Package ‘flowWorkspace’

April 3, 2024

Type Package

Title Infrastructure for representing and interacting with gated and un gated 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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License_restricts_use no

LazyLoad yes

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1
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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

Package: flowWorkspace
Type: Package
Version: 0.5.40
Date: 2011-03-04
License: Artistic 2.0
LazyLoad: yes
Depends: R (>= 2.16.0)

Author(s)

Greg Finak, Mike Jiang

References

http://www.rglab.org/

asinhtGml2_trans

Inverse hyperbolic sine transformation.

Description

Used to construct inverse hyperbolic sine transform object.

Usage

asinhtGml2_trans(...)
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

asinhtGml2 transformation object

Examples

trans.obj <- asinhtGml2_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)

Arguments

T numeric the maximum value of input data

M numeric the full width of the transformed display in asymptotic decades

A numeric Additional negative range to be included in the display in asymptotic decades

inverse whether to return the inverse function

Value

fasinh/fsinh transform function
Examples

```r
trans <- asinh_Gml2()
data.raw <- c(1, 1e2, 1e3)data.trans <- trans(data.raw)
data.trans

inverse.trans <- asinh_Gml2(inverse = TRUE)
inverse.trans(data.trans)
```

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

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

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

Arguments

- `expr` expression
- `...` further arguments to the expression
- `filterId` character identifier

See Also

add GatingHierarchy

Examples

```r
# "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)
```
cf_append_cols: Append data columns to a flowFrame

**Description**

Append data columns to a flowFrame

**Usage**

```r
cf_append_cols(cf, cols)
```

**Arguments**

- **cf**: A cytoframe.
- **cols**: A numeric matrix containing the new data columns to be added. Must have column names to be used as new channel names.

**Details**

It is used to add extra data columns to the existing flowFrame. It handles keywords and parameters properly to ensure the new flowFrame can be written as a valid FCS through the function `write.FCS`.

**Examples**

```r
library(flowCore)
data(GvHD)
tmp <- GvHD[[1]]
cf <- flowFrame_to_cytoframe(tmp)
kf <- kmeansFilter("FSC-H"=c("Pop1","Pop2","Pop3"), filterId="myKmFilter")
fres <- filter(cf, kf)
cols <- as.numeric(fres@subSet)
cols <- matrix(cols, dimnames = list(NULL, "km"))
cf <- cf_append_cols(cf, cols)
```

cf_backend_type: return the cytoframe backend storage format

**Description**

return the cytoframe backend storage format
Usage

cf_backend_type(cf)

Arguments

cf cytoframe

Value

one of "mem","h5", "tile"

---

cf_get_uri  Return the file path of the underlying h5 file

Description

Return the file path of the underlying h5 file

Usage

cf_get_uri(cf)

cf_get_h5_file_path(cf)

Arguments

cf cytoframe object

Details

For the in-memory version of cytoframe, it returns an empty string. This can be used to check whether it is on-disk format.

See Also

Other cytoframe/cytoset IO functions: cf_write_disk(), cf_write_h5(), cs_get_uri(), load_cytoframe_from_fcs(), load_cytoframe(), load_cytoset_from_fcs()
**cf_is_subsetted**

*check whether a cytoframe/cytoset is a subsetted (by column or by row) view*

**Description**

check whether a cytoframe/cytoset is a subsetted (by column or by row) view

**Usage**

```r
cf_is_subsetted(x)
```

```r
cs_is_subsetted(x)
```

**Arguments**

- `x` - a cytoset or cytoframe

---

**cf_write_disk**

*Save the cytoframe to disk*

**Description**

Save the cytoframe to disk

**Usage**

```r
cf_write_disk(cf, filename, backend = get_default_backend())
```

**Arguments**

- `cf` - cytoframe object
- `filename` - the full path of the output file
- `backend` - either "h5" or "tile"

**See Also**

Other cytoframe/cytoset IO functions: `cf_get_uri()`, `cf_write_h5()`, `cs_get_uri()`, `load_cytoframe_from_fcs()`, `load_cytoframe()`, `load_cytoset_from_fcs()`
**cf_write_h5**

Save the cytoframe as h5 format

**Description**

Save the cytoframe as h5 format

**Usage**

```r
cf_write_h5(cf, filename)
```

**Arguments**

- `cf` cytoframe object
- `filename` the full path of the output h5 file

**See Also**

Other cytoframe/cytoset IO functions: `cf_get_uri()`, `cf_write_disk()`, `cs_get_uri()`, `load_cytoframe_from_fcs()`, `load_cytoframe()`, `load_cytoset_from_fcs()`

**cleanup**

Remove on-disk files associated with flowWorkspace data classes

**Description**

These methods immediately delete the on-disk storage associated with cytoframe, cytoset, GatingHierarchy, or GatingSet objects

**Usage**

```r
cf_cleanup(cf)
```

**Arguments**

- `cf` a cytoframe, cytoset, GatingHierarchy, or GatingSet object

**Details**

this will override tempdir() in determining the top directory under which files can safely be removed.
cleanup_temp

Remove temporary files associated with flowWorkspace data classes

Description

These methods immediately delete the on-disk h5 storage associated with cytoframe, cytoset, GatingHierarchy, or GatingSet objects, but only if it is under the directory pointed to by tempdir() or alternatively specified by the temp_dir option. The temp_dir option should be used with caution as it acts as a guard against accidental removal of non-temporary storage.

Usage

```r
cf_cleanup_temp(x, temp_dir = NULL)
cs_cleanup_temp(x, temp_dir = NULL)
gh_cleanup_temp(x, temp_dir = NULL)
gs_cleanup_temp(x, temp_dir = NULL)
```

Arguments

- `x`: a cytoframe, cytoset, GatingHierarchy, or GatingSet object
- `temp_dir`: an optional argument designating another path as temporary storage. If specified this will override tempdir() in determining the top directory under which files can safely be removed.

Details

Use of these functions will generally be unnecessary for most users, but they are provided for workflows that involve repeated creation of such data structures within the same R session to avoid overwhelming temporary storage.

compensate

compensate the flow data associated with the GatingSet

Description

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

Usage

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

x  GatingSet, GatingSetList, cytoframe, or cytoset
spillover compensation object or spillover matrix or a list of compensation objects

Value

a GatingSet, GatingSetList, cytoframe, or cytoset 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)
```

Methods for conversion between flowCore and flowWorkspace data classes

Description

These methods perform conversions between flowWorkspace classes (cytoframe/cytoset) and flowCore classes (flowFrame/flowSet) as well as between single-sample and aggregated classes (e.g. between cytoset and a list of cytoframes).

Usage

```r
cytoframe_to_flowFrame(cf)
flowFrame_to_cytoframe(fr, ...)
cytoset_to_flowSet(cs)
flowSet_to_cytoset(fs,
    path = tempfile(),
    backend = get_default_backend(),
    tmp = tempfile(),
    ...
)
cytoset_to_list(cs)
```
Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cf</td>
<td>cytoframe object</td>
</tr>
<tr>
<td>fr</td>
<td>flowframe</td>
</tr>
<tr>
<td>...</td>
<td>additional arguments passed to <code>load_cytoframe_from_fcs</code> or <code>load_cytoset_from_fcs</code>.</td>
</tr>
<tr>
<td>cs</td>
<td>cytoset</td>
</tr>
<tr>
<td>fs</td>
<td>flowSet or ncdfFlowSet</td>
</tr>
<tr>
<td>path</td>
<td>the h5 path for cytoset</td>
</tr>
<tr>
<td>tmp</td>
<td>the temp folder when the temporary files are written to during conversion by default, it is system temp path. And it can be changed to the customized location when there is not enough space at system path.</td>
</tr>
</tbody>
</table>

Details

The first set of methods consist of a pair of methods to coerce a cytoframe to or from a flowFrame and another pair to coerce a cytoset to or from a flowSet.

The conversion between the two sets of data container classes mostly entails a conversion of the back-end representation of the data. cytoframe and cytoset objects contain flowFrame and flowSet objects respectively, so coercion of a cytoframe to flowFrame entails moving the data from the 'C'-level data structure to the corresponding exprs, description, and parameters slots. Coercion of a flowFrame to a cytoframe entails creation of the 'C'-level data structure from the flowFrame slots. The names of each of the methods are pretty self-explanatory.

The second set of methods perform disaggregation of data objects that represent multiple samples in to lists of data objects that represent a single sample. The opposite direction is handled by the constructors for the aggregate data classes.

Methods

`cytoframe_to_flowFrame(object = "cytoframe")` Returns a flowFrame object coerced from a cytoframe object.

`flowFrame_to_cytoframe(object = "flowFrame")` Returns a cytoframe object coerced from a flowFrame object.

`cytoset_to_flowSet(object = "cytoset")` Returns a flowSet object coerced from a cytoset object.

`flowSet_to_cytoset(object = "flowSet")` Returns a cytoset object coerced from a flowSet object.

`flowSet_to_list(object = "flowSet")` Returns a list of cytoframe objects with names provided by the sampleNames of the original cytoset

`flowSet(object = "list")` Constructs a cytoset object from a list of cytoframe objects. See documentation for `cytoset`

`cytoset_to_list(object = "cytoset")` Returns a list of cytoframe objects with names provided by the sampleNames of the original cytoset

`cytoset(object = "list")` Constructs a cytoset object from a list of cytoframe objects. See documentation for `flowSet`
### Examples

```r
library(flowCore)
data("GvHD")
fs <- GvHD[[1]]
cs <- flowSet_to_cytoset(fs)
cf <- cs[[1, returnType="cytoframe"]]
ff <- cytoframe_to_flowFrame(cf)
```

---

**convert_backend**

Convert h5 based gs archive to tiledb

**Description**

Convert h5 based gs archive to tiledb

**Usage**

```r
convert_backend(gs_dir, output_dir)
```

**Arguments**

- `gs_dir`: existing gs archive path
- `output_dir`: the new gs path

---

**convert_legacy_gs**

Convert the legacy GatingSet archive (mixed with R and C++ files) to the new format (C++ only)

**Description**

Older versions of flowWorkspace represented GatingSet-class objects using a combination of R and C++ files, while newer versions have moved the representation entirely to the C++ level for the sake of efficiency. In order to use GatingSet or GatingSetList archives created in older versions, they will need to be converted to the new format.

**Usage**

```r
convert_legacy_gs(from, to, ...)
convert_legacy_gsitlist(from, to, ...)
```
cs_add_cytoframe

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
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<tbody>
<tr>
<td>from</td>
<td>the old archive path</td>
</tr>
<tr>
<td>to</td>
<td>the new archive path</td>
</tr>
<tr>
<td>...</td>
<td>tmp the path where the temporary files will be written to during the conversion. By default it is system temp folder and sometime it is helpful to be able to customize it to other location when system temp folder is full or not sufficient when converting big data sets.</td>
</tr>
</tbody>
</table>

**Details**

Note that it is likely some of the keyword values (mainly offsets e.g. BEGINDATA) may change slightly after the conversion due to the process of rewriting data to FCS files through write.FCS.

**Examples**

```r
## Not run:
convert_legacy_gs(old_gs_path, new_gs_path)
## End(Not run)
```

---

**cs_add_cytoframe**  
Add a cytoframe to a cytoset

**Description**

Add a cytoframe to a cytoset

**Usage**

```r
cs_add_cytoframe(cs, sn, cf)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cs</td>
<td>cytoset</td>
</tr>
<tr>
<td>sn</td>
<td>sample name to be added</td>
</tr>
<tr>
<td>cf</td>
<td>cytoframe to be added</td>
</tr>
</tbody>
</table>
cs_get_uri

Return the path of the underlying data files

Description

Return the path of the underlying data files

Usage

\[ \text{cs_get_uri}(x) \]

\[ \text{cs_get_h5_file_path}(x) \]

\[ \text{gs_get_uri}(x) \]

See Also

Other cytoframe/cytoset IO functions: \text{cf_get_uri()}, \text{cf_write_disk()}, \text{cf_write_h5()}, \text{load_cytoframe_from_fcs()}, \text{load_cytoframe()}, \text{load_cytoset_from_fcs()} 

---

cs_set_cytoframe

update a cytoframe in a cytoset

Description

update a cytoframe in a cytoset

Usage

\[ \text{cs_set_cytoframe}(cs, sn, cf) \]

Arguments

- \text{cs} \quad \text{cytoset}
- \text{sn} \quad \text{sample name}
- \text{cf} \quad \text{cytoframe}
cytoframe

**Description**

This class serves the same purpose as the `flowFrame` class from the `flowCore` package: to store quantitative data on cell populations from a single FCS run. The primary difference is in the underlying representation of the data. While `flowFrame` objects store the underlying data matrix in the `exprs` slot as an R object, `cytoframe` objects store the matrix (as well as the data from the other slots) in a C data structure that is accessed through an external pointer. This allows for greater optimization of data operations including I/O, parsing, transformation, and gating.

