.

Description

It is usually called after groupByTree and checkRedundantNodes. The operation is done in place through external pointers which means all the original GatingSets are modified.

Usage

dropRedundantNodes(x, toRemove)

Arguments

- x: GatingSet or list of groups (each group is a list of 'GatingSet'). When it is a list, it is usually the outcome from groupByTree.
- toRemove: list of the node sets to be removed. Its length must equal to the length of 'x'. When x is a list, toRemove is usually the outcome from checkRedundantNodes.
estimateLogicle.GatingHierarchy

Examples

```r
## Not run:
gslist <- list(gs1, gs2, gs3, gs4, gs5)
gs_groups <- groupByTree(gslist)
toRm <- checkRedundantNodes(gs_groups)
dropRedundantNodes(gs_groups, toRm)

#Now they can be merged into a single GatingSetList.
#Note that the original gs objects are all modified in place.
GatingSetList(gslist)

## End(Not run)
```

estimateLogicle.GatingHierarchy

*Compute logicle transformation from the flowData associated with a GatingHierarchy*

Description

See details in `estimateLogicle`

Usage

```r
## S3 method for class 'GatingHierarchy'
estimateLogicle(x, channels, ...)
```

Arguments

- `x` a `GatingHierarchy`
- `channels` channels or markers for which the logicle transformation is to be estimated.
- `...` other arguments

Value

`transformerList` object

Examples

```r
## Not run:
# gs is a GatingSet
trans.list <- estimateLogicle(gs[[1]], c("CD3", "CD4", "CD8"))
# trans.list is a transformerList that can be directly applied to GatingSet
gs <- transform(gs, trans.list)

## End(Not run)
```
**extract_cluster_pop_name_from_node**

Description

Extract the population name from the node path. Itstrips the parent path and cluster method name.

Usage

```
extract_cluster_pop_name_from_node(node, cluster_method_name)
```

Arguments

- `node`: population node path
- `cluster_method_name`: the name of the clustering method

Examples

```
extract_cluster_pop_name_from_node("cd3/flowClust_pop1", "flowClust")
#returns "pop1"
```

**filterObject,rectangleGate-method**

Convert flowCore filter to a list. It converts the flowCore gate to a list whose structure can be understood by underlying C++ data structure.

Usage

```
## S4 method for signature 'rectangleGate'
filterObject(x)

## S4 method for signature 'polygonGate'
filterObject(x)

## S4 method for signature 'booleanFilter'
filterObject(x)

## S4 method for signature 'ellipsoidGate'
filterObject(x)

## S4 method for signature 'logical'
filterObject(x)
```
flowData,GatingSet-method

Arguments

x filter a flowCore gate. Currently supported gates are: "rectangleGate", "polygonGate", "ellipsoidGate" and "booleanFilter"

Value

a list

fix_channel_slash toggle the channel names between '/' and '_' character

Description

FlowJoX tends to replace '/' in the original channel names with '_' in gates and transformations. We need to do the same to the flow data but also need to change it back during the process since the channel names of the flowSet can’t be modified until the data is fully compensated.

Usage

fix_channel_slash(chnls, slash_loc = NULL)

Arguments

chnls the channel names
slash_loc a list that records the locations of the original slash character within each channel name so that when restoring slash it won’t tamper the original '_' character.

Value

the toggled channel names

flowData,GatingSet-method

Fetch or replace the flowData object associated with a GatingSet.

Description

Accessor method that gets or replaces the flowset/ncdfFlowSet object in a GatingSet or GatingHierarchy.

Usage

## S4 method for signature 'GatingSet'
flowData(x)

## S4 replacement method for signature 'GatingSet'
flowData(x) <- value
**Arguments**

- **x**: A GatingSet
- **value**: The replacement flowSet or ncdfFlowSet object

**Details**

Accessor method that sets or replaces the ncdfFlowSet object in the GatingSet or GatingHierarchy.

**Value**

the object with the new flowSet in place.

---

**Description**

hyperbolic sine/inverse hyperbolic sine (flowJo-version) transform function constructor

**Usage**

```r
flowJo.fasinh(m = 4, t = 12000, a = 0.7, length = 256)
flowJo.fsinh(m = 4, t = 12000, a = 0.7, length = 256)
```

**Arguments**

- **m**: numeric the full width of the transformed display in asymptotic decades
- **t**: numeric the maximum value of input data
- **a**: numeric Additional negative range to be included in the display in asymptotic decades
- **length**: numeric the maximum value of transformed data

**Value**

fasinh/fsinh transform function

**Examples**

```r
trans <- flowJo.fasinh()
data.raw <- c(1, 1e2, 1e3)
data.trans <- trans(data.raw)
data.trans
inverse.trans <- flowJo.fsinh()
inverse.trans(data.trans)
```
flowJo.flog  flog transform function

Description
flog transform function constructor. It is different from flowCore version of logtGml2 in the way that it reset negative input so that no NAN will be returned.

Usage
flowJo.flog(decade = 4.5, offset = 1, max_val = 262144, min_val = 0, scale = 1, inverse = FALSE)

Arguments
decade  number of decades
offset  offset to the original input
max_val  top of scale value
min_val  lower bound of scaled value (where negative raw value gets truncated at)
scale  the linear scale factor
inverse  whether return the inverse function

Value
flog(or its inverse) transform function

Examples
trans <- flowJo.flog()
data.raw <- c(1,1e2,1e3)
data.trans <- trans(data.raw)
data.trans
inverse.trans <- flowJo.flog(inverse = TRUE)
inverse.trans(data.trans)

#negative input
data.raw <- c(-10,1e2,1e3)
data.trans <- trans(data.raw)
data.trans
inverse.trans(data.trans)#we lose the original value at lower end since flog can't restore negative value

#different
trans <- flowJo.flog(decade = 3, max_val = 1e3)
data.trans <- trans(data.raw)
data.trans
inverse.trans <- flowJo.flog(decade = 3, max_val = 1e3, inverse = TRUE)
inverse.trans(data.trans)
flowJoTrans

construct the flowJo-type biexponential transformation function

**Description**

Normally it was parsed from flowJo xml workspace. This function provides the alternate way to construct the flowJo version of logicle transformation function within R.

**Usage**

```r
flowJoTrans(channelRange = 4096, maxValue = 262144, pos = 4.5, neg = 0, widthBasis = -10, inverse = FALSE)
```

**Arguments**

- `channelRange` numeric: the maximum value of transformed data
- `maxValue` numeric: the maximum value of input data
- `pos` numeric: the full width of the transformed display in asymptotic decades
- `neg` numeric: Additional negative range to be included in the display in asymptotic decades
- `widthBasis` numeric unkown.
- `inverse` logical: whether to return the inverse transformation function.

**Examples**

```r
trans <- flowJoTrans()
data.raw <- c(-1, 1e3, 1e5)
data.trans <- trans(data.raw)
round(data.trans)
inv <- flowJoTrans(inverse = TRUE)
round(inv(data.trans))
```

---

**flowJoWorkspace-class**

*An R representation of a flowJo workspace.*

**Description**

Objects can be created by calls of the form `new("flowJoWorkspace.xml",...)`.

**Slots**

- `version`: Object of class "character". The version of the XML workspace.
- `file`: Object of class "character". The file name.
- `.cache`: Object of class "environment". An environment for internal use.
- `path`: Object of class "character". The path to the file.
- `doc`: Object of class "XMLInternalDocument". The XML document object.
- `options`: Object of class "integer". The XML parsing options passed to `xmlTreeParse`.
flowJo_biexp_trans

flowJo biexponential transformation.

Description

Used for constructing biexponential transformation object.

Usage

flowJo_biexp_trans(..., n = 6, equal.space = FALSE)

Arguments

... parameters passed to flowJoTrans
n desired number of breaks (the actual number will be different depending on the data range)
equal.space whether breaks at equal-spaced intervals

Value

biexponential transformation object

Examples

data(GvHD)
fr <- GvHD[[1]]
data.raw <- exprs(fr)[, "FL1-H"]
trans.obj <- flowJo_biexp_trans(equal.space = TRUE)
brks.func <- trans.obj[["breaks"]]
brks <- brks.func(data.raw)
brks # biexp space displayed at raw data scale

#transform it to verify it is equal-spaced at transformed scale
trans.func <- trans.obj[["transform"]]
print(trans.func(brks))
flowJo_fasinh_trans
flowJo inverse hyperbolic sine transformation.

Description
Used to construct the inverse hyperbolic sine transform object.

Usage
flowJo_fasinh_trans(..., n = 6, equal.space = FALSE)

Arguments
... parameters passed to flowJo.fasinh
n desired number of breaks (the actual number will be different depending on the data range)
equal.space whether breaks at equal-spaced intervals

Value
fasinh transformation object

Examples
trans.obj <- flowJo_fasinh_trans(equal.space = TRUE)
data <- 1:1e3
brks.func <- trans.obj["breaks"]
brks <- brks.func(data)
brks # fasinh space displayed at raw data scale
# transform it to verify it is equal-spaced at transformed scale
trans.func <- trans.obj["transform"]
round(trans.func(brks))

flowWorkspace.par.init
workspace version is parsed from xml node '/Workspace/version' in flowJo workspace and matched with this list to dispatch to the one of the three workspace parsers

Description
workspace version is parsed from xml node '/Workspace/version' in flowJo workspace and matched with this list to dispatch to the one of the three workspace parsers

Usage
flowWorkspace.par.init()
flowWorkspace.par.set

Sets a set of parameters in the flowWorkspace package namespace.

**Description**

flowWorkspace.par.get gets a set of parameters in the flowWorkspace package namespace.

**Usage**

```r
flowWorkspace.par.set(name, value)
flowWorkspace.par.get(name = NULL)
```

**Arguments**

- `name`: The name of a parameter category to get or set.
- `value`: A named list of values to set for category name or a list of such lists if name is missing.

**Details**

It is currently used to add/remove the support for a specific flowJo versions (parsed from xml node `/Workspace/version` in flowJo workspace)

**Examples**

```r
# get the flowJo versions currently supported
old <- flowWorkspace.par.get("FlowJo_versions")

# add the new version
old["win"] <- c(old["win"], "1.7")
flowWorkspace.par.set("FlowJo_versions", old)

flowWorkspace.par.get("FlowJo_versions")
```

---

**flow_breaks**

Generates the breaks that makes sense for flow data visualization.

