Package ‘flowWorkspace’

March 25, 2024

Type Package

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

Version 4.14.3

Date 2011-06-10

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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

Imports Biobase, BiocGenerics, cytolib (>= 2.13.1), XML, ggplot2, graph, graphics, grDevices, methods, stats, stats4, utils, RBGL, tools, Rgraphviz, data.table, dplyr, scales(>= 1.3.0), matrixStats, RProtoBufLib, flowCore(>= 2.1.1), ncdfFlow(>= 2.25.4), DelayedArray, S4Vectors


Suggests testthat, flowWorkspaceData (>= 2.23.2), knitr, rmarkdown, ggcyto, parallel, CytoML, openCyto

LinkingTo cpp11, BH(>= 1.62.0-1), RProtoBufLib(>= 1.99.4), cytolib (>= 2.3.7), Rhdf5lib

1
VignetteBuilder  knitr
biocViews  ImmunoOncology, FlowCytometry, DataImport, Preprocessing, DataRepresentation
SystemRequirements  GNU make, C++11
Encoding  UTF-8
RoxygenNote  7.2.3
git_url  https://git.bioconductor.org/packages/flowWorkspace
git_branch  RELEASE_3_18
git_last_commit  7447e9e
git_last_commit_date  2024-03-16
Repository  Bioconductor 3.18
Date/Publication  2024-03-25

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flowWorkspace-package

Import and replicate flowJo workspaces and gating schemes using flowCore.

Description

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

Details

<table>
<thead>
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</tr>
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<td>Type:</td>
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<tr>
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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(..., n = 6, equal.space = FALSE)
Arguments

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

Value

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

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

asinhtGml2(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

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

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"

---

**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

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

Usage
cf_is_subsetted(x)
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
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

**Usage**

```octave
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**

```octave
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.
compensate

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

```
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

Description

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

Usage

```
## 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

## 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)

convert 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

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

- cf: cytoframe object
- fr: flowframe
- ... additional arguments passed to `load_cytoframe_from_fcs` or `load_cytoset_from_fcs`.
- cs: cytoset
- fs: flowSet or ncdfFlowSet
- path: the h5 path for cytoset
- tmp: 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.

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`.
**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_gslist(from, to, ...)
```
Arguments

- from: the old archive path
- to: the new archive path
- ... 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.

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

- cs: cytoset
- sn: sample name to be added
- cf: cytoframe to be added
cs_get_uri

Return the path of the underlying data files

Description

Return the path of the underlying data files

Usage

cs_get_uri(x)
cs_get_h5_file_path(x)
gs_get_uri(x)

See Also

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

cs_set_cytoframe

update a cytoframe in a cytoset

Description

update a cytoframe in a cytoset

Usage

cs_set_cytoframe(cs, sn, cf)

Arguments

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>cs</td>
<td>cytoset</td>
</tr>
<tr>
<td>sn</td>
<td>sample name</td>
</tr>
<tr>
<td>cf</td>
<td>cytoframe</td>
</tr>
</tbody>
</table>
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:

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-
Parameter 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)
cytoset

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

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

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

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:*

`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:*

`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:*

`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:*

`Subset(cytoset, filter)`
delete_gs  

delete the archive of GatingSet

---

**Description**

delete the archive of GatingSet

**Usage**
delete_gs(path)

**Arguments**

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>path</td>
<td>either a local path or s3 path (e.g. &quot;s3://bucketname/gs_path&quot;)</td>
</tr>
</tbody>
</table>
estimateLogicle

Description

Compute logicle transformation from the flowData associated with a GatingHierarchy

Usage

## 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

## 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

extract_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

```r
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

```r
filter_to_list(x)
```

Arguments

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

Value

- **a list**

---

flowjo_biexp

construct the flowJo-type biexponential transformation function

Description

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

```r
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: unknown.
- `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

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

```r
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

```r
flowjo_fasinh(m = 4, t = 12000, a = 0.7, length = 256)
flowjo_fsinh(m = 4, t = 12000, a = 0.7, length = 256)
```

Arguments

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

Value

fasinh/fsinh transform function
Examples

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

inverse.trans <- flowjo_fsinh()
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