**Details**

From the user's standpoint, interacting with a `cytoframe` is very similar to interacting with a `flowframe`, with one important difference. While operations such as subsetting or copying a `flowFrame` using the standard R assignment operator (`<-`) will perform a deep copy of the data in its slots, the same operations on a `cytoframe` will produce a view to the same underlying data as the original object. This means that changes made to the `cytoframe` resulting from subsetting or copying will affect the original `cytoframe`. If a deep copy of the underlying data is desired, the `realize_view` method will accomplish this.

Because the `cytoframe` class inherits from `flowFrame`, the `flowFrame` slots are present but not utilized. Thus, attempting to access them directly will yield empty data structures. However, the `exprs`, `parameters`, or `description` methods work in a manner similar to a `flowFrame` by accessing the same information from the underlying data structure.

**Methods**

Many of the methods here have their own documentation pages or are more extensively explained in the documentation for `flowFrame`, so those documentation pages may be consulted as well for more details.

[ Subsetting. Returns an object of class `cytoframe`. The syntax for subsetting is similar to that of `data.frames`. In addition to the usual index vectors (integer and logical by position, character by parameter names), `cytoframes` can be subset via `filterResult` and `filter` objects.

*Usage:*

```r

cytoframe[i,j]
cytoframe[filter,]
cytoframe[filterResult,]
```

Note that the value of argument `drop` is ignored when subsetting `cytoframes`. 
Subsetting by channel name. This is similar to subsetting of columns of data.frames, i.e., `frame$FSC.H` is equivalent to `frame[, "FSC.H"]`. Note that column names may have to be quoted if they are not valid R symbols (e.g. `frame$"FSC-H"` or `frame$`FSC-H``).

`exprs, exprs<-` exprs returns an object of class matrix containing the measured intensities. Rows correspond to cells, columns to the different measurement channels. The colnames attribute of the matrix should hold the names or identifiers for the channels. The rownames attribute would usually not be set.

`exprs<-` replaces the raw data intensities. The replacement value must be a numeric matrix with colnames matching the parameter definitions. Implicit subsetting is allowed (i.e. less columns in the replacement value compared to the original cytoframe), but all columns must be defined in the original cytoframe.

**Usage:**

`exprs(cytoframe)`

`exprs(cytoframe) <- value`

`head, tail` Show first/last elements of the raw data matrix

**Usage:**

`head(cytoframe)`

`tail(cytoframe)`

`keyword, keyword<-` Extract all entries or a single entry from the annotations by keyword or replace the entire list of key/value pairs with a new named list. See `keyword` for details.

**Usage:**

`keyword(cytoframe)`

`keyword(cytoframe, character)`

`keyword(cytoframe) <- list(value)`

`parameters, parameters<-` Extract parameters and return an object of class `AnnotatedDataFrame` containing information about each column of the cytoframe, or replace such an object.

This information will generally be filled in by `load_cytoframe_from_fcs` or similar functions using data from the FCS keywords describing the parameters. To access the actual pa-
replacement annotation, use pData(parameters(cytoframe)).

Replacement is only valid with AnnotatedDataFrames containing all varLabels name, desc, range, minRange and maxRange, and matching entries in the name column to the colnames of the exprs matrix. See parameters for more details.

Usage:

parameters(cytoframe)

parameters(cytoframe) <- value

show  Display details about the cytoframe object.

summary  Return descriptive statistical summary (min, max, mean and quantile) for each channel

Usage:

summary(cytoframe)

plot  Basic plots for cytoframe objects. If the object has only a single parameter this produces a histogram. For exactly two parameters we plot a bivariate density map (see smoothScatter) and for more than two parameters we produce a simple splom plot. To select specific parameters from a flowFrame for plotting, either subset the object or specify the parameters as a character vector in the second argument to plot. The smooth parameters lets you toggle between density-type smoothScatter plots and regular scatterplots. For far more sophisticated plotting of flow cytometry data, see the ggcyto package.

Usage:

plot(cytoframe, ...)

plot(cytoframe, character, ...)

plot(cytoframe, smooth=FALSE, ...)

ncol, nrow, dim  Extract the dimensions of the data matrix.

Usage:

ncol(cytoframe)

nrow(cytoframe)
dim(cytoframe)

**featureNames, colnames, colnames**: colnames and featureNames are synonyms. They extract parameter names (i.e., the colnames of the data matrix). For colnames there is also a replacement method. This will update the name column in the parameters slot as well.

*Usage:*

featureNames(cytoframe)

colnames(cytoframe)

colnames(cytoframe) <- value

**markernames, markernames**: Access or replace the marker names associated with the channels of the cytoframe. For replacement, value should be a named list or character vector where the names correspond to the channel names and the values correspond to the marker names.

*Usage:*

markernames(object)

markernames(object) <- value

**names** Extract pretty formatted names of the parameters including parameter descriptions.

*Usage:*

names(cytoframe)

**identifier** Extract GUID of a cytoframe. Returns the file name if no GUID is available. See identifier for details.

*Usage:*

identifier(cytoframe)

**range** Get instrument or actual data range of the cytoframe. Note that instrument dynamic range is not necessarily the same as the range of the actual data values, but the theoretical range of values the measurement instrument was able to capture. The values of the dynamic range will be transformed when using the transformation methods for cytoframe objects.
**Parameters:**

x: cytoframe object.

type: Range type. either "instrument" or "data". Default is "instrument"

**Usage:**

range(x, type = "data")

each_row, each_col  Apply functions over rows or columns of the data matrix. These are convenience methods. See each_col for details.

**Usage:**

each_row(cytoframe, function, ...)

each_col(cytoframe, function, ...)

transform  Apply a transformation function on a cytoframe object. This uses R’s transform function by treating the cytoframe like a regular data.frame. flowCore provides an additional inline mechanism for transformations (see %on%) which is strictly more limited than the out-of-line transformation described here.

**Usage:**

transform(cytoframe, translist, ...)

filter  Apply a filter object on a cytoframe object. This returns an object of class filterResult, which could then be used for subsetting of the data or to calculate summary statistics. See filter for details.

**Usage:**

filter(cytoframe, filter)

split  Split cytoframe object according to a filter, a filterResult or a factor. For most types of filters, an optional flowSet=TRUE parameter will create a flowSet rather than a simple list. See split for details.

**Usage:**

split(cytoframe, filter, flowSet=FALSE, ...)
split(cytoframe, filterResult, flowSet=FALSE, ...)
split(cytoframe, factor, flowSet=FALSE, ...)

Subset  Subset a cytoframe according to a filter or a logical vector. The same can be done using the standard subsetting operator with a filter, filterResult, or a logical vector as first argument.

Usage:

Subset(cytoframe, filter)
Subset(cytoframe, logical)

cbind2  Not yet implemented.
Expand a cytoframe by the data in a numeric matrix of the same length. The matrix must have column names different from those of the cytoframe. The additional method for numerics only raises a useful error message.

Usage:

cbind2(cytoframe, matrix)
cbind2(cytoframe, numeric)

compensate  Apply a compensation matrix (or a compensation object) on a cytoframe object. This returns a compensated cytoframe.

Usage:

compensate(cytoframe, matrix)
compensate(cytoframe, data.frame)
compensate(cytoframe, compensation)

decompensate  Not yet implemented.
Reverse the application of a compensation matrix (or a compensation object) on a cytoframe object. This returns a decompensated cytoframe.

Usage:

decompensate(cytoframe, matrix)
decompensate(cytoframe, data.frame)

**spillover** Extract spillover matrix from description slot if present. It is equivalent to `keyword(x, c("spillover", "SPILL"))` Thus will simply return a list of keyword values for "spillover" and "SPILL".

*Usage:*

spillover(cytoframe)

**realize_view** Returns a new cytoframe with its own copy of the underlying data (a deep copy). The optional filepath argument accepts a string to specify a full filename for storing the new copy of the data in h5 format.

*Usage:*

realize_view(cytoframe, filepath)

**See Also**

`flowSet`, `read.FCS`

---

**cytoframe-labels** *Methods to change channel and marker names for cytoframe and cytoset objects*

**Description**

The methods allow direct alteration of channel names or marker names of `cytoframe` and `cytoset` objects. These objects are accessed by reference and changed in place, so there is no need to assign the return value of these methods.

**Usage**

`cf_swap_colnames(x, col1, col2)`

`cf_rename_channel(x, old, new)`

`cf_rename_marker(x, old, new)`

`cs_swap_colnames(x, col1, col2)`
Arguments

- **x**: a cytoframe
- **col1**: first channel name to swap
- **col2**: second channel name to swap
- **old**: old channel or marker name to be changed
- **new**: new channel or marker name after change

---

cytoset: a reference class for efficiently managing the data representation of a flowSet

Description

This class is a container for a set of cytoframe objects, analogous to a flowSet.

Details

Similar to the distinction between the cytoframe and flowFrame classes, the primary difference between the cytoset and flowSet classes is in the underlying representation of the data. Because cytoset is a reference class, copying or subsetting a cytoset object will return a cytoset pointing to the same underlying data. A deep copy of the data can be obtained via the realize_view method.

There is one notable exception to the typical behavior of most methods returning a cytoframe. The standard extraction operator ([[]]) will by default perform a deep copy of the subset being extracted and return a flowFrame. This is for the sake of compatibility with existing user scripts.