**Description**

It is mainly used as helper function to construct breaks function used by `trans_new`.

**Usage**

```r
flow_breaks(x, n = 6, equal.space = FALSE, trans.fun, inverse.fun)
```
flow_trans

Arguments

- x: the raw data values
- n: desired number of breaks (the actual number will be different depending on the data range)
- equal.space: whether breaks at equal-spaced intervals
- trans.fun: the transform function (only needed when equal.space is TRUE)
- inverse.fun: the inverse function (only needed when equal.space is TRUE)

Value

either $10^n$ intervals or equal-spaced(after transformed) intervals in raw scale.

Examples

data(GvHD)
fr <- GvHD[[1]]
data.raw <- exprs(fr)[, "FL1-H"]
flow_breaks(data.raw)

trans <- logicleTransform()
inv <- inverseLogicleTransform(trans = trans)
myBrks <- flow_breaks(data.raw, equal.space = TRUE, trans = trans, inv = inv)
round(myBrks)
#to verify it is equally spaced at transformed scale
print(trans(myBrks))

---

flow_trans  
**helper function to generate a trans objects Used by other specific trans constructor**

Description

helper function to generate a trans objects Used by other specific trans constructor

Usage

flow_trans(name, trans.fun, inverse.fun, equal.space = FALSE, n = 6)

Arguments

- name: transformation name
- trans.fun: the transform function (only needed when equal.space is TRUE)
- inverse.fun: the inverse function (only needed when equal.space is TRUE)
- equal.space: whether breaks at equal-spaced intervals
- n: desired number of breaks (the actual number will be different depending on the data range)
GatingHierarchy-class  

Class GatingHierarchy

Description

GatingHierarchy is a class for representing the gating hierarchy, which can be either imported from a flowJo workspace or constructed in R.

Details

There is a one-to-one correspondence between GatingHierarchy objects and FCS files in the flowJo workspace. Each sample (FCS file) is associated with its own GatingHierarchy. It is also more space efficient by storing gating results as logical/bit vector instead of copying the raw data.

Given a GatingHierarchy, one can extract the data associated with any subpopulation, extract gates, plot gates, and extract population proportions. This facilitates the comparison of manual gating methods with automated gating algorithms.

See Also

GatingSet

Examples

```r
require(flowWorkspaceData)
d<-system.file("extdata",package="flowWorkspaceData")
wsfile<-list.files(d,pattern="A2004Analysis.xml",full=TRUE)
ws <- openWorkspace(wsfile);
G<-try(parseWorkspace(ws,path=d,name=1));
gh <- G[[1]]
getPopStats(gh);
plotPopCV(gh)

nodes <- getNodes(gh)
thisNode <- nodes[4]
plotGate(gh,thisNode);
getGate(gh,thisNode);
getData(gh,thisNode)
```

GatingSet,character,character-method

constructors for GatingSet

Description

construct object from xml workspace file and a list of sampleIDs (not intended to be called by user.)
construct a gatingset with empty trees (just root node)
construct object from existing gating hierarchy(gating template) and flow data
Usage

## S4 method for signature 'character,character'
GatingSet(x, y, guids,
   includeGates = FALSE, sampNloc = "keyword", xmlParserOption, wsType)

## S4 method for signature 'flowSet,ANY'
GatingSet(x)

## S4 method for signature 'GatingHierarchy,character'
GatingSet(x, y, path = ".", ...)

Arguments

x character or flowSet or GatingHierarchy
y character or missing
guids character vectors to uniquely identify each sample (Sometime FCS file names alone may not be unique)
includeGates logical whether to parse the gates or just simply extract the flowJo stats
sampNloc character scalar indicating where to get sampleName(or FCS filename) within xml workspace. It is either from "keyword" or "sampleNode".
xmlParserOption integer option passed to xmlTreeParse
wsType character workspace type, can be value of "win", "macII", "vX", "macIII".
path character specifies the path to the flow data (FCS files)
... other arguments. see parseWorkspace

Examples

## Not run:
#fdata could be a flowSet or ncdfFlowSet
gs <- GatingSet(fdata)

## End(Not run)

GatingSet-class

Class "GatingSet"

Description

GatingSet holds a set of GatingHierarchy objects, representing a set of samples and the gating scheme associated with each.

[ subsets a GatingSet or GatingSetList using the familiar bracket notation
[[ extract a GatingHierarchy object from a GatingSet or GatingSetList
Usage

```r
## S4 method for signature 'GatingSet,ANY'
x[i, j, ..., drop = TRUE]
## S4 method for signature 'GatingSet,numeric'
x[[i, j, ...]]
## S4 method for signature 'GatingSetList,ANY'
x[i, j, ..., drop = TRUE]
```

Arguments

- `x` GatingSet or GatingSetList
- `i` numeric or logical or character used as sample index
- `j` not used
- `...` not used
- `drop` not used

Details

Objects stores a collection of GatingHierarchies and represent a group in a flowJo workspace. A GatingSet can have two “states”. After a call to parseWorkspace(..., execute=FALSE), the workspace is imported but the data is not. Setting `execute` to `TRUE` is needed in order to load, transform, compensate, and gate the associated data. Whether or not a GatingHierarchy has been applied to data is encoded in the `flag` slot. Some methods will warn the user, or may not function correctly if the GatingHierarchy has not been executed. This mechanism is in place, largely for the purpose of speed when working with larger workspaces. It allows the use to load a workspace and subset desired samples before proceeding to load the data.

Slots

- `FCSPath`: deprecated
- `data`: Object of class "FlowSet". flow data associated with this GatingSet
- `flag`: Object of class "logical". A flag indicating whether the gates, transformations, and compensation matrices have been applied to data, or simply imported.
- `axis`: Object of class "list". stores the axis information used for plotGate.
- `pointer`: Object of class "externalptr". points to the gating hierarchy stored in C data structure.
- `guid`: Object of class "character". the unique identifier for GatingSet object.
- `transformation`: Object of class "list". a list of transformation objects used by GatingSet.
- `compensation`: Object of class "ANY". compensation objects.

See Also

- `GatingHierarchy`
- `flowJoWorkspace`
- `parseWorkspace`
Examples

```r
require(flowWorkspaceData)
d<-system.file("extdata",package="flowWorkspaceData")
wsfile<-list.files(d,pattern="A2004Analysis.xml",full=TRUE)
ws <- openWorkspace(wsfile);
G<-try(parseWorkspace(ws,execute=TRUE,path=d,name=1));
plotPopCV(G);
```

GatingSetList-class  Class "GatingSetList"

Description

A list of of GatingSet objects. This class exists for method dispatching.

use GatingSetList constructor to create a GatingSetList from a list of GatingSet

Usage

```r
GatingSetList(x, samples = NULL)

## S4 method for signature 'GatingSetList,missing'
rbind2(x, y = "missing", ...)
```

Arguments

- **x**: a list of GatingSet
- **samples**: character vector specifying the order of samples. if not specified, the samples are ordered as the underlying stored order.
- **y**: missing not used.
- **...**: other arguments passed to rbind2 method for ncdfFlowList

Details

Objects store a collection of GatingSets, which usually has the same gating trees and markers. Most GatingSets methods can be applied to GatingSetList.

See Also

- GatingSet
- GatingHierarchy

Examples

```r
## Not run:
#load several GatingSets from disk
gs_list<-lapply(list.files("../gs_toMerge",full=T) ,function(this_folder){
  load_gs(this_folder)
})

#gs_list is a list
gs_groups <- merge(gs_list)
```
#returns a list of GatingSetList objects
gslist2 <- gs_groups[[2]]
#gslist2 is a GatingSetList that contains multiple GatingSets and they share the same gating and data structure
gslist2
class(gslist2)
sampleNames(gslist2)

#reference a GatingSet by numeric index
gslist2[[1]]
#reference a GatingSet by character index
gslist2["30104.fcs"]

#loop through all GatingSets within GatingSetList
lapply(gslist2,sampleNames)

#subset a GatingSetList by [
sampleNames(gslist2[1:4])
sampleNames(gslist2[1:4])
gslist2[30104.fcs]

#get flow data from it
data(gslist2)
#get gated flow data from a particular population
data(gslist2, "3+"

#extract the gates associated with one population
data(gslist2,"3+")
data(gslist2,5)

#extract the pheno data
data(gslist2[3:1])
#modify the pheno data
pd <- data(gslist2)
pd$id <- 1:nrow(pd)
data(gslist2) <- pd
data(gslist2[3:2])

#plot the gate
plotGate(gslist2[1:2],5,smooth=T)
plotGate_labkey(gslist2[3:4],4,x="<APC Cy7-A>",y="<PE Tx RD-A>",smooth=T)

#remove cerntain gates by loop through GatingSets
getNodes(gslist2[[1]])
lapply(gslist2,function(gs)Rm("Excl",gs))

#extract the stats
dataPopStats(gslist2)
#extract statistics by using getQAStats defined in QUALIFIER package
res<-getQAStats(gslist2[c(4,2)],isMFI=F,isSpike=F,nslaves=1)

#archive the GatingSetList
save_gslist(gslist2, path="/rglab/workspace/flowIncubator/output/gslist",overwrite=T)
gslist2 <- load_gslist(path="/rglab/workspace/flowIncubator/output/gslist")

#convert GatingSetList into one GatingSet by rbind
gs_merged2 <- rbind2(gslist2,ncdfFile=path.expand(tempfile(tmpdir="/rglab/workspace/flowIncubator/output/",fileext=".nc")))
gs_merged2
getCompensationMatrices,GatingHierarchy-method

Retrieve the compensation matrices from a GatingHierarchy.

Description

Retrieve the compensation matrices from a GatingHierarchy.

Usage

## S4 method for signature 'GatingHierarchy'
getCompensationMatrices(x)

Arguments

x

A GatingHierarchy object.

Details

Return all the compensation matrices in a GatingHierarchy.