Description

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

Usage

flowjo_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**

- `getStats` -> `gs(/gh)_pop_get_stats`
- `getProp` -> `gh_pop_get_proportion`
- `getTotal` -> `gh_pop_get_count`
- `getPopStats` -> `gs(/gh)_pop_get_stats`
- `getNodes` -> `gs_get_pop_paths`
- `getParent` -> `gs_pop_get_parent`
- `getChildren` -> `gs_pop_get_children`
- `getGate` -> `gs(/gh)_get_gate`
- `getIndices` -> `gh_pop_get_indices`
- `isGated` -> `gh_pop_is_gated`
- `isNegated` -> `gh_pop_is_negated`
- `isHidden` -> `gh_pop_is_hidden`
- `getData` -> `gs(/gh)_get_data`
- `getTransformations` -> `gh_get_transformations`
- `getCompensationMatrices` -> `gh_get_compensations`
- `setNode` -> `gs(/gh)_set_node_name/gs(/gh)_set_node_visible`
- `isNcdf` -> `gs_is_h5`
- `flowData` -> `gs_cyto_data`
- `flowData<-` -> `gs_cyto_data<-`
- `getLoglevel` -> `get_log_level`
- `setLoglevel` -> `set_log_level`
- `rbind2` -> `gslist_to_gs`
- `filterObject` -> `filter_to_list`
- `add` -> `gs_pop_add`
- `Rm` -> `gs_pop_remove`
copyNode -> gh_copy_gate
openWorkspace -> open_flowjo_xml
flowJo.flog -> flowjo_log_trans
flowJoTrans -> flowjo_biexp
flowJo_biexp_trans -> flowjo_biexp_trans
flowJo.fasinh -> flowjo_fasinh
flowJo.fsinh -> flowjo_fsinh
flowJo_fasinh_trans -> flowjo_fasinh_trans
getDescendants -> gh_pop_get_descendants
getSingleCellExpression -> gs_get_singlecell_expression
groupByTree -> gs_split_by_tree
groupByChannels -> gs_split_by_channels
checkRedundantNodes -> gs_check_redundant_nodes
dropRedundantNodes -> gs_remove_redundant_nodes
dropRedundantChannels -> gs_drop_redundant_channels
updateChannels -> gs_update_channels
setGate -> gs(/gh)_pop_set_gate
updateIndices -> gh_pop_set_indices
getMergedStats -> gs_pop_get_count_with_meta
set.count.xml -> gh_pop_set_xml_count

---

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**

```r
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)
GatingHierarchy-class  

Class GatingHierarchy

Description

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

Details

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

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

See Also

GatingSet

Examples

```r
## 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,path=d,name=1));
gh <- G[[1]]
gh_pop_compare_stats(gh);
gh_plot_pop_count_cv(gh)
nodes <- 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)
```
**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.
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

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

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

gslist2
class(gslist2)
sampleNames(gslist2)

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

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

#subset a GatingSetList by [
sampleNames(gslist2[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 population
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)
pData(gslist2) <- pd
pData(gslist2[3:2])

#plot the gate
autoplot(gslist2[1:2],5)

#remove certain gates by loop through GatingSets
gs_get_pop_paths(gslist2[[1]])
lapply(gslist2,function(gs)gs_pop_remove("Excl",gs = gs))

#extract the stats
gs_pop_get_count_fast(gslist2)
#extract statistics by using getQAStats defined in QUALIFIER package
res<-getQAStats(gslist2[,c(4,2)],isMF1=F,isSpike=F,nslaves=1)

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

#convert GatingSetList into one GatingSet by merge_list_to_gs
gs_merged2 <- merge_list_to_gs(gslist2)
gs_merged2

## End(Not run)

## Not run:
samleNames(gsA) # return A1, A2
samleNames(gsB) # return B1, B2
gs.list <- list(gsA, gsB)
gslist<- GatingSetList(gs.list)
sampleNames(gslist) #return A1,A2,B1,B2

#set different order when create the GatingSetList
gslist<- GatingSetList(gs.list, samples = c("A1", "B1", "A2", "B2"))
sampleNames(gslist) #return A1,B1,A2,B2

## End(Not run)

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")

**Description**

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

**Usage**

```r
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**

```r
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**

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>gh</td>
<td>GatingHierarchy</td>
</tr>
<tr>
<td>node</td>
<td>the node to be copied</td>
</tr>
<tr>
<td>to</td>
<td>the new parent node under which the node will be copied</td>
</tr>
</tbody>
</table>

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")new.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 collect 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
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
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
Examples

## Not run:
# Assume gh is a GatingHierarchy and gs is a GatingSet
gh_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

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

Arguments

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

Details

Returns a list of the transformations or a transformation in the flowJo workspace. The list is of
length L, where L is the number of distinct transformations applied to samples in the flowjo_workspace.
Each element of L is itself a list of length M, where M is the number of parameters that were trans-
formed for a sample or group of samples in a 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 repre-
sent 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
gh_get_transformations(gh); # return a list transformation functions
gh_get_transformations(gh, inverse = TRUE); # return a list inverse transformation functions
gh_get_transformations(gh, channel = "FL1-H"); # only return the transformation associated with given channel
gh_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
gh_plot_pop_count_cv(x, path = "auto", ...)
gs_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 by n.

Value

Nothing is returned.
gh_pop_compare_stats

See Also

gs_pop_get_count_fast

Examples

## Not run:

```r
#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
**gh_pop_get_data**

### Description

Get gated flow data from a GatingHierarchy/GatingSet/GatingSetList.

### Usage

```r
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 GatingSet 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**

```
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**

```
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.
**gh_pop_get_indices_mat**

**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**

`gh_pop_get_indices_mat(gh, y)`

**Arguments**

- `gh` GatingHierarchy object
- `y` character vector containing the node names
**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
gp_pop.move(gh, node, to, recompute = TRUE)
```

**Arguments**

- `gh`: GatingPriority
- `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_get_proportion**

Get count or proportion from populations

**Description**

Get count or proportion from populations.