Creating Objects

Objects can be created using cytoset() and then adding samples by providing a cytoframe and sample name to cs_add_cytoframe:

```r
cs <- cytoset()
cs_add_cytoframe(cs, "Sample Name", cytoframe)
```

The safest and easiest way to create cytosets directly from FCS files is via the load_cytoset_from_fcs function, and there are alternative ways to specify the files to read. See the separate documentation for details.
Methods

[[, [[ Subsetting. \(x[i]\) where \(i\) is a scalar, returns a cytoset object, and \(x[[i]]\) a flowFrame object. In this respect the semantics are similar to the behavior of the subsetting operators for lists. \(x[i, j]\) returns a cytoset for which the parameters of each cytoframe have been subset according to \(j\). \(x[[i, j]]\) returns the subset of a single flowFrame for all parameters in \(j\).

The reason for the default behavior of the extraction operator [[ returning a flowFrame rather than cytoframe is for backwards compatibility with existing user scripts. This behavior can be overridden to instead return a cytoframe with the additional returnType argument.

Usage:

cytoset[i]
cytoset[i, j]
cytoset[[i]]
cytoset[[i, returnType = "cytoframe"]]

get_cytoframe_from_cs Extract a cytoframe from a cytoset by supplying either a sample name or index and optionally supplying a subset of columns.

The cytoframe to be extracted (i argument) can be specified using its sample name (character) or index in the cytoset (int/numeric). Columns (j argument) can be specified using channel name (character), index (int/numeric), or logical vector. If this argument is missing, all columns will be selected.

Usage:

(Assuming cs is a cytoset and cf is the extracted cytoframe) cf <- get_cytoframe_from_cs(cs, i, j) cf <- get_cytoframe_from_cs(cs, i)

$ Subsetting by frame name. This will return a single cytoframe object. Note that names may have to be quoted if they are not valid R symbols (e.g. cytoset$"sample 1").

colnames, colnames<- Extract or replace the character object with the (common) column names of all the data matrices in the cytoframes.

Usage:

colnames(cytoset)
colnames(cytoset) <- value

identifier, identifier<- Extract or replace the name item from the environment.
Usage:

identifier(cytoset)

identifier(cytoset) <- value

**phenoData, phenoData<-**  Extract or replace the AnnotatedDataFrame containing the phenotypic data for the whole data set. Each row corresponds to one of the cytoframes. The sampleNames of phenoData (see below) must match the names of the cytoframes in the frames environment.

Usage:

phenoData(cytoset)

phenoData(cytoset) <- value

**pData, pData<-**  Extract or replace the data frame (or columns thereof) containing actual phenotypic information from the phenoData of the underlying data.

Usage:

pData(cytoset)

pData(cytoset)$someColumn <- value

**varLabels, varLabels<-**  Not yet implemented.

Extract and set varLabels in the AnnotatedDataFrame of the phenoData of the underlying data.

Usage:

varLabels(cytoset)

varLabels(cytoset) <- value

**sampleNames**  Extract and replace sample names from the phenoData. Sample names correspond to frame identifiers, and replacing them will also replace the GUID for each cytoframe. Note that each sample name needs to be unique.

Usage:

sampleNames(cytoset)
sampleNames(cytoset) <- value

**keyword**  Extract or replace keywords specified in a character vector or a list from the description slot of each frame. See `keyword` for details.

*Usage:*

```r
keyword(cytoset, list(keywords))
keyword(cytoset, keywords)
keyword(cytoset) <- list(foo="bar")
```

**length**  The number of `cytoframe` objects in the set.

*Usage:*

```r
length(cytoset)
```

**show**  display object summary.

**summary**  Return descriptive statistical summary (min, max, mean and quantile) for each channel of each `cytoframe`.

*Usage:*

```r
summary(cytoset)
```

**fsApply**  Apply a function on all frames in a cytoset object. Similar to `sapply`, but with additional parameters. See `fsApply` for details.

*Usage:*

```r
fsApply(cytoset, function, ...)
fsApply(cytoset, function, use.exprs=TRUE, ...)
```

**compensate**  Apply a compensation matrix on all frames in a cytoset object. See `compensate` for details.

*Usage:*

```r```
compensate(cytoset, matrix)

**transform**  Apply a transformation function on all frames of a cytoset object. See `transform` for details.

*Usage:*

```r
transform(cytoset, ...)```

**filter**  Apply a filter on a cytoset object. There are methods for `filter` objects, and lists of `filter` objects. The latter has to be a named list, where names of the list items are matching the `sampleNames` of the cytoset. See `filter` for details.

*Usage:*

```r
filter(cytoset, filter)
filter(cytoset, list(filters))```

**split**  Split all `cytoframe` objects according to a `filter`, `filterResult` or a list of such objects, where the length of the list has to be the same as the length of the cytoset. This returns a list of `cytoframes` or an object of class `cytoset` if the `flowSet` argument is set to `TRUE`. Alternatively, a cytoset can be split into separate subsets according to a factor (or any vector that can be coerced into a factor), similar to the behaviour of `split` for lists. This will return a list of cytosets. See `split` for details.

*Usage:*

```r
split(cytoset, filter)
split(cytoset, filterResult)
split(cytoset, list(filters))
split(cytoset, factor)```

**Subset**  Returns a cytoset of `cytoframes` that have been subset according to a `filter` or `filterResult`, or according to a list of such items of equal length as the cytoset. See `Subset` for details.

*Usage:*

```r
Subset(cytoset, filter)```
Subset(cytoset, filterResult)
Subset(cytoset, list(filters))

**rbind2** Not yet implemented.
Combine two cytoset objects, or one cytoset and one cytoframe object.

*Usage:*

rbind2(cytoset, cytoset)
rbind2(cytoset, cytoframe)

**spillover** Compute spillover matrix from a compensation set. See `spillover` for details.

**realize_view** Returns a new cytoset with its own copy of the underlying data (a deep copy). The optional filepath argument accepts a string to specify a full directory name for storing the new copies of the data from the FCS files in h5 format.

*Usage:*

realize_view(cytoset, filepath)

**cs_add_cytoframe** Adds a cytoframe to the cytoset with sample name given by a string.

*Usage:*

cs_add_cytoframe(cytoset, "SampleName", cytoframe)

---

**delete_gs**

(delete the archive of GatingSet)

**Description**

delete the archive of GatingSet

**Usage**

delete_gs(path)

**Arguments**

- **path** either a local path or s3 path (e.g. "s3://bucketname/gs_path")
estimateLogicle

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

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

Description

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

Usage

```r
eextract_cluster_pop_name_from_node(node, cluster_method_name)
```
flowjo_biexp

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"

filter_to_list

convert flowCore filter to a list It convert the flowCore gate to a list whose structure can be understood by underlying c++ data structure.

Description

convert flowCore filter to a list
It convert the flowCore gate to a list whose structure can be understood by underlying c++ data structure.

Usage

filter_to_list(x)

Arguments

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

Value

alist

flowjo_biexp

construct the flowJo-type biexponentioal 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
flowjo_biexp(
  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 <- flowjo_biexp()
data.raw <- c(-1, 1e3, 1e5)
data.trans <- trans(data.raw)
round(data.trans)
inv <- flowjo_biexp(inverse = TRUE)
round(inv(data.trans))
```

Description

`flowjo_biexp_trans` flowJo biexponential transformation.

Used for constructing biexponential transformation object.

Usage

```r
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

library(flowCore)
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 inverse hyperbolic sine transform function

Description

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

Usage

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

numeric the maximum value of input data

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

trans <- flowjo_fasinh()
data.raw <- c(1,1e2,1e3)
data.trans <- trans(data.raw)
data.trans

inverse.trans <- flowjo_fasinhs()
inverse.trans(data.trans)

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)

flowJo_fasinh_trans(...)

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))
flowjo_log_trans

flowjo_log_trans  

flog transform function

Description

flog transform function constructor. It is different from flowCore version of logGml2 in the way that it reset negative input so that no NAN will be returned.

Usage

flowjo_log_trans(
  decade = 4.5,
  offset = 1,
  scale = 1,
  n = 6,
  equal.space = FALSE
)

Arguments

decade  total number of decades (i.e. log(max)-log(min)
offset   offset to the original input (i.e. min value)
scale    the linear scale factor
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

flog (or its inverse) transform function

Examples

trans <- flowjo_log_trans()
data.raw <- c(1,1e2,1e3)
data.trans <- trans["transform"](data.raw)
data.trans

inverse.trans <- trans["inverse"]
inverse.trans(data.trans)

# negative input
data.raw <- c(-10,1e2,1e3)
data.trans <- trans["transform"](data.raw)
data.trans
inverse.trans(data.trans)# we lose the original value at lower end since flog can't restore negative value
```r
#different
trans <- flowjo_log_trans(decade = 3, offset = 30)
data.trans <- trans[["transform"]](data.raw)
data.trans
inverse.trans <- trans[["inverse"]]
inverse.trans(data.trans)
```

---

**Description**

<table>
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<th>Function</th>
<th>Alias</th>
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<tr>
<td>getProp</td>
<td>gh_pop_get_proportion</td>
</tr>
<tr>
<td>getTotal</td>
<td>gh_pop_get_count</td>
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<td>getPopStats</td>
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<td>gh_pop_get_indices</td>
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<td>gs_pop_remove</td>
</tr>
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</table>

*Deprecated functions in package flowWorkspace.*
flow_breaks

Generate 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

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

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

```r
library(flowCore)
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

```r
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)
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
## Not run:
require(flowWorkspaceData)
d<-system.file("extdata",package="flowWorkspaceData")
wsfiles<-list.files(d,pattern="A2004Analysis.xml",full=TRUE)
library(CytoML)
ws <- open_flowjo_xml(wsfile);
G<-try(flowjo_to_gatingset(ws,path=d,name=1));
gh <- G[[1]]
gh_pop_compare_stats(gh);
gh_plot_pop_count_cv(gh)
nodeValues <- gs_get_pop_paths(gh)
thisNode <- nodes[4]
require(ggcyto)
autoplot(gh,thisNode);
gh_pop_get_gate(gh,thisNode);
gh_pop_get_data(gh,thisNode)
## 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.

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 flowjo_to_gatingset(...,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

pointer: Object of class "externalPtr". points to the gating hierarchy stored in C data structure.

transformation: Object of class "list". a list of transformation objects used by GatingSet.

See Also

GatingHierarchy

Examples