Value

A list of matrix representing the spillover matrix in GatingHierarchy

Examples

## Not run:
#Assume gh is a GatingHierarchy
getCompensationMatrices(gh);

## End(Not run)
**getData, GatingHierarchy, missing-method**

get gated flow data from a GatingHierarchy/GatingSet/GatingSetList

**Description**

get gated flow data from a GatingHierarchy/GatingSet/GatingSetList

**Usage**

```r
## S4 method for signature 'GatingHierarchy,missing'
getData(obj, y, ...)

## S4 method for signature 'GatingHierarchy,character'
getData(obj, y, ...)

## S4 method for signature 'GatingSet,missing'
getData(obj, y, ...)

## S4 method for signature 'GatingSet,character'
getData(obj, y, ...)

## S4 method for signature 'GatingSetList,ANY'
getData(obj, y, ...)
```

**Arguments**

- `obj` A `GatingHierarchy`, `GatingSet` or `GatingSetList` object.
- `y` character the node name or full/partial gating path. If not specified, will return the complete flowFrame/flowSet at the root node.
- `...` arguments passed to `ncdfFlow::`
getDescendants

Details

Returns a flowFrame/flowSet containing the events in the gate defined at node \( y \). Subset membership can be obtained using getIndices. Population statistics can be obtained using getPop and getPopStats. When calling getData on a GatingSet, the trees representing the GatingHierarchy for each sample in the GaingSet are presumed to have the same structure. To update the data, use flowData method.

Value

A flowFrame object if \( \text{obj} \) is a GatingHierarchy. A flowSet or ncdfFlowSet if a GatingSet. A ncdfFlowList if a GatingSetList.

See Also

flowData getIndices getPopStats

Examples

```r
## Not run:
#G is a GatingSet
dataG3 <- getGatingSet(G,3) #get a flowSet constructed from the third node / population in the tree.
dataG4 <- getGatingSet(G,"cd4")

#gh is a GatingHierarchy
dataGh <- getData(gh)

## End(Not run)
```

getDescendants  

get all the descendant nodes for the given ancestor

Description

get all the descendant nodes for the given ancestor

Usage

getDescendants(gh, node, ...)

Arguments

- gh: GatingHierarchy
- node: the node path
- ...: passed to getNode call

Examples

```r
library(flowWorkspace)
dataDir <- system.file("extdata",package="flowWorkspaceData")
suppressMessages(gs <- load_gs(list.files(dataDir, pattern = "gs_manual", full = TRUE)))
getDescendants(gs[[1]], "CD4")
getDescendants(gs[[1]], "CD8", path = "auto")
```
getFJWSubsetIndices
 Fetch the indices for a subset of samples in a flowJo workspace, based on a keyword value pair

Description
This function will calculate the indices of a subset of samples in a flowJoWorkspace, based on a keyword/value filter. It is applied to a specific group of samples in the workspace. The output is meant to be passed to the subset= argument of parseWorkspace.

Usage
getFJWSubsetIndices(ws, key = NULL, value = NULL, group, requiregates = TRUE)

Arguments
ws flowJoWorkspace object
key character The name of the keyword.
value character The value of the keyword.
group numeric The group of samples to subset.
requiregates TRUE or FALSE, specifying whether we include only samples that have gates attached or whether we include any sample in the workspace.

Details
Returns an index vector into the samples in a flowJo workspace for use with parseWorkspace(subset=), based on a keyword/value filter in a specific group of samples.

Value
A numeric vector of indices.

See Also
parseWorkspace

getGate,GatingHierarchy,character-method
Return the flowCore gate definition associated with a node in a GatingHierarchy/GatingSet.

Description
Return the flowCore gate definition object associated with a node in a GatingHierarchy or GatingSet object.
Usage

## S4 method for signature 'GatingHierarchy,character'
getGate(obj, y)

## S4 method for signature 'GatingSet,character'
getGate(obj, y)

## S4 method for signature 'GatingSetList,character'
getGate(obj, y)

Arguments

obj A GatingHierarchy or GatingSet
y A character the name or full/(partial) gating path of the node of interest.

Value

A gate object from flowCore. Usually a polygonGate, but may be a rectangleGate. Boolean gates are represented by a "BooleanGate" S3 class. This is a list boolean gate definition that references populations in the GatingHierarchy and how they are to be combined logically. If obj is a GatingSet, assuming the trees associated with each GatingHierarchy are identical, then this method will return a list of gates, one for each sample in the GatingSet corresponding to the same population indexed by y.

See Also

gData getNodes

Examples

## Not run: #gh is a GatingHierarchy
getGate(gh, "CD3") #return the gate for the fifth node in the tree, but fetch it by name.
#G is a GatingSet
getGate(G, "CD3") #return a list of gates for the fifth node in each tree

## End(Not run)

gIndiceMat

---

Return the single-cell matrix of 1/0 dichotomized expression

Description

Return the single-cell matrix of 1/0 dichotomized expression

Usage

gIndiceMat(gh, y)

Arguments

gh GatingHierarchy object
y character node name
getIndices,GatingHierarchy,character-method

Get the membership indices for each event with respect to a particular gate in a GatingHierarchy

Description

Returns a logical vector that describes whether each event in a sample is included or excluded by this gate.

Usage

```r
## S4 method for signature 'GatingHierarchy,character'
getIndices(obj, y)
```

Arguments

- `obj`: A GatingHierarchy representing a sample.
- `y`: A character giving the name or full/(partial) gating path of the population/node of interest.

Details

Returns a logical vector that describes whether each event in the data file is included in the given gate of this GatingHierarchy. The indices are for all events in the file, and do not reflect the population counts relative to the parent but relative to the root. To get population frequencies relative to the parent one cross-tabulate the indices of `y` with the indices of its parent.

Value

A logical vector of length equal to the number of events in the FCS file that determines whether each event is or is not included in the current gate.

Note

Generally you should not need to use getIndices but the more convenient methods getProp and getPopStats which return population frequencies relative to the parent node. The indices returned reference all events in the file and are not directly suitable for computing population statistics, unless subsets are taken with respect to the parent populations.

See Also

- `getPopStats`

Examples

```r
## Not run:
#G is a gating hierarchy
#Return the indices for population 5 (topological sort)
getIndices(G,getNodes(G,tsort=TRUE)[5]);

## End(Not run)
```
getIndices,GatingSet,name-method

routine to return the indices by specify boolean combination of reference nodes:

Description

It adds the boolean gates and does the gating on the fly, and return the indices associated with that bool gate, and remove the bool gate the typical use case would be extracting any-cytokine-expressed cells

Usage

```r
## S4 method for signature 'GatingSet,name'
getIndices(obj, y)
```

Arguments

- `obj` : GatingSet
- `y` : a quoted expression.

Examples

```r
## Not run:
getIndices(gs, quote('4+/TNFa+|4+/IL2+'))
```

getKeywords,flowJoWorkspace,character-method

Get Keywords

Description

Retrieve keywords associated with a workspace

Usage

```r
## S4 method for signature 'flowJoWorkspace,character'
getKeywords(obj, y, ...)
```

```r
## S4 method for signature 'flowJoWorkspace,numeric'
getKeywords(obj, y, ...)
```
getLoglevel

Arguments

obj A flowJoWorkspace
y character or numeric specifying the sample name or sample ID
... other arguments sampNloc a character the location where the sample name is specified. See parseWorkspace for more details.

Details

Retrieve a list of keywords from a flowJoWorkspace

Value

A list of keyword - value pairs.

Examples

require(flowWorkspaceData)
d<-system.file("extdata", package="flowWorkspaceData")
wsfile<-list.files(d, pattern="manual.xml", full=TRUE)
ws <- openWorkspace(wsfile);

getsSamples(ws)
res <- try(getKeywords(ws, "CytoTrol_CytoTrol_1.fcs"), silent = TRUE)
print(res[[1]])
getKeywords(ws, 1)

---

getLoglevel

get/set the log level

Description

It is helpful sometime to get more detailed print out for the purpose of trouble shooting

Usage

getLoglevel()

setLoglevel(level = "none")

Arguments

level a character that represents the log level, can be value of c("none", "GatingSet", "GatingHierarchy", "Population", "gate") default is "none", which does not print any information from C parser.

Value

a character that represents the internal log level
**getMergedStats**

*Get Cell Population Statistics and Sample Metadata*

### Description

Get Cell Population Statistics and Sample Metadata

### Usage

```
getMergedStats(object, ...) 
```

### Arguments

- `object` a `GatingSet` or `GatingSetList`
- `...` additional arguments passed to `getPopStats`

### Value

A `data.table` of merged population statistics with sample metadata.

### Examples

```r
## Not run:
#G is a GatingSetList
stats = getMergedStats(G)
## End(Not run)
```

---

**getNodes,GatingSet-method**

*Get the names of all nodes from a gating hierarchy.*

### Description

`getNodes` returns a character vector of names of the nodes (populations) in the GatingSet.

### Usage

```r
## S4 method for signature 'GatingSet'
getNodes(x, y = NULL, order = "regular", path = "full", showHidden = FALSE, ...)
```
getParent, GatingSet, character-method

Arguments

- **x**: A GatingSet. Assuming the gating hierarchy are identical within the GatingSet, the Gating tree of the first sample is used to query the node information.
- **y**: A character not used.
- **order**: `order=c("regular","tsort","bfs")` returns the nodes in regular, topological or breadth-first sort order. "regular" is default.
- **path**: A character or numeric scalar. When numeric, it specifies the fixed length of gating path (length 1 displays terminal name). When character, it can be either 'full' (full path, which is default) or 'auto' (display the shortest unique gating path from the bottom of gating tree).
- **showHidden**: logical whether to include the hidden nodes.
- **...**: Additional arguments.

Details

Integer indices of nodes are based on regular order, so whenever need to map from character node name to integer node ID, make sure to use default order which is regular.

Value

`getNodes` returns a character vector of node/population names, ordered appropriately.

Description

Returns the name of the parent population or a character/numeric vector of all the children of the current population in the given GatingHierarchy.

Usage

```r
## S4 method for signature 'GatingSet,character'
g getParent(obj, y, ...)

## S4 method for signature 'GatingSet,character'
g getChildren(obj, y, showHidden = TRUE, ...)
```

Arguments

- **obj**: A GatingHierarchy
- **y**: a character/numeric the name or full/(partial) gating path or node indices of the node / population.
- **...**: other arguments passed to `getNodes` methods
- **showHidden**: logical whether to include the hidden children nodes.
Value

`getParent` returns a character vector, the name of the parent population. `getChildren` returns a character or numeric vector of the node names or node indices of the child nodes of the current node. An empty vector if the node has no children.

See Also

`getNodes`

Examples

```r
## Not run:
# G is a gatinghierarchy
# return the name of the parent of the fifth node in the hierarchy.
getParent(G, getNodes(G)[[1]][5])

n <- getNodes(G, tsort = T)[4];
getChildren(G, n); # Get the names of the child nodes of the 4th node in this gating hierarchy.
getChildren(G, 4); # Get the ids of the child nodes

## End(Not run)
```

getProp, GatingHierarchy, character-method

*Return a table of population statistics for all populations in a GatingHierarchy/GatingSet or the population proportions or the total number of events of a node (population) in a GatingHierarchy*

Description

`getProp` calculates the population proportion (events in the gate / events in the parent population) associated with a node in the GatingHierarchy. `getPopStats` is more useful than `getPop`. Returns a table of population statistics for all populations in a GatingHierarchy/GatingSet. Includes the xml counts, openCyto counts and frequencies. `getTotal` returns the total number of events in the gate defined in the GatingHierarchy object.

Usage

```r
## S4 method for signature 'GatingHierarchy, character'
getProp(x, y, xml = FALSE)

## S4 method for signature 'GatingHierarchy, character'
getTotal(x, y, xml = FALSE)

## S4 method for signature 'GatingHierarchy'
getPopStats(x, path = "auto", ...)

## S4 method for signature 'GatingSet'
getPopStats(x, statistic = c("freq", "count"),
    xml = FALSE, subpopulations = NULL, format = c("long", "wide"),
    path = "auto", ...)

## S4 method for signature 'GatingSetList'
getPopStats(x, format = c("long", "wide"), ...)
```
Arguments

- `x`: A `GatingHierarchy` or `GatingSet`
- `y`: character node name or path
- `xml`: logical indicating whether the statistics come from xml (if parsed from xml workspace) or from openCyto.
- `path`: character see `getNodes`
- `statistic`: character specifies the type of population statistics to extract. (only valid when format is "wide"). Either "freq" or "count" is currently supported.
- `subpopulations`: character vector to specify a subset of populations to return. (only valid when format is "long")
- `format`: character value of c("wide", "long") specifying whether to organize the output in long or wide format

Details

getPopStats returns a table population statistics for all populations in the gating hierarchy. The output is useful for verifying that the import was successful, if the xml and openCyto derived counts don’t differ much (i.e. if they have a small coefficient of variation.) for a GatingSet, returns a matrix of proportions for all populations and all samples getProp returns the proportion of cells in the gate, relative to its parent. getTotal returns the total number of events included in this gate. The contents of "thisTot" variable in the "metadata" environment of the nodeData element associated with the gating tree and gate / population.

Value

getPopStats returns a `data.frame` with columns for the population name, xml derived counts, openCyto derived counts, and the population proportions (relative to their parent population). getProp returns a population frequency numeric. getTotal returns a numeric value of the total number of elements in the population.

See Also

- `getNodes`

Examples

```R
## Not run:
#gh is a GatingHierarchy
getPopStats(gh);
#proportion for the fifth population
getProp(gh, getNodes(gh)[5])
getTotal(gh, getNodes(gh, tsort=T)[5])

#gs is a GatingSet
getPopStats(gs)
#optionally output in long format as a data.table
getPopStats(gs, format = "long", path = "auto")
#only get stats for a subset of populations
getPopStats(gs, format = "long", subpopulations = getNodes(gs)[4:6])

## End(Not run)
```
getSampleGroups, flowJoWorkspace-method

Get a table of sample groups from a flowJo workspace

Description

Return a data frame of sample group information from a flowJo workspace

Usage

```r
## S4 method for signature 'flowJoWorkspace'
getSampleGroups(x)
```

Arguments

- `x`: A `flowJoWorkspace` object.

Details

Returns a table of samples and groups defined in the flowJo workspace

Value

A data.frame containing the `groupName`, `groupID`, and `sampleID` for each sample in the workspace. Each sample may be associated with multiple groups.

See Also

- `flowJoWorkspace-class`
- `openWorkspace`

Examples

```r
## Not run:
# ws is a flowJoWorkspace
getSampleGroups(ws);
## End(Not run)
```

getSamples, flowJoWorkspace-method

Get a list of samples from a flowJo workspace

Description

Return a data frame of samples contained in a flowJo workspace

Usage

```r
## S4 method for signature 'flowJoWorkspace'
getSamples(x, sampNloc = "keyword")
```

Examples

```r
## Not run:
# ws is a flowJoWorkspace
getSamples(ws, sampNloc = "keyword")
## End(Not run)
```
getSingleCellExpression,GatingSetList,character-method

Arguments

x A flowJoWorkspace

sampNloc character either "keyword" or "sampleNode". see parseWorkspace

Details

Returns a data.frame of samples in the flowJoWorkspace, including their sampleID, name, and compID (compensation matrix ID).

Value

A data.frame with columns sampleID, name, and compID if x is a flowJoWorkspace.

Examples

## Not run:
# ws is a flowJoWorkspace
getSamples(ws);

## End(Not run)

getSingleCellExpression,GatingSetList,character-method

Return the cell events data that express in any of the single populations defined in y

Description

Returns a list of matrix containing the events that expressed in any one of the populations defined in y

Usage

## S4 method for signature 'GatingSetList,character'
getSingleCellExpression(x, nodes, ...)

## S4 method for signature 'GatingSet,character'
getSingleCellExpression(x, nodes, ...)

getSingleCellExpressionByGate(...)

Arguments

x A GatingSet or GatingSetList object.

nodes character vector specifying different cell populations

... other arguments

other.markers character vector specifying the extra markers/channels to be returned besides the ones derived from "nodes" and "map" argument. It is only valid when threshold is set to FALSE.

swap logical indicates whether channels and markers of flow data are swapped.
getSingleCellExpression, GatingSetList, character-method

threshold logical indicates whether to threshold the flow data by setting intensity value to zero when it is below the gate threshold.

marginal logical indicates whether to gate is treated as 1d marginal gate. Default is TRUE, which means markers are determined either by node name or by 'map' argument explained below. When FALSE, the markers are determined by the gate dimensions. and node name and 'map' argument are ignored.

map a named list providing the mapping between node names (as specified in the gating hierarchy of the gating set) and channel names (as specified in either the desc or name columns of the parameters of the associated flowFrames in the GatingSet). see examples.

ignore.case whether to ignore case when match the marker names. Default is FALSE.

mc.cores passed to mclapply. Default is 1, which means the process runs in serial mode. When it is larger than 1, parallel mode is enabled.

Value

A list of numeric matrices

Author(s)

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See Also

getIndices getPopStats

Examples

## Not run:
#G is a GatingSet
nodes <- c("4+/TNFa+", "4+/IL2+")
res <- getSingleCellExpression(gs, nodes)
res[[1]]

# if it fails to match the given nodes to the markers, then try to provide the mapping between node and marker explicitly
res <- getSingleCellExpression(gs, nodes , map = list("4+/TNFa+" = "TNFa", "4+/IL2+" = "IL2"))

# It can also operate on the 2d gates by setting marginal to FALSE
# The markers are no longer deduced from node names or supplied by map
# Instead, it retrieves the markers that are associated with the gates
nodes <- c("4+/TNFa+IFNg+", "4+/IL2+IL3+")
res <- getSingleCellExpression(gs, nodes, marginal = FALSE)
# or simply call convenient wrapper
getSingleCellExpressionByGate(gs, nodes)

## End(Not run)
getStats

**Exact MFI from populations(or nodes) for all the markers**

**Description**

It calculates the MFI for each marker.

**Usage**

```r
getStats(x, ...)
```

## S3 method for class 'GatingSetList'

```r
getStats(x, ...)
```

## S3 method for class 'GatingSet'

```r
getStats(x, ...)
```

## S3 method for class 'GatingHierarchy'

```r
getStats(x, nodes = NULL, type = "count", inverse.transform = FALSE, stats.fun.arg = list(), ...)
```

**Arguments**

- `x`: a GatingSet or GatingHierarchy
- `...`: arguments passed to `getNodes` method.
- `nodes`: the character vector specifies the populations of interest. default is all available nodes
- `type`: the character vector specifies the type of pop stats or a function used to compute population stats. when character, it is expected to be either "count" or "percent". Default is "count" (total number of events in the populations). when a function, it takes a flowFrame object through 'fr' argument and return the stats as a named vector.
- `inverse.transform`: logical flag. Whether inverse transform the data before computing the stats.
- `stats.fun.arg`: a list of arguments passed to 'type' when 'type' is a function.

**Value**

a data.table that contains MFI values for each marker per column along with 'pop' column and 'sample' column (when used on a 'GatingSet')

**Examples**

```r
## Not run:
dataDir <- system.file("extdata",package="flowWorkspaceData")
suppressMessages(gs <- load_gs(list.files(dataDir, pattern = "gs_manual",full = TRUE)))

# get stats all nodes
dt <- getStats(gs) #default is "count"

nodes <- c("CD4", "CD8")
```
getStats(gs, nodes, "percent")

# pass a build-in function
getStats(gs, nodes, type = pop.MFI)

# compute the stats based on the raw data scale
getStats(gs, nodes, type = pop.MFI, inverse.transform = TRUE)

# supply user-defined stats fun
pop.quantiles <- function(fr)
  chnls <- colnames(fr)
  res <- matrixStats::colQuantiles(exprs(fr), probs = 0.75)
  names(res) <- chnls
  res
getStats(gs, nodes, type = pop.quantiles)

## End(Not run)

getTransformations, GatingHierarchy-method

Return a list of transformations or a transformation in a GatingHierarchy

Description

Return a list of all the transformations or a transformation in a GatingHierarchy

Usage

## S4 method for signature 'GatingHierarchy'
getTransformations(x, channel = NULL,
  inverse = FALSE, only.function = TRUE, ...)

Arguments

x A GatingHierarchy object
channel character channel name
inverse logical whether to return the inverse transformation function. Valid when
  only.funtion is TRUE
only.function logical whether to return the function or the entire transformer object(see
  scales package) that contains transform and inverse and breaks function.
...
other arguments equal.spaced logical passed to the breaks functio to determine
whether to break at 10^n or equally spaced intervals

Details

Returns a list of the transformations or a transformation in the flowJo workspace. The list is of
length L, where L is the number of distinct transformations applied to samples in the flowJoWorkspace. Each
element of L is itself a list of length M, where M is the number of parameters that were trans-
formed for a sample or group of samples in a flowJoWorkspace. For example, if a sample has 10
parameters, and 5 are transformed during analysis, using two different sets of transformations, then L will be of length 2, and each element of L will be of length 5. The elements of L represent channel- or parameter-specific transformation functions that map from raw intensity values to channel-space used by flowJo.