```r
## Not run:
require(flowWorkspaceData)
d<-system.file("extdata",package="flowWorkspaceData")
wsfile<-list.files(d,pattern="A2004Analysis.xml",full=TRUE)
library(CytoML)
ws <- open_flowjo_xml(wsfile);
G<-try(flowjo_to_gatingset(ws,execute=TRUE,path=d,name=1));
gs_plot_pop_count_cv(G);
## End(Not run)
```
GatingSet-methods

constructors for GatingSet

Description

construct a gatingset with empty trees (just root node)

Usage

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

Arguments

x
a flowSet, ncdfFlowSet, or cytoset

... arguments passed to flowSet_to_cytoset() when x is a flowSet

Examples

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

## End(Not run)

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

GatingSetList(x, samples = NULL)

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.
**GatingSetList-class**

**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

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[c(4,1)])
sampleNames(gslist2[c(1,4)])
gslist2[c("30104.fcs")]

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

# extract the gates associated with one popoulation
gs_pop_get_gate(gslist2, "3+")
gs_pop_get_gate(gslist2, 5)

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

get/set the default backend format of cytoframe

Description

get/set the default backend format of cytoframe

Usage

get_default_backend()

set_default_backend(backend = c("h5", "mem", "tile"))
get_log_level

Arguments
backend one of c("h5", "mem", "tile")

get_log_level get/set the log level

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

Usage
get_log_level()

set_log_level(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

Examples
get_log_level()
set_log_level("Population")
get_log_level()

gh_apply_to_cs Construct a GatingSet using a template

Description
This uses a GatingHierarchy as a template to apply to other loaded samples in the form of a cytoset, resulting in a GatingSet. The transformations and gates from the template are applied to all samples. The compensation applied to each of the samples can be controlled via the compensation_source argument.

Usage
gh_apply_to_cs(x, cs, swap_cols = FALSE, compensation_source = "sample", ...)

**gh_apply_to_new_fcs**

**Arguments**

- `x` GatingHierarchy
- `cs` a cytoset
- `swap_cols` for internal usage
- `compensation_source`

  One of the following options:
  - "sample" – each cytoframe will be compensated with the spillover matrix included in its own FCS
  - "template" – all cytoframes will be compensated with the spillover matrix of the template GatingHierarchy
  - "none" – no compensation will be applied

- ... not currently used

**Value**

a GatingSet

---

**gh_apply_to_new_fcs**  
*Construct a GatingSet using a template and FCS files*

**Description**

This uses a GatingHierarchy as a template to apply to other loaded samples in the form of a list of FCS files, resulting in a GatingSet. The transformations and gates from the template are applied to all samples.

**Usage**

```r
gh_apply_to_new_fcs(
  x,
  files,
  swap_cols = FALSE,
  backend = get_default_backend(),
  compensation_source = "sample",
  ...
)
```

**Arguments**

- `x` GatingHierarchy
- `swap_cols` for internal usage
- `backend` the backend storage mode to use for load_cytoset_from_fcs
- `compensation_source`

  One of the following options:
• "sample" – each cytoframe will be compensated with the spillover matrix included in its own FCS
• "template" – all cytoframes will be compensated with the spillover matrix of the template GatingHierarchy
• "none" – no compensation will be applied

... other arguments passed to load_cytoset_from_fcs

Details

This method is still included to support legacy scripts but will be deprecated for the more modular workflow of loading a cytoset via load_cytoset_from_fcs followed by gh_apply_to_cs.

---

gh_copy_gate

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

Description

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

Usage

gh_copy_gate(gh, node, to)

Arguments

gh
  GatingHierarchy

node
  the node to be copied

to
  the new parent node under which the node will be copied

Examples

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 <- gs_pop_get_parent(gh, "CD4")
nh.parent <- "singlets"
gh_copy_gate(gh, "CD4", new.parent)
gs_get_pop_paths(gh)
**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

**gh_get_compensations**  
*Retrieve the compensation matrices from a GatingHierarchy or GatingSet*

**Description**

Retrieve the compensation matrices from a GatingHierarchy or GatingSet.

**Usage**

```r
gh_get_compensations(x)
gs_get_compensations(x)
```

**Arguments**

- `x`: A GatingHierarchy or GatingSet object.

**Details**

Return all the compensation matrices in a GatingHierarchy or GatingSet

**Value**

A list of matrix representing the spillover matrix in GatingHierarchy or GatingSet
gh_get_transformations

Examples

## Not run:
# Assume gh is a GatingHierarchy and gs is a GatingSet
g_get_compensations(gh)
gs_get_compensations(gs)

## End(Not run)

gh_get_transformations

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

g_get_transformations(
  x,
  channel = NULL,
  inverse = FALSE,
  only.function = TRUE,
  ...
)

Arguments

x
channel
inverse
only.function

A GatingHierarchy object
character channel name
logical whether to return the inverse transformation function. Valid when only.function is TRUE
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 function 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 flowjo_workspace. Each element of L is itself a list of length M, where M is the number of parameters that were transformed for a sample or group of samples in a flowjo_workspace. 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
g_h_get_transformations(gh); # return a list transformation functions
g_h_get_transformations(gh, inverse = TRUE); # return a list inverse transformation functions
g_h_get_transformations(gh, channel = "FL1-H") # only return the transformation associated with given channel
g_h_get_transformations(gh, channel = "FL1-H", only.function = FALSE) # return the entire transform object

## End(Not run)
```

**gh_plot_pop_count_cv**  
Plot the coefficient of variation between xml and openCyto population statistics for each population in a gating hierarchy.

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.

Usage

```r
g_h_plot_pop_count_cv(x, path = "auto", ...)
g_s_plot_pop_count_cv(x, scales = list(x = list(rot = 90)), path = "auto", ...)
```

Arguments

- **x**  
  A GatingHierarchy from or a GatingSet.

- **path**  
  character see `gs_get_pop_paths`

- **...**  
  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.
gh_pop_compare_stats

See Also

gs_pop_get_count_fast

Examples

## Not run:

# G is a GatingHierarchy
gs_plot_pop_count_cv(G, 4, 4);

## End(Not run)

gh_pop_compare_stats

Compare the stats(count/freq) between the version parsed from xml and the one recalculated/gated from R

Description

Compare the stats(count/freq) between the version parsed from xml and the one recalculated/gated from R

Usage

gh_pop_compare_stats(x, path = "auto", ...)

Arguments

x GatingHierarchy
path see gs_get_pop_paths
... not used

gh_pop_get_cluster_name

check if a node is clustering node

Description

check if a node is clustering node

Usage

gh_pop_get_cluster_name(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_pop_get_data
get gated flow data from a GatingHierarchy/GatingSet/GatingSetList

Description

get gated flow data from a GatingHierarchy/GatingSet/GatingSetList

Usage

gh_pop_get_data(obj, y = "root", inverse.transform = FALSE, ...)

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.
- **inverse.transform**: logical flag indicating whether to inverse transform the data
- **...**: arguments passed to ncdfFlow::[

Details

Returns a flowFrame/flowSet containing the events in the gate defined at node y. Subset membership can be obtained using gh_pop_get_indices. Population statistics can be obtained using getPop and gh_pop_compare_stats. When calling gh_pop_get_data 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 gs_cyto_data method.

Value

A flowFrame object if obj is a GatingHierarchy. A flowSet or ncdfFlowSet if a GatingSet. A ncdfFlowList if a GatingSetList.

See Also

gs_cyto_data gh_pop_get_indices gh_pop_compare_stats
**gh_pop_get_descendants**

get all the descendant nodes for the given ancestor

**Description**

get all the descendant nodes for the given ancestor

**Usage**

gh_pop_get_descendants(gh, node, showHidden = TRUE, ...)

**Arguments**

- **gh**
  - GatingHierarchy
- **node**
  - the node path
- **showHidden**
  - whether show hidden nodes
- **...**
  - 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)))
gh_pop_get_descendants(gs[[1]], "CD4")
gh_pop_get_descendants(gs[[1]], "CD8", path = "auto")
```
gh_pop_get_full_path  *convert the partial gating path to the full path*

**Description**

convert the partial gating path to the full path

**Usage**

```r
gh_pop_get_full_path(gh, path)
```

**Arguments**

- `gh` GatingHierarchy object
- `path` the partial gating path

**Value**

the full gating path

---

gh_pop_get_indices  *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
gh_pop_get_indices(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 `gh_pop_get_indices` but the more convenient methods `gh_pop_get_proportion` and `gh_pop_compare_stats` 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**

`gh_pop_compare_stats`

**Examples**

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

---

**gh_pop_get_indices_mat**

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

**Description**

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

**Usage**

```r
gh_pop_get_indices_mat(gh, y)
```

**Arguments**

- `gh` GatingHierarchy object
- `y` character vector containing the node names
gh_pop_get_proportion  
*Get count or proportion from populations*

**Description**

Get count or proportion from populations

**Usage**

```r
gh_pop_get_proportion(x, y, xml = FALSE)
gh_pop_get_count(x, y, xml = FALSE)
```

**Arguments**

- **x**  
  GatingHierarchy
- **y**  
  character node name or path
- **xml**  
  whether to extract xml stats or openCyto stats

gh_pop_move  
*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
gh_pop_move(gh, node, to, recompute = TRUE)
```

**Arguments**

- **gh**  
  GatingHierarchy
- **node**  
  the node to be moved
- **to**  
  the new parent node under which the node will be moved to
- **recompute**  
  whether to recompute the gates after the node is moved. Default is TRUE.
**gh_pop_set_indices**

directly update event indices without changing gates

**Description**

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

**Usage**

```
gh_pop_set_indices(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**

```
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 <- gh_pop_get_parent(gh, "CD4")
new.parent <- "singlets"
gh_pop_move(gh, "CD4", new.parent)
gh_pop_get_parent(gh, "CD4")
```

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

gh_pop_set_xml_count
save the event counts parsed from xml into c++ tree structure

Description
It is for internal use by the diva parser

Usage
gh_pop_set_xml_count(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
## Not run:
gh_pop_set_xml_count(gh, "CD3", 10000)
## End(Not run)

gslist_to_gs
Merge a GatingSetList into a single GatingSet

Description
Merge a GatingSetList into a single GatingSet

Usage
gslist_to_gs(x, ...)

Arguments
x GatingSetList
... other arguments passed to gslist_to_gs method for ncdfFlowList
gs_check_redundant_nodes

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

Description

These leaf nodes make the gating trees to be different from one another and can be removed by the subsequent convenient call gs_remove_redundant_nodes.

Usage

gs_check_redundant_nodes(x, path = "auto", ...)

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 gs_split_by_tree.

path argumented passed to gs_get_pop_paths. The default value is "auto".

... other arguments passed to gs_get_pop_paths.

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 <- gs_split_by_tree(gslist)
toRm <- gs_check_redundant_nodes(gs_groups)

## End(Not run)

---

gs_cyto_data

Fetch or replace the flowData object associated with a GatingSet.

Description

Accessor method that gets or replaces the cytoset/flowSet/ncdfFlowSet object in a GatingSet or GatingHierarchy
Usage

```
gs.cyto.data(x, ...)
```

```
## S4 method for signature 'GatingSet'
gs.cyto.data(x, inverse.transform = FALSE)
```

```
gs.cyto.data(x) <- value
```

Arguments

- `x`: A `GatingSet`
- `...`: other arguments
- `inverse.transform`: logical flag indicating whether to inverse transform the data
- `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.

gs.get_compensation_internal

extract compensation object from GatingSet

Description

extract compensation object from GatingSet

Usage

```
gs.get_compensation_internal(gs, sampleName)
```

Arguments

- `gs`: `GatingSet`
- `sampleName`: sample name
gs_get_leaf_nodes

get all the leaf nodes

Description

get all the leaf nodes

Usage

hs.get_leaf_nodes(x, ancestor = "root", ...)

gh_get_leaf_nodes(x, ancestor = "root", ...)

Arguments

- `x`: GatingHierarchy/GatingSet object
- `ancestor`: ancestor node where the leaf nodes descend from. Default is 'root'.
- `...`: arguments passed to 'gs.get_pop_paths" method

Value

the leaf nodes

gs_get_pop_paths

Get the names of all nodes from a gating hierarchy.

Description

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

Usage

hs.get_pop_paths(
  x,
  y = NULL,
  order = "regular",
  path = "full",
  showHidden = FALSE,
  ...
)

gh_get_pop_paths(
  x,
  y = NULL,
  order = "regular",
  path = "full",
  showHidden = FALSE,
  ...)
gs_get_singlecell_expression

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

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

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

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

Examples

## Not run:
# G is a gating hierarchy
gs_get_pop_paths(G, path = 1)# return node names (without prefix)
gs_get_pop_paths(G, path = "full")# return the full path
gs_get_pop_paths(G, path = 2)# return the path as length of two
gs_get_pop_paths(G, path = "auto")# automatically determine the length of path
gs_pop_set_name(G, "L", "lymph")

## End(Not run)
Description

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

Usage