Value

Lists of functions (or transform objects when only.function is FALSE), with each element of the list representing a transformation applied to a specific channel/parameter of a sample.

Examples

```r
## Not run:
# Assume gh is a GatingHierarchy
getTransformations(gh); # return a list transformation functions
getTransformations(gh, inverse = TRUE); # return a list inverse transformation functions
getTransformations(gh, channel = "FL1-H"); # only return the transformation associated with given channel
getTransformations(gh, channel = "FL1-H", only.function = FALSE) # return the entire transform object
## End(Not run)
```

gh_check_cluster_node  check if a node is clustering node

Description

check if a node is clustering node

Usage

`gh_check_cluster_node(gh, node)`

Arguments

- `gh` GatingHierarchy
- `node` the population/node name or path

Value

The name of the clustering method. If it is not cluster node, returns NULL.
**gh_get_cluster_labels**  
*Retrieve the cluster labels from the cluster nodes*

**Description**

Clustering results are stored as individual gated nodes. This helper function collects all the gating indices from the same clustering run (identified by 'parent' node and 'cluster_method_name' and merge them as a single factor.

**Usage**

```r
gh_get_cluster_labels(gh, parent, cluster_method_name)
```

**Arguments**

- `gh`: GatingHierarchy
- `parent`: the parent population/node name or path
- `cluster_method_name`: the name of the clustering method

**groupByChannels**  
*split GatingSets into groups based on their flow channels*

**Description**

Sometimes, gates are defined on different dimensions across different GatingSets. (e.g. ‘FSC-W’ or ‘SSC-H’ may be used for Y axis for cytokines) These differences in dimensions may not be critical since they are usually just used for visualization (instead of thresholding events). But this prevents the gs from merging because they may not be collected across batches. Thus we have to separate them if we want to visualize the gates.

**Usage**

```r
groupByChannels(x)
```

**Arguments**

- `x`: a list of GatingSets

**Examples**

```r
## Not run:
gslist <- list(gs1, gs2, gs3, gs4, gs5)  
gs_groups <- groupByChannels(gslist)

## End(Not run)
```
**groupByTree**

*split GatingSets into groups based on their gating schemes Be careful that the splitted results still points to the original data set!!*

**Description**

It allows isomorphism in Gating tree and ignore difference in hidden nodes i.e. tree is considered to be the same as long as getNode(gh, path = "auto", showHidden = F) returns the same set.

**Usage**

```r
groupByTree(x)
```

**Arguments**

- `x` a list of GatingSets or one GatingSet

**Value**

when `x` is a GatingSet, this function returns a list of sub-GatingSets When `x` is a list of GatingSets, it returns a list of list, each list itself is a list of GatingSets, which share the same gating tree.

**Examples**

```r
## Not run:
gslist <- list(gs1, gs2, gs3, gs4, gs5)
gs_groups <- groupByTree(gslist)
## End(Not run)
```

**insertGate**

*insert a dummy gate to the GatingSet*

**Description**

Is is useful trick to make the tree structure of GatingSet same with other so that they can be combined into a 'GatingSetList' object. (deprecated by 'moveNode')

**Usage**

```r
insertGate(gs, gate, parent, children)
```

**Arguments**

- `gs` GatingSet to work with
- `gate` filter a dummy gate to be inserted, its 'filterId' will be used as the population name
- `parent` character full path of parent node where the new dummy gate to be added to
- `children` character full path of children nodes that the new dummy gate to be parent of
Value

A new `GatingSet` object with the new gate added but share the same flow data with the input `GatingSet`.

Examples

```r
## Not run:
# construct a dummy singlet gate
dummyGate <- rectangleGate("FSC-A" = c(-Inf, Inf), "FSC-H" = c(-Inf, Inf), filterId = "singlets")
# insert it between the 'not debris' node and "lymph" node
gs_clone <- insertGate(gs, dummyGate, "not debris", "lymph")
## End(Not run)
```

isGated

The flags of gate nodes `isGated` checks if a node is already gated `isNegated` checks if a node is negated. `isHidden` checks if a node is hidden.

Description

The flags of gate nodes `isGated` checks if a node is already gated `isNegated` checks if a node is negated. `isHidden` checks if a node is hidden.

Usage

```r
isGated(obj, y, ...)

## S4 method for signature 'GatingHierarchy,character'
isGated(obj, y)

isNegated(obj, y, ...)

## S4 method for signature 'GatingHierarchy,character'
isNegated(obj, y)

isHidden(obj, y, ...)

## S4 method for signature 'GatingHierarchy,character'
isHidden(obj, y)
```

Arguments

- `obj` GatingHierarchy
- `y` node/gating path
- `...` not used
### isNcdf

**determine the flow data associated with a Gating Hierarchy is based on 'ncdfFlowSet' or 'flowSet'**

**Description**

- determine the flow data associated with a Gating Hierarchy is based on 'ncdfFlowSet' or 'flowSet'

**Usage**

```r
isNcdf(x)
```

**Arguments**

- `x` GatingHierarchy object

**Value**

- logical

---

### keyword,GatingHierarchy,character-method

**Retrieve a specific keyword for a specific sample in a GatingHierarchy or or set of samples in a GatingSet or GatingSetList**

**Description**

- Retrieve a specific keyword for a specific sample in a GatingHierarchy or or set of samples in a GatingSet or GatingSetList

**Usage**

```r
## S4 method for signature 'GatingHierarchy,character'
keyword(object, keyword)

## S4 method for signature 'GatingHierarchy,missing'
keyword(object, keyword = "missing", ...)

## S4 method for signature 'GatingSet,missing'
keyword(object, keyword = "missing", ...)

## S4 method for signature 'GatingSet,character'
keyword(object, keyword)

## S4 method for signature 'GatingSetList,missing'
keyword(object, keyword = "missing", ...)

## S4 method for signature 'GatingSetList,character'
keyword(object, keyword)
```
**Arguments**

- **object**: GatingHierarchy or GatingSet or GatingSetList
- **keyword**: character specifying keyword name. When missing, extract all keywords.
- **...**: other arguments passed to `keyword-methods`

**Details**

See keyword in Package ‘flowCore’

**See Also**

`keyword-methods`

**Examples**

```r
## Not run:
# get all the keywords from all samples
keyword(G)
# get all the keywords from one sample
keyword(G[[1]])
# filter the instrument setting
keyword(G[[1]], compact = TRUE)
# get single keyword from all samples
keyword(G, "FILENAME")
# get single keyword from one sample
keyword(G[[1], "FILENAME"])

## End(Not run)
```

---

**Description**

apply FUN to each sample (i.e. GatingHierarchy)

**Usage**

```r
## S4 method for signature 'GatingSet'
lapply(X, FUN, ...)
```

**Arguments**

- **X**: GatingSet
- **FUN**: function to be applied to each sample in 'GatingSet'
- **...**: other arguments to be passed to 'FUN'
Methods to get the length of a GatingSet

Description

Return the length of a GatingSet or GatingSetList object (number of samples).

Usage

```r
## S4 method for signature 'GatingSet'
length(x)

## S4 method for signature 'GatingSet'
show(object)
```

Arguments

- `x` GatingSet
- `object` object

logicleGml2_trans

GatingML2 version of logicle transformation.

Description

The only difference from logicle_trans is it is scaled to c(0,1) range.

Usage

```r
logicleGml2_trans(T = 262144, M = 4.5, W = 0.5, A = 0, n = 6, equal.space = FALSE)
```

Arguments

- `T, M, W, A` see logicleGml2
- `n` desired number of breaks (the actual number will be different depending on the data range)
- `equal.space` whether breaks at equal-spaced intervals

Value

a logicleGml2 transformation object
Examples

trans.obj <- logicleGml2_trans(equal.space = TRUE)
data <- 1:1e3
brks.func <- trans.obj[["breaks"]]
brks <- brks.func(data)
brks # logicle space displayed at raw data scale
#transform it to verify the equal-spaced breaks at transformed scale
print(trans.obj[["transform"]](brks))

Description

Used for construct logicle transform object.

Usage

logicle_trans(..., n = 6, equal.space = FALSE)

Arguments

... arguments passed to logicleTransform.
n desired number of breaks (the actual number will be different depending on the data range)
equal.space whether breaks at equal-spaced intervals

Value

a logicle transformation object

Examples

trans.obj <- logicle_trans(equal.space = TRUE)
data <- 1:1e3
brks.func <- trans.obj[["breaks"]]
brks <- brks.func(data)
brks # logicle space displayed at raw data scale
#transform it to verify the equal-spaced breaks at transformed scale
print(trans.obj[["transform"]](brks))
Description

Used to construct flog transformer object. (which uses a specialized flowJo.flog)

Usage

logtGml2_trans(M = 4.5, T = 262144, n = 6, equal.space = FALSE)

Arguments

- **M**: number of decades
- **T**: top scale value
- **n**: desired number of breaks (the actual number will be different depending on the data range)
- **equal.space**: whether breaks at equal-spaced intervals

Value

logtGml2 transformation object

Examples

trans.obj <- logtGml2_trans(M = 1, T = 1e3, equal.space = TRUE)
data <- 1:1e3
brks.func <- trans.obj["breaks"]
brks <- brks.func(data)
brks #fasinh space displayed at raw data scale

#transform it to verify it is equal-spaced at transformed scale
trans.func <- trans.obj["transform"]
brks.trans <- trans.func(brks)
brks.trans

Description

Get/set the column(channel) or marker names

It simply calls the methods for the underlying flow data (flowSet/ncdfFlowSet/ncdfFlowList).
Usage

```r
## S4 method for signature 'GatingHierarchy'
markernames(object)

## S4 replacement method for signature 'GatingHierarchy'
markernames(object) <- value

## S4 method for signature 'GatingHierarchy'
colnames(x, do.NULL = "missing",
           prefix = "missing")

## S4 replacement method for signature 'GatingHierarchy'
colnames(x) <- value

## S4 method for signature 'GatingSet'
markernames(object)

## S4 replacement method for signature 'GatingSet'
markernames(object) <- value

## S4 method for signature 'GatingSet'
colnames(x, do.NULL = "missing",
           prefix = "missing")

## S4 replacement method for signature 'GatingSet'
colnames(x) <- value
```

Arguments

- `value`: named character vector for markernames<-, regular character vector for colnames<-
- `x, object`: GatingHierarchy/GatingSet/GatingSetList
- `do.NULL, prefix`: not used.

Examples

```r
## Not run:
markers.new <- c("CD4", "CD8")
chnls <- c("<B710-A>", "<R780-A>")
names(markers.new) <- chnls
markernames(gs) <- markers.new

chnls <- colnames(gs)
chnls.new <- chnls
chnls.new[c(1,4)] <- c("fsc", "ssc")
colnames(gs) <- chnls.new

## End(Not run)
```
mkformula  

*make a formula from a character vector*

**Description**

construct a valid formula to be used by flowViz::xyplot

**Usage**

```r
mkformula(dims, isChar = FALSE)
```

**Arguments**

- `dims`  
a character vector that contains \( y, x \) axis, if it is unnamed, then treated as the order of \( c(y,x) \)
- `isChar`  
logical flag indicating whether to return a formula or a pasted string

**Value**

when `isChar` is `TRUE`, return a character, otherwise coerce it as a formula

**Examples**

```r
all.equal(mkformula(c("SSC-A", "FSC-A")), "\text{~}SSC-A \text{~}FSC-A")# unnamed vector
all.equal(mkformula(c(x = "SSC-A", y = "FSC-A")), "\text{~}FSC-A \text{~}SSC-A")# named vector
```

moveNode  

*move a node along with all of its descendant nodes to the given ancestor*

**Description**

move a node along with all of its descendant nodes to the given ancestor

**Usage**

```r
moveNode(gh, node, to)
```

**Arguments**

- `gh`  
GatingHierarchy
- `node`  
the node to be moved
- `to`  
the new parent node under which the node will be moved to
Examples

```r
library(flowWorkspace)
dataDir <- system.file("extdata", package="flowWorkspaceData")
suppressMessages(gs <- load_gs(list.files(dataDir, pattern = "gs_manual", full = TRUE)))
gh <- gs[[1]]
old.parent <- getParent(gh, "CD4")
new.parent <- "singlets"
moveNode(gh, "CD4", new.parent)
getParent(gh, "CD4")
```

ncFlowSet

*Fetch the flowData object associated with a GatingSet.*

Description

Deprecated by flowData method

Deprecated by flowData method

openWorkspace, character-method

*Open/Close a flowJo workspace*

Description

Open a flowJo workspace and return a flowJoWorkspace object. Close a flowJoWorkspace, destroying the internal representation of the XML document, and freeing the associated memory.

Usage

```r
## S4 method for signature 'character'
openWorkspace(file, options = 0, ...)

## S4 method for signature 'flowJoWorkspace'
closeWorkspace(workspace)
```

Arguments

- **file**: Full path to the XML flowJo workspace file.
- **options**: xml parsing options passed to xmlTreeParse
- **workspace**: A flowJoWorkspace

Details

Open an XML flowJo workspace file and return a flowJoWorkspace object. The workspace is represented using a XMLInternalDocument object. Close a flowJoWorkspace after finishing with it. This is necessary to explicitly clean up the C-based representation of the XML tree. (See the XML package).
parseWorkspace, flowJoWorkspace-method

Value

a flowJoWorkspace object.

Examples

```r
## Not run:
file<-'myworkspace.xml'
ws<-openWorkspace(file);
class(ws); #flowJoWorkspace
closeWorkspace(ws);
## End(Not run)
```

parseWorkspace, flowJoWorkspace-method

Parse a flowJo Workspace

Description

Function to parse a flowJo Workspace, generate a GatingHierarchy or GatingSet object, and associated flowCore gates. The data are not loaded or acted upon until an explicit call to `recompute()` is made on the GatingHierarchy objects in the GatingSet.

Usage

```r
## S4 method for signature 'flowJoWorkspace'
parseWorkspace(obj, ...)
```

Arguments

- `obj` A flowJoWorkspace to be parsed.
- `...`
  - `name` numeric or character. The name or index of the group of samples to be imported. If NULL, the groups are printed to the screen and one can be selected interactively. Usually, multiple groups are defined in the flowJo workspace file.
  - `execute` TRUE|FALSE a logical specifying if the gates, transformations, and compensation should be immediately calculated after the flowJo workspace have been imported. TRUE by default.
  - `isNcdf` TRUE|FALSE logical specifying if you would like to use netcdf to store the data, or if you would like to keep all the flowFrames in memory. For a small data set, you can safely set this to FALSE, but for larger data, we suggest using netcdf. You will need the netcdf C library installed.
  - `subset` numeric vector specifying the subset of samples in a group to import. Or a character specifying the FCS filenames to be imported. Or an expression to be passed to `subset` function to filter samples by `pData` (Note that the columns referred by the expression must also be explicitly specified in `keywords` argument)
  - `requiregates` logical Should samples that have no gates be included?
  - `includeGates` logical Should gates be imported, or just the data with compensation and transformation?
parseWorkspace, flowJoWorkspace-method

- **path** either a character scalar or data.frame. When character, it is a path to the fcs files that are to be imported. The code will search recursively, so you can point it to a location above the files. When it is a data.frame, it is expected to contain two columns: 'sampleID' and 'file', which is used as the mapping between 'sampleID' and FCS file (absolute) path. When such mapping is provided, the file system searching is avoided.

- **sampNloc** a character scalar indicating where to get sampleName(or FCS filename) within xml workspace. It is either from "keyword" or 'sampleNode".

- **compensation=NULL**: a compensation or a list of compensations that allow the customized compensation matrix to be used instead of the one specified in flowJo workspace.

- **options=0**: an integer option passed to xmlTreeParse

- **channel.ignore.case** a logical flag indicates whether the colnames(channel names) matching needs to be case sensitive (e.g. compensation, gating..)

- **extend_val numeric** the threshold that determine wether the gates need to be extended. default is 0. It is triggered when gate coordinates are below this value.

- **extend_to numeric** the value that gate coordinates are extended to. Default is -4000. Usually this value will be automatically detected according to the real data range. But when the gates needs to be extended without loading the raw data (i.e. execute is set to FALSE), then this hard-coded value is used.

- **leaf.bool** a logical whether to compute the leaf boolean gates. Default is TRUE. It helps to speed up parsing by turning it off when the statistics of these leaf boolean gates are not important for analysis. (e.g. COMPASS package will calculate them by itself.) If needed, they can be calculated by calling recompute method at later stage.

- **additional.keys** character vector: The keywords (parsed from FCS header) to be combined(concatenated with "_") with FCS filename to uniquely identify samples. Default is "$TOT" (total number of cells) and more keywords can be added to make this GUID.

- **keywords** character vector specifying the keywords to be extracted as pData of GatingSet

- **keywords.source** character the place where the keywords are extracted from, can be either "XML" or "FCS"

- **keyword.ignore.case** a logical flag indicates whether the keywords matching needs to be case sensitive.

- **...**: Additional arguments to be passed to read.ncdfFlowSet or read.flowSet.

**Details**

A flowJoWorkspace is generated with a call to openWorkspace(), passing the name of the xml workspace file. This returns a flowJoWorkspace, which can be parsed using the parseWorkspace() method. The function can be called non-interactively by passing the index or name of the group of samples to be imported via parseWorkspace(obj, name=x), where x is either the numeric index, or the name. The subset argument allows one to select a set of files from the chosen sample group. The routine will take the intersection of the files in the sample group, the files specified in subset and the files available on disk, and import them.
Value

a GatingSet, which is a wrapper around a list of GatingHierarchy objects, each representing a single sample in the workspace. The GatingHierarchy objects contain graphNEL trees that represent the gating hierarchy of each sample. Each node in the GatingHierarchy has associated data, including the population counts from flowJo, the parent population counts, the flowCore gates generated from the flowJo workspace gate definitions. Data are not yet loaded or acted upon at this stage. To execute the gating of each data file, a call to execute() must be made on each GatingHierarchy object in the GatingSet. This is done automatically by default, and there is no more reason to set this argument to FALSE.

See Also

getSampleGroups,GatingSet

Examples

## Not run:
#f is a xml file name of a flowJo workspace
ws <- openWorkspace(f)
#parse the second group
gs <- parseWorkspace(ws, name = 2); #assume that the fcs files are under the same folder as workspace

gs <- parseWorkspace(ws, name = 4, path = dataDir) #specify the FCS path
, subset = "CytoTrol_CytoTrol_1.fcs" #subset the parsing by FCS filename
, isNcdf = FALSE)#turn off cdf storage mode (normally you don't want to do this for parsing large datasets)

gs <- parseWorkspace(ws, path = dataDir, name = 4, keywords = c("PATIENT ID", "SAMPLE ID", "$TOT", "EXPERIMENT NAME")) #tell the parser to extract these keywords
, keywords.source = "XML" #keywords are extracted from xml workspace (alternatively can be set to "FCS"
, additional.keys = c("PATIENT ID") #use additional keywords together with FCS filename to uniquely identify samples
, execute = F) #parse workspace without the actual gating (can save time if just want to get the info)

#subset by pData (extracted from keywords)
gs <- parseWorkspace(ws, path = dataDir, name = 4, subset = 1\(^{\text{TUBE NAME}}\) \%in\% c("CytoTrol_1", "CytoTrol_2")
, keywords = 1\(^{\text{TUBE NAME}}\))

#override the default compensation defined in xml with the customized compensations
ws <- parseWorkspace(ws, name = 2, compensation = comps); #comp is either a compensation object or a list of compensation objects

## End(Not run)
**Description**

Accessor method that gets or replaces the pData of the flowSet/ncdfFlowSet object in a GatingSet or GatingSetList

**Usage**

```
## S4 method for signature 'GatingHierarchy'
pData(object)

## S4 method for signature 'GatingSet'
pData(object)

## S4 replacement method for signature 'GatingSet,data.frame'
pData(object) <- value

## S4 replacement method for signature 'GatingSetList,data.frame'
pData(object) <- value
```

**Arguments**

- **object** GatingSet or GatingSetList
- **value** data.frame The replacement of pData for flowSet or ncdfFlowSet object

**Value**

a data.frame

---

**plot,GatingSet,missing-method**

*plot a gating tree*

**Description**

Plot a tree/graph representing the GatingHierarchy

**Usage**

```
## S4 method for signature 'GatingSet,missing'
plot(x, y, ...)

## S4 method for signature 'GatingSet,character'
plot(x, y, ...)
```

**Arguments**

- **x** GatingHierarchy or GatingSet. If GatingSet, the first sample will be used to extract gating tree.
- **y** missing or character specifies.
- **...** other arguments:
• boolean: TRUE|FALSE logical specifying whether to plot boolean gate nodes.
  Defaults to FALSE.
• showHidden: TRUE|FALSE logical whether to show hidden nodes
• layout: See layoutGraph in package Rgraphviz
• width: See layoutGraph in package Rgraphviz
• height: See layoutGraph in package Rgraphviz
• fontsize: See layoutGraph in package Rgraphviz
• labelfontsize: See layoutGraph in package Rgraphviz
• fixedsize: See layoutGraph in package Rgraphviz

Examples

## Not run:
#gs is a GatingSet
plot(gs) # the same as plot(gs[[1]])
#plot a substree rooted from 'CD4'
plot(gs, "CD4")

## End(Not run)

plotGate

Plot gates and associated cell population contained in a GatingHierarchy or GatingSet

Description

When applied to a GatingHierarchy, arrange is set as TRUE, then all the gates associated with it are plotted as different panel on the same page. If arrange is FALSE, then it plots one gate at a time. By default, merge is set as TRUE, plot multiple gates on the same plot when they share common parent population and axis. When applied to a GatingSet, if lattice is TRUE, it plots one gate (multiple samples) per page, otherwise, one sample (with multiple gates) per page.