```r
gs_get_singlecell_expression(
  x,
  nodes,
  other.markers = NULL,
  swap = FALSE,
  threshold = TRUE,
  marginal = TRUE,
  mc.cores = getOption("mc.cores", 1L),
  inverse.transform = FALSE,
  ...
)
```

```r
gs_get_singlecell_expression_by_gate(...)
```

Arguments

- `x`: A GatingSet or GatingSetList object.
- `nodes`: character vector specifying different cell populations.
- `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.
- `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 the gate is treaded 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.
- `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.
- `inverse.transform`: logical flag indicating whether to inverse transform the data.
- `...`: other arguments 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.
gs_is_persistent

determine whether the flow data associated with a GatingSet is persistent(on-disk) or in-memory

description

determine whether the flow data associated with a GatingSet is persistent(on-disk) or in-memory

Usage

  gs_is_persistent(x)

  gs_is_h5(x)

  isNcdf(x)
**gs_plot_diff_tree**

**Arguments**
- **x**  
  GatingSet object

**Value**
- logical

**gs_plot_diff_tree**  
visualize the tree structure difference among the GatingSets

**Description**
visualize the tree structure difference among the GatingSets

**Usage**

```
gs_plot_diff_tree(x, path = "auto", ...)
```

**Arguments**
- **x**  
  list of groups(each group is a list of 'GatingSet'). it is usually the outcome from `gs_split_by_tree`.
- **path**  
  passed to `getNodes`
- **...**  
  passed to `getNodes`

**Examples**

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

**gs_pop_add**  
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. gs_pop_set_gate 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

gs_pop_add(gs, gate, validityCheck = TRUE, ...)

gs_pop_remove(gs, node, ...)

Arguments

gs A GatingSet
gate A flowCore::filter or a list of flowCore::filters or logical vectors to be added to the GatingSet. When logical vectors, they represent the indices of events to be included in the populations. It can be global that represents the index to the original full events or local index that is relative to the parent population cell events. See examples for more details.
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.
... some other arguments to specify how the gates are added to the gating tree.
  • names a character vector of length four, which specifies the population names resulted by adding a quadGate. The order of the names is clock-wise starting from the top left quadrant population.
  • 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
  • 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.

node A character identifies the population node in a GatingHierrarchy or GatingSet to remove

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

## Not run:
library(flowCore)
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

gs_get_pop_paths(gs[[1]]) #only contains root node

#add one gate

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

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

#add a quadGate

qg <- quadGate("FL1-H"=2, "FL2-H"=4)
nodeIDs<-gs_pop_add(gs,qg,parent="rectangle")
nodeIDs #quadGate produces four population nodes

gs_get_pop_paths(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<-gs_pop_add(gs,bg,parent="rectangle")
nodeID2

gs_get_pop_paths(gs[[1]])

#do the actual gating

recompute(gs)

#plot one gate for one sample

autoplot(gs[[1]],"rectangle")
autoplot(gs[[1]],nodeIDs) #may be smoothed automatically if there are not enough events after gating

#plot gates across samples

autoplot(gs,nodeID)

#plot all gates for one sample

autoplot(gs[[1]])#boolean gate is skipped by default
autoplot(gs[[1]],bool=TRUE)

#plot the gating hierarchy

plot(gs[[1]])

#remove one node causing the removal of all the descendants

gs_pop_remove('rectangle', gs = gs)

gs_get_pop_paths(gs[[1]])

#add logical vectors as gate

lg <- sapply(sampleNames(gs), function(sn){
  gh <- gs[[sn]]
  dat <- exprs(gh_pop_get_data(gh, "cd3+"))#get events data matrix for this sample at cd3+ node

  dat <- exprs(gh_pop_get_data(gh, "cd3+"))#get events data matrix for this sample at cd3+ node
})
gs_pop_get_count_fast

vec <- dat[, "FSC-A"] > 1e4 & data[, "SSC-A"] > 1e5
vec
})
gs_pop_add(gs, lg, name = "new_bool", parent = "cd3+)

## End(Not run)

**Description**

`gs_pop_get_count_fast` is more useful than `getPop`. Returns 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.

**Usage**

```r
gs_pop_get_count_fast(
x, 
statistic = c("count", "freq"), 
xml = FALSE, 
subpopulations = NULL, 
format = c("long", "wide"), 
path = "full", 
...)

gs_pop_get_count_with_meta(x, ...)
```

**Arguments**

- `x` a GatingSet or GatingSetList
- `statistic` character; specifies the type of population statistics to extract. (only valid when format is "wide"). Either "freq" or "count" is currently supported.
- `xml` logical; indicating whether the statistics come from xml (if parsed from xml workspace) or from openCyto.
- `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
- `path` character; see `gs_get_pop_paths`
- `...` additional arguments passed to `gs_pop_get_count_fast`
Details

gs_pop_get_count_fast 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.

Value

gs_pop_get_count_fast 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).

a data.table of merged population statistics with sample metadata.

See Also

gs_get_pop_paths

Examples

```r
## Not run:
#gh is a GatingHierarchy
gs_pop_get_count_fast(gh);
gh_pop_get_stats(gh,gs_get_pop_paths(gh,tsort=T)[5])

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

## End(Not run)
```

Description

Return the flowCore gate definition associated with a node in a GatingHierarchy/GatingSet.
Usage

gh_pop_get_gate(obj, y)

gs_pop_get_gate(obj, y)

Arguments

obj      A GatingHierrarchy 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

gh_pop_get_data gs_get_pop_paths

Examples

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

## End(Not run)

---

gs_pop_get_gs  

subset gs by population node

Description

Basically it returns a new GatingSet with only the substree of the given population node

Usage

gs_pop_get_gs(gs, pop)

Arguments

gs     GatingSet
pop    the population node that will become the new root node
Value

a new GatingSet that share the underlying events data

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

gs_pop_get_parent(obj, y, ...)
gh_pop_get_parent(obj, y, ...)
gs_pop_get_children(obj, y, showHidden = TRUE, ...)
gh_pop_get_children(obj, y, showHidden = TRUE, ...)

Arguments

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

Value

gs_pop_get_parent returns a character vector, the name of the parent population. gs_pop_get_children 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

gs_get_pop_paths
Examples

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

## End(Not run)
```

---

**gs_pop_get_stats**  
Extract stats from populations(or nodes)

**Description**

Extract stats from populations(or nodes)

**Usage**

```r
gs_pop_get_stats(x, ...

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

**Arguments**

- `x`: a GatingSet or GatingHierarchy
- `...`: arguments passed to `gs_get_pop_paths` 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.
- `xml`: whether to extract xml stats or openCyto stats
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 stats values (if MFI, 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 <- gs_pop_get_stats(gs) #default is "count"

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

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

# compute the stats based on the raw data scale
gs_pop_get_stats(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
}
gs_pop_get_stats(gs, nodes, type = pop.quantiles)

## End(Not run)
```

**gs_pop_get_stats_tfilter**

Extract stats from populations(or nodes) within a restricted time window

**Description**

Extract stats from populations(or nodes) within a restricted time window
Usage

gs_pop_get_stats_tfilter(x, ...)

gh_pop_get_stats_tfilter(
  x,
  nodes = NULL,
  type = c("Count", "Frequency"),
  inverse.transform = FALSE,
  stats.fun.arg = list(),
  tfilter = NULL,
  path = c("full", "auto"),
  ...
)

Arguments

x GatingSet or GatingHierarchy

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 it is a character, it is expected to be either "Count" or "Frequency". Default is "Count" (total number of events in the populations). When it is a function, it takes a flowFrame object through the 'fr' argument and returns the stats as a named vector.

inverse.transform logical flag. Whether to inverse transform the data before computing the stats.

stats.fun.arg a list of arguments passed to 'type' when 'type' is a function.

tfilter Either a list (tmin, tmax) specifying the minimum and maximum of a the time window filter or a GatingHierarchy, whose minimum and maximum time will be used to determine the window. For both x and the reference GatingHierarchy in tfilter, the only channels that will match this filter are "Time" or "time" and the filter will be applied to each event such that only events with time value t where tmin <= t <= tmax will be evaluated.

path, ... arguments passed to 'gh_get_pop_paths()'

Description

update the population node with a flowCore-compatible gate object

Usage

gh_pop_set_gate(obj, y, value, negated = FALSE, ...)

gs_pop_set_gate(obj, y, value, ...)

**gs_pop_set_name**

**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**

```r
## Not run:
rg1 <- rectangleGate("FSC-H"=c(200,400), "SSC-H"=c(250, 400), filterId="rectangle")
rg2 <- rectangleGate("FSC-H"=c(200,400), "SSC-H"=c(250, 400), filterId="rectangle")
flist <- list(rg1,rg2)
names(flist) <- sampleNames(gs[1:2])
gs_pop_set_gate(gs[1:2], "lymph", flist)
recompute(gs[1:2], "lymph")

## End(Not run)
```

---

**gs_pop_set_name**

*Update the name of one node in a gating hierarchy/GatingSet.*

**Description**

`gh_pop_set_name/gs_pop_set_name` update the name of one node in a gating hierarchy/GatingSet.

**Usage**

```r
gh_pop_set_name(x, y, value)
gs_pop_set_name(x, y, value)
```

**Arguments**

- **x**: GatingHierarchy
- **y**: pop name/path
- **value**: A character the name of the node
Example

```r
# G is a GatingHierarchy
gs_get_pop_paths(G[[1]]) # return node names
gs_pop_set_name(G,"L","lymph")
```

## Examples

```
## Not run:
gh_pop_set_visibility(gh, 4, FALSE) # hide a node
gh_pop_set_visibility(gh, 4, TRUE) # unhide a node
## End(Not run)
```

---

**gs_pop_set_visibility**  
hide/unhide a node

### Description

hide/unhide a node

### Usage

```r
gh_pop_set_visibility(x, y, value)
gs_pop_set_visibility(x, y, value)
```

#### Arguments

- `x`: GatingHierarchy object
- `y`: character node name or path
- `value`: TRUE/FALSE to indicate whether to hide a node

#### Examples

```
## Not run:
gh_pop_set_visibility(gh, 4, FALSE) # hide a node
gh_pop_set_visibility(gh, 4, TRUE) # unhide a node
## End(Not run)
```

---

**gs_remove_redundant_channels**  
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.
gs_remove_redundant_channels

Usage

gs_remove_redundant_channels(gs, ...)

Arguments

gs a GatingSet
...
other arguments passed to gs_get_pop_paths 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

## Not run:
gs_new <- gs_remove_redundant_channels(gs)

## End(Not run)

gs_remove_redundant_nodes

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

Description

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

Usage

gs_remove_redundant_nodes(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 gs_split_by_tree.
toRemove list of the node sets to be removed. its length must equals to the length of 'x'. When x is a list, toRemove is usually the outcome from gs_check_redundant_nodes.
Examples

```r
## Not run:
gslist <- list(gs1, gs2, gs3, gs4, gs5)
gs_groups <- gs_split_by_channels(gslist)
toRm <- gs_check_redundant_nodes(gs_groups)
gs_remove_redundant_nodes(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)
```

---

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

**Description**

Sometimes it is gates are defined on the different dimensions across different GatingSets, (e.g. ‘FSC-W’ or ‘SSC-H’ may be used for Y axis for cytokines) These difference 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
gs_split_by_channels(x)
```

**Arguments**

- `x`  a list of GatingSets

**Examples**

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

## End(Not run)
```
gs_split_by_tree

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 `gs_get_pop_paths(gh, path = "auto", showHidden = F)` returns the same set.

Usage

`gs_split_by_tree(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 <- gs_split_by_tree(gslist)
## End(Not run)
```

gs_update_channels

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

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

- **gs**: a GatingSet object
- **map**: data.frame contains 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 <- gs_update_channels(gs, map = data.frame(old = c("Qdot 655-A"),
                                            new = c("QDot 655-A")))
## End(Not run)
```

identifier-methods

Retrieve/replace the GUID of a GatingSet or GatingSetList

Description

Retrieve or replace the GUID (globally unique identifier) for a GatingSet or GatingSetList

Usage

```r
identifier(object)
```

## S4 replacement method for signature 'GatingSet,ANY'
`identifier(object) <- value`

## S4 replacement method for signature 'GatingSetList,character'
`identifier(object) <- value`

Arguments

- **object**: a GatingSet or GatingSetList
- **value**: string
**keyword**

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", ...)
```

**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)
```
Methods to alter keywords in cytoframe, cytoset, GatingHierarchy, or GatingSet objects

Description

These methods allow for direct insertion, deletion, or renaming of keywords in cytoframe, cytoset, GatingHierarchy, or GatingSet objects.

Usage

```python
cf_keyword_insert(cf, keys, values)
cf_keyword_delete(cf, keys)
cf_keyword_rename(cf, old_keys, new_keys)
cf_keyword_set(cf, keys, values)

cs_keyword_insert(cs, keys, values)
cs_keyword_delete(cs, keys)
cs_keyword_rename(cs, old_keys, new_keys)
cs_keyword_set(cs, keys, values)

gh_keyword_insert(gh, keys, values)
gh_keyword_delete(gh, keys)
gh_keyword_rename(gh, old_keys, new_keys)
gh_keyword_set(gh, keys, values)

gs_keyword_insert(gs, keys, values)
gs_keyword_delete(gs, keys)
gs_keyword_rename(gs, old_keys, new_keys)
gs_keyword_set(gs, keys, values)
```

Arguments

- `cf` a cytoframe
- `keys` the keyword names to insert/delete/replace – single value or vector
values the values to associate with the supplied keywords – single value or vector of sample length as keys

old_keys the old keyword name (for renaming)

new_keys the new keyword name (for renaming)

cs a cytoset

gh a GatingHierarchy

gs a GatingSet

Details

Each of the methods taking two character vectors (keys/values or old_keys/new_keys) will also accept a single named vector for flexibility in usage.

For the functions that take a vector of keys and a vector of values (the keyword_insert and keyword_set functions), the names of this vector should be the keys to which the values of the vector will be assigned.

For the keyword_rename functions, the names of this vector should be the existing keyword names (old_keys) while the values should be the replacement keyword names (new_keys).

See examples for details

Examples

library(flowCore)
data(GvHD)
cs <- flowSet_to_cytoset(GvHD[1:2])

keys <- c("CYTNUM", "CREATOR")

# Values before changes
keyword(cs, keys)

# Set two keyword values using separate key and values vectors
values <- c("E3598", "CELLQuest 3.4")
cs_keyword_set(cs, keys, values)

# Values after changes
keyword(cs, keys)

# Change the values again using a single named vector
values <- c("E3599", "CELLQuest 3.5")
names(values) <- keys
cs_keyword_set(cs, values)

# Values after changes
keyword(cs, keys)
lapply-methods

apply FUN to each sample (i.e. GatingHierarchy or cytoframe) in a
GatingSet or cytoset

Description

sample names are used for names of the returned list

Usage

lapply(X, FUN, ...)

Arguments

X GatingSet or cytoset
FUN function to be applied to each sample in 'GatingSet' or 'cytoset'
... other arguments to be passed to 'FUN'

length

Methods to get the length of a GatingSet

Description

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

Usage

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

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

Arguments

x GatingSet
object object
load_cytoframe

Load the cytoframe from disk

Description

Load the cytoframe from disk

Usage

load_cytoframe(uri, on_disk = TRUE, readonly = on_disk)

Arguments

uri           path to the cytoframe file
on_disk       logical flag indicating whether to keep the data on disk and load it on demand. Default is TRUE.
readonly      logical flag indicating whether to open h5 data as readonly. Default is TRUE. And it is valid when on_disk is set to true.

See Also

Other cytoframe/cytoset IO functions: cf_get_uri(), cf_write_disk(), cf_write_h5(), cs_get_uri(), load_cytoframe_from_fcs(), load_cytoset_from_fcs()

load_cytoframe_from_fcs

Read a single FCS file in to a cytoframe

Description

Similar to read.FCS, this takes a filename for a single FCS file and returns a cytoframe.

Usage

load_cytoframe_from_fcs(
  filename,
  transformation = "linearize",
  which.lines = NULL,
  decades = 0,
  is_h5 = NULL,
  backend = get_default_backend(),
  uri = NULL,
  h5_filename = NULL,
  min.limit = NULL,
  truncate_max_range = TRUE,
load_cytoframe_from_fcs

dataset = NULL,
emptyValue = TRUE,
num_threads = 1,
ignore.text.offset = FALSE,
text.only = FALSE
)

Arguments

filename The filename of the single FCS file to be read
transformation A character string that defines the type of transformation. Valid values are
linearize (default), linearize-with-PnG-scaling, or scale. The linearize
transformation applies the appropriate power transform to the data. The linearize-with-PnG-scaling
transformation applies the appropriate power transform for parameters stored
on log scale, and also a linear scaling transformation based on the "gain" (FCS
$PnG keywords) for parameters stored on a linear scale. The scale transfor-
mation scales all columns to $[0, 10^{\text{decades}}]$, defaulting to decades = 0 as in the
FCS4 specification. A logical can also be used: TRUE is equal to linearize and
FALSE (or NULL) corresponds to no transformation. Also, when the transforma-
tion keyword of the FCS header is set to "custom" or "applied", no transfor-
mation will be used.
which.lines Numeric vector to specify the indices of the lines to be read. If it is NULL, all
the records are read. If it is of length 1, a random sample of the size indicated
by which.lines is read in.
decades When scaling is activated, the number of decades to use for the output.
is_h5 Logical indicating whether the data should be stored in h5 format
h5_filename String specifying a name for the h5 file if is_h5 is TRUE
min.limit The minimum value in the data range that is allowed. Some instruments produce
extreme artifactual values. The positive data range for each parameter is com-
pletely defined by the measurement range of the instrument and all larger values
are set to this threshold. The lower data boundary is not that well defined, since
compensation might shift some values below the original measurement range of
the instrument. This can be set to an arbitrary number or to NULL (the default
value), in which case the original values are kept.
truncate_max_range Logical. Default is TRUE. can be optionally turned off to avoid truncating the
extreme positive value to the instrument measurement range, i.e. '$PnR'.
dataset The FCS file specification allows for multiple data segments in a single file.
Since the output of load_cytoframe_from_cytoset is a single cytoframe we
can't automatically read in all available sets. This parameter allows the user to
choose one of the subsets for import. Its value should be an integer in the range
of available data sets. This argument is ignored if there is only a single data
segment in the FCS file.
emptyValue Logical indicating whether or not to allow empty values for keywords in TEXT
segment. It affects how double delimiters are treated. If TRUE, double delimi-
ters are parsed as a pair of start and end single delimiters for an empty value.
load_cytoset_from_fcs

Description

Similar to `read.flowSet`, this takes a list of FCS filenames and returns a cytoset.
Usage

load_cytoset_from_fcs(
    files = NULL,
    path = ".",
    pattern = NULL,
    phenoData = NULL,
    descriptions,
    name.keyword,
    transformation = "linearize",
    which.lines = NULL,
    decades = 0,
    is_h5 = NULL,
    h5_dir = NULL,
    backend = get_default_backend(),
    backend_dir = tempdir(),
    min.limit = NULL,
    truncate_max_range = TRUE,
    dataset = NULL,
    emptyValue = TRUE,
    num_threads = 1,
    ignore.text.offset = FALSE,
    sep = "\t",
    as.is = TRUE,
    name,
    file_col_name = NULL,
    ...
)

Arguments

files  Optional character vector with filenames.
path   Directory where to look for the files.
pattern This argument is passed on to dir, see details.
phenoData An object of class AnnotatedDataFrame, character or a list of values to be extracted from the cytoframe object, see details.
descriptions Character vector to annotate the object of class cytoset.
name.keyword An optional character vector that specifies which FCS keyword to use as the sample names. If this is not set, the GUID of the FCS file is used for sample Names, and if that is not present (or not unique), then the file names are used.
transformation see load_cytoframe_from_fcs for details.
which.lines see load_cytoframe_from_fcs for details.
decades see load_cytoframe_from_fcs for details.
is_h5 logical indicating whether the data should be stored in h5 format
h5_dir String specifying a name for the h5 directory for the h5 files if is_h5 is TRUE
min.limit see load_cytoframe_from_fcs for details.
load_cytoset_from_fcs

truncation_max_range
see load_cytoframe_from_fcs for details.
dataset
see load_cytoframe_from_fcs for details.
emptyValue
see load_cytoframe_from_fcs for details.
num_threads
Integer allowing for parallelization of the parsing operation by specifying a number of threads
ignore.text.offset
see load_cytoframe_from_fcs for details.
sep
Separator character that gets passed on to read.AnnotatedDataFrame.
as.is
logical that gets passed on to read.AnnotatedDataFrame. This controls the automatic coercion of characters to factors in the phenoData.
name
An optional character scalar used as name of the object.
file_col_name
optionally specify the column name that stores the fcs filename when phenoData is supplied read.AnnotatedDataFrame, see details.
...
Further arguments that get passed on to

Details

There are four different ways to specify the file from which data is to be imported:

First, if the argument phenoData is present and is of class AnnotatedDataFrame, then the file names are obtained from its sample names (i.e. row names of the underlying data.frame). Also column name will be generated based on sample names if it is not there. This column is mainly used by visualization methods in flowViz. Alternatively, the argument phenoData can be of class character, in which case this function tries to read an AnnotatedDataFrame object from the file with that name by calling read.AnnotatedDataFrame(file.path(path,phenoData),{}).

In some cases the file names are not a reasonable selection criterion and the user might want to import files based on some keywords within the file. One or several keyword value pairs can be given as the phenoData argument in form of a named list.

Third, if the argument phenoData is not present and the argument files is not NULL, then files is expected to be a character vector with the file names.