Usage

plotGate(x, y, ...)

## S4 method for signature 'GatingHierarchy,numeric'
plotGate(x, y, ...)

## S4 method for signature 'GatingSet,missing'
plotGate(x, y, ...)

## S4 method for signature 'GatingSetList,character'
plotGate(x, y, ...)
plotGate

Arguments

- `x` - GatingSet or GatingHierarchy object
- `y` - character, the node name or full/(partial) gating path or numeric representing the node index in the GatingHierarchy. or missing which will plot all gates and one gate per page. It is useful for generating plots in a multi-page pdf.

Nodes can be accessed with `getNodes`.

- `...`
  - `bool` logical specifying whether to plot boolean gates.
  - `arrange.main` character, The title of the main page of the plot. Default is the sample name. Only valid when `x` is GatingHierarchy
  - `arrange` logical indicating whether to arrange different populations/nodes on the same page via `arrangeGrob` call.
  - `merge` logical indicating whether to draw multiple gates on the same plot if these gates share the same parent population and same x,y dimensions/parameters;
  - `projections` list of character vectors used to customize x,y axis. By default, the x,y axis are determined by the respective gate parameters. The elements of the list are named by the population name or path (see `y`). Each element is a pair of named character specifying the channel name(or marker name) for x, y axis. Short form of channel or marker names (e.g., "APC" or "CD3") can be used as long as they can be uniquely matched to the dimensions of flow data. For example, `projections = list("lymph" = c(x = "SSC-A", y = "FSC-A"), "CD3" = c(x = "CD3", y = "SSC-A"))`
  - `par.settings` list of graphical parameters passed to `lattice`;
  - `gpar` list of grid parameters passed to `grid.layout`;
  - `lattice` logical deprecated;
  - `formula` formula a formula passed to `xyplot` function of `flowViz`, by default it is NULL, which means the formula is generated according to the x,y parameters associated with gate.
  - `cond` character the conditioning variable to be passed to lattice plot.
  - `overlayNode` names. These populations are plotted on top of the existing gates(defined by `y` argument) as the overlaid dots.
  - `overlay.symbol` A named (lattice graphic parameter) list that defines the symbol color and size for each overlaid population. If not given, we automatically assign the colors.
  - `keyLattice` legend parameter for overlay symbols.
  - `default.y` character specifying y channel for `xyplot` when plotting a 1d gate. Default is "SSC-A" and session-wise setting can be stored by `flowWorkspace.par.set("plotGate", list(default.y = "FSC-A"))`
  - `type` character either "xyplot" or "densityplot". Default is "xyplot" and session-wise setting can be stored by `flowWorkspace.par.set("plotGate", list(type = "xyplot"))`
  - `fitGate` used to disable behavior of plotting the gate region in 1d density-plot. Default is FALSE and session-wise setting can be stored by `flowWorkspace.par.set("plotGate", list(fitGate = FALSE))`
  - `strip` logical specifies whether to show pop name in strip box, only valid when `x` is GatingHierarchy
  - `strip.text` either "parent" (the parent population name) or "gate "(the gate name).
• raw.scale logical whether to show the axis in raw (untransformed) scale. Default is TRUE and can be stored as session-wise setting by `flowWorkspace.par.set("plotGate", list(raw.scale = TRUE))`.

• xlim, ylim character can be either "instrument" or "data" which determines the x, y axis scale either by instrument measurement range or the actual data range. or numeric which specifies customized range. They can be stored as session-wise setting by `flowWorkspace.par.set("plotGate", list(xlim = "instrument"))`.

• path A character or numeric scalar passed to `getNodes` method (used to control how the gating/node path is displayed).

... The other additional arguments to be passed to `xyplot`.

Value

A trellis object if arrange is FALSE.

References

http://www.rglab.org/

Examples

```r
## Not run:
projections <- list("cd3" = c(x = "cd3", y = "AViD"), 
  "cd4" = c(x = "cd8", y = "cd4"), 
  "cd4/IL2" = c(x = "IL2", y = "IFNg"), 
  "cd4/IFNg" = c(x = "IL2", y = "IFNg")
)
plotGate(gh, c("cd3", "cd4", "cd4/IL2", "cd4/IFNg"), path = "auto", projections = projections, gpar = c(nrow = 2))
## End(Not run)
## Not run:
#G is a GatingHierarchy
plotGate(G, getNodes(G)[5]);#plot the gate for the fifth node
## End(Not run)
```

Description

This function plots the coefficient of variation calculated between the xml population statistics and the openCyto population statistics for each population in a gating hierarchy extracted from a xml Workspace.
## plot_pop_cv

### Usage

```r
## S4 method for signature 'GatingHierarchy'
plotPopCV(x, m = 2, n = 2, path = "auto", ...)

## S4 method for signature 'GatingSet'
plotPopCV(x, scales = list(x = list(rot = 90)), path = "auto", ...)
```

### Arguments

- **x**
  - A `GatingHierarchy` from or a `GatingSet`.
- **m**
  - numeric The number of rows in the panel plot. Now deprecated, uses lattice.
- **n**
  - numeric The number of columns in the panel plot. Now deprecated, uses lattice.
- **path**
  - character see `getNodes`
- **...**
  - Additional arguments to the `barplot` methods.
- **scales**
  - list see `barchart`

### Details

The CVs are plotted as barplots across panels on a grid of size $m \times n$.

### Value

Nothing is returned.

### See Also

- `getPopStats`

### Examples

```r
## Not run:
#G is a GatingHierarchy
plotPopCV(G, 4, 4);
## End(Not run)
```

---

## plot_diff_tree

### Description

visualize the tree structure difference among the `GatingSets`

### Usage

```r
plot_diff_tree(x, path = "auto", ...)
```
Arguments

x list of groups (each group is a list of 'GatingSet'). It is usually the outcome from `groupByTree`.

Examples

```r
## Not run:
gslist <- list(gs1, gs2, gs3, gs4, gs5)
gs_groups <- groupByTree(gslist)
plot_diff_tree(gs_groups)
## End(Not run)
```

pop.MFI `built-in stats functions`.

Description

`pop.MFI` computes and returns the median fluorescence intensity for each marker. They are typically used as the arguments passed to `getStats` method to perform the sample-wise population stats calculations.

Usage

```r
pop.MFI(fr)
```

Arguments

fr a flowFrame represents a gated population

Value

a named numeric vector

prettyAxis `Determine tick mark locations and labels for a given channel axis`

Description

Determine tick mark locations and labels for a given channel axis

Usage

```r
prettyAxis(gh, channel)
```

Arguments

gh `GatingHierarchy`

channel character channel name
Value

when there is transformation function associated with the given channel, it returns a list of that contains positions and labels to draw on the axis otherwise returns NULL.

Examples

```r
## Not run:
prettyAxis(gh, "<B710-A>")
## End(Not run)
```

Description

Compute each cell event to see if it falls into the gate stored within the gating tree and store the result as cell count.

Usage

```r
## S4 method for signature 'GatingSet'
recompute(x, y = "root", alwaysLoadData = FALSE, ...

## S4 method for signature 'GatingSetList'
recompute(x, ...)
```

Arguments

- `x`: GatingSet
- `y`: character node name or node path. Default "root". Optional.
- `alwaysLoadData`: logical. Specifies whether to load the flow raw data for gating boolean gates. Default "FALSE". Optional. Sometime it is more efficient to skip loading the raw data if all the reference nodes and parent are already gated. "FALSE" will check the parent node and reference to determine whether to load the data. This check may not be sufficient since the further upstream ancestor nodes may not be gated yet. In that case, we allow the gating to fail and prompt user to recompute those nodes explicitly. When TRUE, then it forces data to be loaded to guarantee the gating process to be uninterrupted at the cost of unnecessary data IO.
- `...`: other arguments leaf.bool whether to compute the leaf boolean gate, default is TRUE

Details

It is usually used immediately after `add` or `setGate` calls.
sampleNames,GatingHierarchy-method

Get/update sample names in a GatingSet

Description

Return a sample names contained in a GatingSet

Usage

## S4 method for signature 'GatingHierarchy'
sampleNames(object)

## S4 method for signature 'GatingSet'
sampleNames(object)

## S4 replacement method for signature 'GatingSet'
sampleNames(object) <- value

Arguments

object or a GatingSet

value character new sample names

Details

The sample names comes from pdata of fs.

Value

A character vector of sample names

Examples

## Not run:
#G is a GatingSet
sampleNames(G)

## End(Not run)

save_gs

save/load a GatingSet/GatingSetList to/from disk.