Fourth, if neither the argument phenoData is present nor files is not NULL, then the file names are obtained by calling dir(path, pattern).

Value

An object of class cytoset.

See Also

Other cytoframe/cytoset IO functions: cf_get_uri(), cf_write_disk(), cf_write_h5(), cs_get_uri(), load_cytoframe_from_fcs(), load_cytoframe()
load_meta  
*Flush/load meta data (keywords, pData, channels/markers) to/from disk (only valid for on-disk cytoset/cytoframe)*

**Description**
Flush/load meta data (keywords, pData, channels/markers) to/from disk (only valid for on-disk cytoset/cytoframe)

**Usage**
- `cf_flush_meta(cf)`
- `cf_load_meta(cf)`
- `cs_flush_meta(cs)`
- `cs_load_meta(cs)`

**Arguments**
- `cf`  cytoframe object
- `cs`  cytoset object

lock  
*Lock/Unlock the cytoset/cytoframe by turning on/off its read-only flag*

**Description**
Lock/Unlock the cytoset/cytoframe by turning on/off its read-only flag

**Usage**
- `cf_lock(cf)`
- `cf_unlock(cf)`
- `cs_lock(cs)`
- `cs_unlock(cs)`

**Arguments**
- `cf`  cytoframe object
- `cs`  cytoset object
logicleGml2_trans  

Description

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

Usage

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))
logicle_trans  

**Description**  
Used for construct logicle transform object.

**Usage**  
```r  
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**  
```r  
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))  
```

logtGml2_trans  

**Description**  
Used to construct GML 2.0 flog transformer object.

**Usage**  
```r  
logtGml2_trans(t = 262144, m = 4.5, n = 6, equal.space = FALSE)  
```
Arguments

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

Details

GML 2.0 standard log transform function constructor. The definition is as in the GML 2.0 standard section 6.2 "parametrized logarithmic transformation – flog" This deviates from standard only in the following way. Before applying the logarithmic transformation, non-positive values are assigned the smallest positive value from the input rather than having undefined values (NA) under the transformation.

Value

logtGml2 transformation object

Examples

```r
trans.obj <- logtGml2_trans(t = 1e3, m = 1, 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
```

markernames

Get/set the column(channel) or marker names

Description

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
```
merge_list_to_gs

Merge a list of GatingSets into a single GatingSet

Description

It also checks the consistency of the cyto data and gates.

Usage

merge_list_to_gs(x, ...)

Arguments

x          a list of GatingSets
...
    other arguments (not used)
ncFlowSet

Fetch the flowData object associated with a GatingSet.

Description

Deprecated by flowData method
Deprecated by flowData method

nodeflags

The flags of gate nodes

Description

gh_pop_is_gated checks if a node is already gated. gh_pop_is_negated checks if a node is negated.
gh_pop_is_hidden checks if a node is hidden.

Usage

gh_pop_is_gated(obj, y)
gh_pop_is_negated(obj, y)
gh_pop_is_hidden(obj, y)
gh_pop_is_bool_gate(obj, y)

Arguments

obj GatingHierarchy
y node/gating path

openWorkspace

It is now moved along with entire flowJo parser to CytoML package

Description

It is now moved along with entire flowJo parser to CytoML package

Usage

openWorkspace(file, ...)

Arguments

file xml file
... other arguments
pData-methods

read/set pData of flow data associated with GatingHierarchy, GatingSet, or GatingSetList

Description
Accessor method that gets or replaces the pData of the flowset/ncdfFlowSet object in a GatingHierarchy, GatingSet, or GatingSetList

Usage
pData(object)

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-methods
plot a gating tree

Description
Plot a tree/graph representing the GatingHierarchy

Usage
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
Description
Add populations to a GatingHierarchy

Usage
pop_add(gate, gh, ...)

## S3 method for class 'filter'
pop_add(gate, gh, ...)

## S3 method for class 'filters'
pop_add(gate, gh, names = NULL, ...)

## S3 method for class 'quadGate'
pop_add(gate, gh, names = NULL, ...)

## S3 method for class 'logical'
pop_add(gate, gh, parent, name, recompute, cluster_method_name = NULL, ...)

## S3 method for class 'factor'
pop_add(gate, gh, name = NULL, ...)

## S3 method for class 'logicalFilterResult'
pop_add(gate, gh, ...)

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)
## S3 method for class 'multipleFilterResult'

```r
pop_add(gate, gh, name = NULL, ...)
```

```r
gh_pop_remove(gh, node, ...)
```

### Arguments

- **gate**: a gate object that extends `flowCore::filter` or `flowCore::filters`
- **gh**: `GatingHierarchy`
- **...**: other arguments
- **names**: a character vector of length four, which specifies the population names resulted by adding a quadGate. The order of the names is clock-wise starting from the top left quadrant population.
- **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**: the population name
- **recompute**: whether to recompute the gates
- **cluster_method_name**: when adding the logical vectors as the gates, the name of the cluster method can be used to tag the populations as the extra meta information associated with the gates.
- **node**: population name/path

---

### 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 other wise returns NULL
recompute

Examples

```r
## Not run:
prettyAxis(gh, "<B71O-A>")

## End(Not run)
```

recompute

**Compute the cell events by the gates stored within the gating tree.**

**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
recompute(
  x,
  y = "root",
  alwaysLoadData = FALSE,
  verbose = FALSE,
  leaf.bool = TRUE
)
```

**Arguments**

- `x`  
  GatingSet or GatingSetList

- `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.
rotate_gate

verbose default is FALSE
leaf.bool whether to compute the leaf boolean gate, default is TRUE
... arguments

Details

It is usually used immediately after add or gs_pop_set_gate calls.

rotate_gate

Simplified geometric rotation of gates associated with nodes

Description

Rotate a gate associated with a node of a GatingHierarchy or GatingSet. This method is a wrapper for rotate_gate that enables updating of the gate associated with a node of a GatingHierarchy or GatingSet.

rotate_gate calls gs_pop_set_gate to modify the provided GatingHierarchy or GatingSet directly so there is no need to re-assign its output. The arguments will be essentially identical to the flowCore method, except for the specification of the target gate. Rather than being called on an object of type flowCore:filter, here it is called on a GatingHierarchy or GatingSet object with an additional character argument for specifying the node whose gate should be transformed. The rest of the details below are taken from the flowCore documentation.

Usage

## S3 method for class 'GatingHierarchy'
rotate_gate(obj, y, deg = NULL, rot_center = NULL, ...)

Arguments

obj A GatingHierarchy or GatingSet object
y A character specifying the node whose gate should be modified
deg An angle in degrees by which the gate should be rotated in the counter-clockwise direction
rot_center A separate 2-dimensional center of rotation for the gate, if desired. By default, this will be the center for ellipsoidGate objects or the centroid for polygonGate objects. The rot_center argument is currently only supported for polygonGate objects.
... not used
Details

This method allows for geometric rotation of filter types defined by simple geometric gates (ellipsoidGate, and polygonGate). The method is not defined for rectangleGate or quadGate objects, due to their definition as having 1-dimensional boundaries.

The angle provided in the deg argument should be in degrees rather than radians. By default, the rotation will be performed around the center of an ellipsoidGate or the centroid of the area encompassed by a polygonGate. The rot_center argument allows for specification of a different center of rotation for polygonGate objects (it is not yet implemented for ellipsoidGate objects) but it is usually simpler to perform a rotation and a translation individually than to manually specify the composition as a rotation around a shifted center.

See Also

transform_gate flowCore::rotate_gate

Examples

```r
## Not run:
#
#' # Rotates the original gate 15 degrees counter-clockwise
rotate_gate(gs, node, deg = 15)
#' # Rotates the original gate 270 degrees counter-clockwise
rotate_gate(gs, node, 270)

## End(Not run)
```

---

description

Get/update sample names in a GatingSet

Description

Return a sample names contained in a GatingSet

Usage

sampleNames(object)

sampleNames(object) <- value

Arguments

  object       a GatingSet
  value        character new sample names

Details

The sample names comes from pdata of fs.
save_cytoset

Value
A character vector of sample names

Examples

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

### End(Not run)

save_cytoset save/load a cytoset to/from disk.

Description

load_cytoset() can load a cytoset from either the archive previously saved by save_cytoset() call or from a folder that contains a collection of inidivudal cytoframe files (either in h5 format or tiledb format)

Usage

save_cytoset(cs, path, ...)

load_cytoset(path, verbose = FALSE, ...)

Arguments
cs A cytoset
path A character scalar giving the path to save/load the cytoset to/from.
... other arguments passed to save_gs/load_gs
verbose whether to print details. Default is FALSE.

Value
load_cytoset returns a cytoset object

Examples

### Not run:
#cs is a cytoset
save_cytoset(cs, outdir)
cs <- load_cytoset(outdir)

# or from cytoframe on-disk files
# e.g. h5_dir contains the cytoframes in h5 format
cs <- load_cytoset(h5_dir)
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 contains the internal C data structure (gating tree).\emph{ncdfFlowSet} object (if applicable).

Retrieve sample names by scanning h5 files from a GatingSet folder.

Usage

```r
save_gs(
  gs,  
  path,  
  cdf = NULL,  
  backend_opt = c("copy", "move", "skip", "symlink", "link"),  
  ...  
)
```

```r
load_gs(
  path,  
  h5_readonly = NULL,  
  backend_readonly = TRUE,  
  select = character(),  
  verbose = FALSE  
)
```

```r
## S4 method for signature 'character'
sampleNames(object)
```

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

```r
load_gslist(path)
```

Arguments

- **gs**
  - A GatingSet

- **path**
  - A character scalar giving the path to save/load the GatingSet to/from.

- **backend_opt**
  - A character scalar. The valid options are: "copy", "move", "skip", "symlink" specifying what to do with the backend data file. Sometimes it is more efficient to move or create a symlink of the existing backend file to the archived folder. It is useful to "skip" archiving backend file if raw data has not been changed.
scale_gate

... other arguments: not used.

h5_readonly whether to open h5 data as read-only. Default is TRUE
select an integer or character vector to select a subset of samples to load
verbose logical flag to optionally print the versions of the libraries that were used to archive the GatingSet for troubleshooting purpose.
object a GatingSet folder
gslist A GatingSetList

See Also

GatingSet-class,GatingSetList-class

Examples

## 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)
    ## Not run:
    ## Not run:
        sampleNames(gsdir)
    
## End(Not run)

scale_gate

Simplified geometric scaling of gates associated with nodes

Description

Scale a gate associated with a node of a GatingHierarchy or GatingSet. This method is a wrapper for scale_gate that enables updating of the gate associated with a node of a GatingHierarchy or GatingSet.

scale_gate calls gs_pop_set_gate to modify the provided GatingHierarchy or GatingSet directly so there is no need to re-assign its output. The arguments will be essentially identical to the flowCore method, except for the specification of the target gate. Rather than being called on an object of type filter, here it is called on a GatingHierarchy or GatingSet object with an additional character argument for specifying the node whose gate should be transformed. The rest of the details below are taken from the flowCore documentation.
Usage

```r
## S3 method for class 'GatingHierarchy'
scale_gate(obj, y, scale = NULL, ...)
```

Arguments

- `obj`: A `GatingHierarchy` or `GatingSet` object
- `y`: A character specifying the node whose gate should be modified
- `scale`: Either a numeric scalar (for uniform scaling in all dimensions) or numeric vector specifying the factor by which each dimension of the gate should be expanded (absolute value > 1) or contracted (absolute value < 1). Negative values will result in a reflection in that dimension.
- `...`: not used

Details

This method allows uniform or non-uniform geometric scaling of filter types defined by simple geometric gates (`quadGate`, `rectangleGate`, `ellipsoidGate`, and `polygonGate`). Note that these methods are for manually altering the geometric definition of a gate. To easily transform the definition of a gate with an accompanying scale transformation applied to its underlying data, see `?ggcyto::rescale_gate`

The `scale` argument passed to `scale_gate` should be either a scalar or a vector of the same length as the number of dimensions of the gate. If it is scalar, all dimensions will be multiplicatively scaled uniformly by the scalar factor provided. If it is a vector, each dimension will be scaled by its corresponding entry in the vector.

The scaling behavior of `scale_gate` depends on the type of gate passed to it. For `rectangleGate` and `quadGate` objects, this amounts to simply scaling the values of the 1-dimensional boundaries. For `polygonGate` objects, the values of `scale` will be used to determine scale factors in the direction of each of the 2 dimensions of the gate (`scale_gate` is not yet defined for higher-dimensional `polytopeGate` objects). **Important**: For `ellipsoidGate` objects, `scale` determines scale factors for the major and minor axes of the ellipse, *in that order*. Scaling by a negative factor will result in a reflection in the corresponding dimension.

See Also

- `transform_gate` `flowCore::scale_gate`

Examples

```r
## Not run:
# Scales both dimensions by a factor of 5
scale_gate(gs, node, 5)

# Shrinks the gate in the first dimension by factor of 1/2
# and expands it in the other dimension by factor of 3
scale_gate(gs, node, c(0.5,3))
## End(Not run)
```
**shift_gate**

*Simplified geometric translation of gates associated with nodes*

**Description**

Shift the location of a gate associated with a node of a GatingHierarchy or GatingSet. This method is a wrapper for `shift_gate` that enables updating of the gate associated with a node of a GatingHierarchy or GatingSet.

`shift_gate` calls `gs_pop_set_gate` to modify the provided GatingHierarchy or GatingSet directly so there is no need to re-assign its output. The arguments will be essentially identical to the `flowCore` method, except for the specification of the target gate. Rather than being called on an object of type `flowCore::filter`, here it is called on a GatingHierarchy or GatingSet object with an additional character argument for specifying the node whose gate should be transformed. The rest of the details below are taken from the `flowCore` documentation.

**Usage**

```r
## S3 method for class 'GatingHierarchy'
shift_gate(obj, y, dx = NULL, dy = NULL, center = NULL, ...)
```

**Arguments**

- `obj` A GatingHierarchy or GatingSet object
- `y` A character specifying the node whose gate should be modified
- `dx` Either a numeric scalar or numeric vector. If it is scalar, this is just the desired shift of the gate in its first dimension. If it is a vector, it specifies both dx and dy as (dx, dy). This provides an alternate syntax for shifting gates, as well as allowing shifts of ellipsoidGate objects in more than 2 dimensions.
- `dy` A numeric scalar specifying the desired shift of the gate in its second dimension.
- `center` A numeric vector specifying where the center or centroid should be moved (rather than specifying dx and/or dy)
- `...` not used

**Details**

This method allows for geometric translation of filter types defined by simple geometric gates (rectangleGate, quadGate, ellipsoidGate, or polygonGate). The method provides two approaches to specify a translation. For rectangleGate objects, this will shift the min and max bounds by the same amount in each specified dimension. For quadGate objects, this will simply shift the dividing boundary in each dimension. For ellipsoidGate objects, this will shift the center (and therefore all points of the ellipse). For polygonGate objects, this will simply shift all of the points defining the polygon.

The method allows two different approaches to shifting a gate. Through the `dx` and/or `dy` arguments, a direct shift in each dimension can be provided. Alternatively, through the `center` argument, the gate can be directly moved to a new location in relation to the old center of the gate. For quadGate
objects, this center is the intersection of the two dividing boundaries (so the value of the boundary slot). For rectangleGate objects, this is the center of the rectangle defined by the intersections of the centers of each interval. For ellipsoidGate objects, it is the center of the ellipsoid, given by the mean slot. For polygonGate objects, the centroid of the old polygon will be calculated and shifted to the new location provided by center and all other points on the polygon will be shifted by relation to the centroid.

See Also

transform_gate flowCore::shift_gate

Examples

## Not run:
# Moves the entire gate +500 in its first dimension and 0 in its second dimension
shift_gate(gs, node, dx = 500)

# Moves the entire gate +250 in its first dimension and +700 in its second dimension
shift_gate(gs, node, dx = 500, dy = 700)

# Same as previous
shift_gate(gs, node, c(500, 700))

# Move the gate based on shifting its center to (700, 1000)
shift_gate(gs, node, center = c(700, 1000))

## End(Not run)
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.

- `gs_split_by_tree` splits the GatingSets into groups based on the gating tree structures.
- `gs_split_by_channels` split GatingSets into groups based on their flow channels.
- `gs_check_redundant_nodes` 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.
- `gs_remove_redundant_nodes` removes the terminal(or leaf) nodes that are detected as redundant by `gs_check_redundant_nodes`.
- `gs_remove_redundant_channels` remove the redundant channels that are not used by any gate defined in the GatingSet.
- `gs_update_channels` modifies the channel names in place. (Usually used to standardize the channels among GatingSets due to the letter case discrepancies or typo).
- `gh_pop_move` 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 `gs_remove_redundant_nodes`.
- `gs_pop_set_visibility` hide a node/gate in a GatingSet. It is useful to deal with the non-leaf node that causes the tree structure discrepancy.

---

**stats.fun**

*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 `gh_pop_get_stats` 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
subset

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 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

```r
library(flowCore)
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 the flow data associated with the GatingSet

Description

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

Usage

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

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:
library(flowCore)
data(GvHD)
fs <- GvHD[1:2]
gs <- GatingSet(fs)

# construct biexponential transformation function
biexpTrans <- flowjo_biexp_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)
```
transformerList

#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
library(flowCore)
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))
transform_gate

Simplified geometric transformations of gates associated with nodes

Description

Perform geometric transformations of a gate associated with a node of a GatingHierarchy or GatingSet. This method is a wrapper for transform_gate that enables updating of the gate associated with a node of a GatingHierarchy or GatingSet.

transform_gate calls gs_pop_set_gate to modify the provided GatingHierarchy or GatingSet directly so there is no need to re-assign its output. The arguments will be essentially identical to the flowCore method, except for the specification of the target gate. Rather than being called on an object of type flowCore::filter, here it is called on a GatingHierarchy or GatingSet object with an additional character argument for specifying the node whose gate should be transformed. The rest of the details below are taken from the flowCore documentation.

Usage

```r
## S3 method for class 'GatingHierarchy'
transform_gate(
  obj,
  y,
  scale = NULL,
  deg = NULL,
  rot_center = NULL,
  dx = NULL,
  dy = NULL,
  center = NULL,
  ...
)
```

Arguments

- `obj` A GatingHierarchy or GatingSet object
- `y` A character specifying the node whose gate should be modified
- `scale` Either a numeric scalar (for uniform scaling in all dimensions) or numeric vector specifying the factor by which each dimension of the gate should be expanded (absolute value > 1) or contracted (absolute value < 1). Negative values will result in a reflection in that dimension. For rectangleGate and quadGate objects, this amounts to simply scaling the values of the 1-dimensional boundaries. For polygonGate objects, the values of scale will be used to determine scale factors in the direction of each of the 2 dimensions of the gate (scale_gate is not yet defined for higher-dimensional polytopeGate objects). **Important:** For ellipsoidGate objects, scale determines scale factors for the major and minor axes of the ellipse, in that order.
- `deg` An angle in degrees by which the gate should be rotated in the counter-clockwise direction.
transform_gate

rot_center  A separate 2-dimensional center of rotation for the gate, if desired. By default, this will be the center for ellipsoidGate objects or the centroid for polygonGate objects. The rot_center argument is currently only supported for polygonGate objects. It is also usually simpler to perform a rotation and a translation individually than to manually specify the composition as a rotation around a shifted center.

dx  Either a numeric scalar or numeric vector. If it is scalar, this is just the desired shift of the gate in its first dimension. If it is a vector, it specifies both dx and dy as (dx, dy). This provides an alternate syntax for shifting gates, as well as allowing shifts of ellipsoidGate objects in more than 2 dimensions.

dy  A numeric scalar specifying the desired shift of the gate in its second dimension.

center  A numeric vector specifying where the center or centroid should be moved (rather than specifying dx and/or dy)

...  Assignments made to the slots of the particular Gate-type filter object in the form "<slot_name> = <value>"

Details

This method allows changes to the four filter types defined by simple geometric gates (quadGate, rectangleGate, ellipsoidGate, and polygonGate) using equally simple geometric transformations (shifting/translation, scaling/dilation, and rotation). The method also allows for directly resetting the slots of each Gate-type object. Note that these methods are for manually altering the geometric definition of a gate. To easily transform the definition of a gate with an accompanying scale transformation applied to its underlying data, see ?ggcyto::rescale_gate.

First, transform_gate will apply any direct alterations to the slots of the supplied Gate-type filter object. For example, if "mean = c(1,3)" is present in the argument list when transform_gate is called on a ellipsoidGate object, the first change applied will be to shift the mean slot to (1,3). The method will carry over the dimension names from the gate, so there is no need to provide column or row names with arguments such as mean or cov for ellipsoidGate or boundaries for polygonGate.

transform_gate then passes the geometric arguments (dx, dy, deg, rot_center, scale, and center) to the methods which perform each respective type of transformation: shift_gate, scale_gate, or rotate_gate. The order of operations is to first scale, then rotate, then shift. The default behavior of each operation follows that of its corresponding method but for the most part these are what the user would expect. A few quick notes:

- rotate_gate is not defined for rectangleGate or quadGate objects, due to their definition as having 1-dimensional boundaries.
- The default center for both rotation and scaling of a polygonGate is the centroid of the polygon. This results in the sort of scaling most users expect, with a uniform scale factor not distorting the shape of the original polygon.

See Also

flowCore::transform_gate
Examples

## Not run:
# Scale the original gate non-uniformly, rotate it 15 degrees, and shift it
transform_gate(gs, node, scale = c(2,3), deg = 15, dx = 500, dy = -700)

# Scale the original gate (in this case an ellipsoidGate) after moving its center to (1500, 2000)
transform_gate(gs, node, scale = c(2,3), mean = c(1500, 2000))

## End(Not run)

### Description

[ subsets a GatingSet or GatingSetList using the familiar bracket notation
[[ extracts a GatingHierarchy object from a GatingSet.

### Usage

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

## S4 method for signature 'GatingSet,numeric'
x[[i, j, ...]]

### Arguments

- **x**: a GatingSet or GatingSetList
- **i**: numeric or logical or character used as sample indices
- **j,..., drop**: unused

### Value

The [ operator returns an object of the same type as x corresponding to the subset of indices in i, while the [[ operator returns a single GatingHierarchy
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