Description

Save/load a GatingSet/GatingSetList which is the gated flow data including gates and populations to/from the disk. The GatingSet object The internal C data structure (gating tree), ncdfFlowSet object (if applicable)
Usage

```r
save_gs(G, path, overwrite = FALSE, cdf = c("copy", "move", "skip", "symlink", "link"), ...)
```

```r
load_gs(path)
```

```r
save_gslist(gslist, path, ...)
```

```r
load_gslist(path)
```

Arguments

- **G**: A `GatingSet`
- **path**: A character scalar giving the path to save/load the `GatingSet` to/from.
- **overwrite**: A logical scalar specifying whether to overwrite the existing folder.
- **cdf**: a character scalar. The valid options are: "copy", "move", "skip", "symlink", "link" specifying what to do with the cdf data file. Sometime it is more efficient to move or create a link of the existing cdf file to the archived folder. It is useful to "skip" archiving cdf file if raw data has not been changed.
- **...**: other arguments: not used.
- **gslist**: A `GatingSetList`

Value

- **load_gs**: returns a `GatingSet` object
- **load_gslist**: returns a `GatingSetList` object

See Also

- `GatingSet-class`
- `GatingSetList-class`

Examples

```r
## Not run:
#G is a GatingSet
save_gs(G, path="tempFolder")
G1<-load_gs(path="tempFolder")
#G is a GatingSet
save_gslist(gslist1, path="tempFolder")
gslist2<-load_gslist(path="tempFolder")
## End(Not run)
```
**set.count.xml**

Save the event counts parsed from xml into c++ tree structure.

**Description**

It is for internal use by the diva parser.

**Usage**

```r
set.count.xml(gh, node, count)
```

**Arguments**

- **gh**
  - GatingHierarchy
- **node**
  - the unique gating path that uniquely identifies a population node
- **count**
  - integer number that is events count for the respective gating node directly parsed from xml file

**Examples**

```r
## Not run:
set.count.xml(gh, "CD3", 10000)
## End(Not run)
```

**setGate**, **GatingHierarchy**, **character**, **filter-method**

Update the gate.

**Description**

Update the population node with a flowCore-compatible gate object.

**Usage**

```r
## S4 method for signature 'GatingHierarchy, character, filter'
setGate(obj, y, value,
    negated = FALSE, ...)
```

```r
## S4 method for signature 'GatingSet, character, filterList'
setGate(obj, y, value, ...)
```
Arguments

obj  GatingHierarchy or GatingSet
y    character node name or path
value filter or filterList or list of filter objects
negated logical see add
... other arguments

Details

Usually recompute is followed by this call since updating a gate doesn’t re-calculating the cell events within the gate automatically. see filterObject for the gate types that are currently supported.

Examples

## Not run:
gr1 <- rectangleGate("FSC-H"=c(200,400), "SSC-H"=c(250, 400), filterId="rectangle")
gr2 <- rectangleGate("FSC-H"=c(200,400), "SSC-H"=c(250, 400), filterId="rectangle")
flist <- list(gr1,gr2)
names(flist) <- sampleNames(gs[1:2])
setGate(gs[1:2], "lymph", flist)
recompute(gs[1:2], "lymph")

## End(Not run)
## Examples

```r
# Not run:
G is a gating hierarchy
gNodes(G[[1]]) # return node names
setNode(G,"L","lymph")

# Not run:
setNode(gh, 4, FALSE) # hide a node
setNode(gh, 4, TRUE) # unhide a node

# Not run
```

## Description

The tools to standardize the tree structures and channel names.

- `groupByTree(x)`
- `groupByChannels(x)`
- `checkRedundantNodes(x)`
- `dropRedundantNodes(x, toRemove)`
- `dropRedundantChannels(gs)`
- `updateChannels(gs, map, all = TRUE)`
- `insertGate(gs, gate, parent, children)`
- `setNode(x, y, FALSE)`

## Details

In order to merge multiple GatingSets into single `GatingSetList`, the gating trees and channel names must be consistent. These functions help removing the discrepancies and standardize the GatingSets so that they are mergable.

- `groupByTree` splits the GatingSets into groups based on the gating tree structures.
- `groupByChannels` split GatingSets into groups based on their flow channels.
- `checkRedundantNodes` returns the terminal(or leaf) nodes that makes the gating trees to be different among GatingSets and thus can be considered to remove as redundant nodes.
- `dropRedundantNodes` removes the terminal(or leaf) nodes that are detected as redundant by `checkRedundantNodes`.
- `dropRedundantChannels` remove the redundant channels that are not used by any gate defined in the GatingSet.
- `updateChannels` modifies the channel names in place. (Usually used to standardize the channels among GatingSets due to the letter case discrepancies or typo).
- `insertGate` inserts a dummy gate to the GatingSet. Is is useful trick to deal with the extra non-leaf node in some GatingSets that can not be simply removed by `dropRedundantNodes`.
- `setNode` hide a node/gate in a GatingSet. It is useful to deal with the non-leaf node that causes the tree structure discrepancy.
subset.GatingSet

subset.GatingSet subset the GatingSet/GatingSetList based on 'pData'

Description
subset the GatingSet/GatingSetList based on 'pData'

Usage
## S3 method for class 'GatingSet'
subset(x, subset, ...)

Arguments
x GatingSet or GatingSetList
subset logical expression(within the context of pData) indicating samples to keep. see subset
... other arguments. (not used)

Value
a codeGatingSet or GatingSetList object

swap_data_cols

swap_data_cols Swap the colnames Perform some validity checks before returning the updated colnames

Description
Swap the colnames Perform some validity checks before returning the updated colnames

Usage
swap_data_cols(cols, swap_cols)

Arguments
cols the original colname vector
swap_cols a named list specifying the pairs to be swapped

Value
the new colname vector that has some colnames swapped

Examples
data(GvHD)
fr <- GvHD[[1]]
colnames(fr)
new <- swap_data_cols(colnames(fr), list('FSC-H' = "SSC-H", 'FL2-H' = "FL2-A"))
colnames(fr) <- new
transform, GatingSet-method

transform the flow data associated with the GatingSet

Description

The transformation functions are saved in the GatingSet and can be retrieved by `getTransformations`. Currently only flowJo-type biexponential transformation (either returned by `getTransformations` or constructed by `flowJoTrans`) is supported.

Usage

```r
## S4 method for signature 'GatingSet'
transform(`_data`, translist, ...)

## S4 method for signature 'GatingSetList'
transform(`_data`, ...)
```

Arguments

- `_data` GatingSet or GatingSetList
- `translist` expect a `transformList` object or a list of `transformList` objects (with names matched to sample names)
- `...` other arguments passed to `transform` method for `ncdfFlowSet` (e.g. `ncdf-File`)

Value

A GatingSet or GatingSetList object with the underlying flow data transformed.

Examples

```r
## Not run:
data(GvHD)
fs <- GvHD[1:2]
gs <- GatingSet(fs)
# construct biexponential transformation function
biexpTrans <- flowJoBiexp_trans(channelRange = 4096, maxValue = 262144, pos = 4.5, neg = 0, widthBasis = -10)
# make a transformList object
chnls <- c("FL1-H", "FL2-H")
transList <- transformerList(chnls, biexpTrans)
# add it to GatingSet
gs_trans <- transform(gs, transList)
```

## End(Not run)
**transformerList**  
*Constructor for transformerList object*

**Description**

Similar to `transformList` function, it constructs a list of transformer objects generated by `trans_new` method from `scales` so that the inverse and breaks functions are also included.

**Usage**

`transformerList(from, trans)`

**Arguments**

- `from` channel names
- `trans` a `trans` object or a list of `trans` objects constructed by `trans_new` method.

**Examples**

```r
library(scales)
# create transformer object from scratch
trans <- logicleTransform(w = 0.5, t = 262144, m = 4.5, a = 0)
inv <- inverseLogicleTransform(trans = trans)
trans.obj <- flow_trans("logicle", trans, inv, n = 5, equal.space = FALSE)

# or simply use convenient constructor
# trans.obj <- logicle_trans(n = 5, equal.space = FALSE, w = 0.5, t = 262144, m = 4.5, a = 0)

transformerList(c("FL1-H", "FL2-H"), trans.obj)

# use different transformer for each channel
trans.obj2 <- asinhGml2_trans()
transformerList(c("FL1-H", "FL2-H"), list(trans.obj, trans.obj2))
```

**updateChannels**  
*Update the channel information of a GatingSet (c++ part)*

**Description**

It updates the channels stored in gates, compensations and transformations based on given mapping between the old and new channel names.

**Usage**

`updateChannels(gs, map, all = TRUE)`
Arguments

- **gs**: a GatingSet object
- **map**: a data.frame containing the mapping from old (case insensitive) to new channel names. Note: Make sure to remove the '<' or '>' characters from 'old' name because the API tries to only look at the raw channel name so that the gates with both prefixed and non-prefixed names could be updated.
- **all**: logical whether to update the flow data as well

Value

When 'all' is set to TRUE, it returns a new GatingSet but it still shares the same underlying C++ tree structure with the original GatingSet otherwise it returns nothing (less overhead.)

Examples

```r
# Not run:
## this will update both "Qdot 655-A" and "<Qdot 655-A>"
gs <- updateChannels(gs, map = data.frame(old = c("Qdot 655-A"),
                  new = c("QDot 655-A")))
```

## End(Not run)

---

**updateIndices, GatingHierarchy, character, logical**

Directly update event indices without changing gates

Description

It is useful when we want to alter the popluation at events level yet without removing or adding the existing gates.

Usage

```r
## S4 method for signature 'GatingHierarchy, character, logical'
updateIndices(obj, y, z)
```

Arguments

- **obj**: GatingHierarchy object
- **y**: character node name or path
- **z**: logical vector as local event indices relative to node y
Examples

```r
library(flowWorkspace)
dataDir <- system.file("extdata", package="flowWorkspaceData")
suppressMessages(gs <- load_gs(list.files(dataDir, pattern = "gs_manual", full = TRUE)))
gh <- gs[[1]]
# get pop counts
pop.stats <- getStats(gh, nodes = c("CD3+", "CD4", "CD8"))
pop.stats

# subsample 30% cell events at CD3+ node
total.cd3 <- pop.stats[pop == "CD3+", count]
gInd <- seq_len(total.cd3) # create integer index for cd3
gInd <- sample.int(total.cd3, size = total.cd3 * 0.3) # randomly select 30%
# convert it to logicle index
gInd.logical <- rep(FALSE, total.cd3)
gInd.logical[gInd] <- TRUE
# replace the original index stored at GatingHierarchy
updateIndices(gh, "CD3+", gInd.logical)
# check the updated pop counts
getStats(gs[[1]], nodes = c("CD3+", "CD4", "CD8")) # note that CD4, CD8 are not updated
# update all the descendants of CD3+
nodes <- getDescendants(gh, "CD3+")
for (node in nodes) suppressMessages(recompute(gh, node))
getStats(gs[[1]], nodes = c("CD3+", "CD4", "CD8")) # now all are update to date
```
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