**Usage**

```r
gp_pop.get_proportion(x, y, xml = FALSE)
gp_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
**Examples**

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

---

**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**

```r
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**

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

```r
## 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, ...)`

```r
## 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

gs_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

gs_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

path = "full",
showHidden = FALSE,
...
)

Arguments

x   A GatingSet Assuming the gating hierarchy are identical within the GatingSet, the Gating tree of the first sample is used to query the node information.

y   A character not used.

order order=c("regular","tsort","bfs") returns the nodes in regular, topological or breadth-first sort order. "regular" is default.

path A character or numeric scalar. when numeric, it specifies the fixed length of gating path (length 1 displays terminal name). When character, it can be either 'full' (full path, which is default) or 'auto' (display the shortest unique gating path from the bottom of gating tree).

showHidden logical whether to include the hidden nodes

... Additional arguments.

Details

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

Value

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)

---

gs_get_singlecell_expression

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

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

Usage

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

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 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)
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

## 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 preferred 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
})
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)

gs_pop_get_count_fast

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

Description

gs_pop_get_count_fast is more useful than getPop. Returns a table of population statistics for all populations in a GatingHierarchy/GatingSet. Includes the xml counts, openCyto counts and frequencies.

Usage

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 origanize 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

## 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)
## Not run:
#G is a GatingSetList
stats = gs_pop_get_count_with_meta(G)

## End(Not run)

---

**gs_pop_get_gate**

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

**Description**

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

Usage

gh_pop_get_gate(obj, y)

gs_pop_get_gate(obj, y)

Arguments

obj A GatingHierarchy or GatingSet

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

Value

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

See Also

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
gs_pop_get_parent

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

## 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_set_gate(x, ...)  
```

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

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**

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

**Description**

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

**Usage**
gs_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

**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)
```
Examples

```r
## Not run:
# G is a GatingHierarchy
gs_get_pop_paths(G[[1]]) # return node names
gh_pop_set_name(G, "L", "lymph")

## End(Not run)
```

---

gs_pop_set_visibility  hide/unhide a node

Description

hide/unhide a node

Usage

```r
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

```r
## 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.
Usage

\texttt{gs\_remove\_redundant\_channels(gs, \ldots)}

Arguments

\begin{itemize}
  \item [\texttt{gs}] a \texttt{GatingSet}
  \item [\texttt{\ldots}] other arguments passed to \texttt{gs\_get\_pop\_paths} method
\end{itemize}

Value

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

Examples

\begin{verbatim}
## Not run:
gs\_new <- gs\_remove\_redundant\_channels(gs)
## End(Not run)
\end{verbatim}

\section*{gs\_remove\_redundant\_nodes}

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

\section*{Description}

It is usually called after \texttt{gs\_split\_by\_tree} and \texttt{gs\_check\_redundant\_nodes}. The operation is done in place through external pointers which means all the original \texttt{GatingSets} are modified.

Usage

\texttt{gs\_remove\_redundant\_nodes(x, toRemove)}

Arguments

\begin{itemize}
  \item [\texttt{x}] \texttt{GatingSet} or list of groups(each group is a list of 'GatingSet'). When it is a list, it is usually the outcome from \texttt{gs\_split\_by\_tree}.
  \item [\texttt{toRemove}] list of the node sets to be removed. its length must equals to the length of 'x'. When \texttt{x} is a list, \texttt{toRemove} is usually the outcome from \texttt{gs\_check\_redundant\_nodes}.
\end{itemize}
## 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

Sometime 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

## 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)
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

```
identifier(object)
```

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

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>a GatingSet or GatingSetList</td>
</tr>
<tr>
<td>value</td>
<td>string</td>
</tr>
</tbody>
</table>

Examples

```
## 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)
```
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)
```
keyword-mutators

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

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

```r
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**

```r
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**

```r
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 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 transformation 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 transformation keyword of the FCS header is set to "custom" or "applied", no transformation 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 completely 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 delimiters are parsed as a pair of start and end single delimiters for an empty value.
load_cytoset_from_fcs

Otherwise, double delimiters are parsed as one part of the string of the keyword value. The default is TRUE.

num_threads Integer allowing for parallelization of the parsing operation by specifying a number of threads

ignore.text.offset Logical indicating whether to ignore the keyword values in TEXT segment when they don't agree with the HEADER. Default is FALSE, which throws the error when such a discrepancy is found. Users can turn it on to ignore the TEXT segment when they are sure of the accuracy of the HEADER segment so that the file still can be read.

text.only whether to only parse text section of FCS (default is FALSE), it is sometime useful to skip loading data section for the faster loading meta data from FCS read.AnnotatedDataFrame, see details

Details

The function load_cytoframe_from_fcs works with the output of the FACS machine software from a number of vendors (FCS 2.0, FCS 3.0 and List Mode Data LMD). However, the FCS 3.0 standard includes some options that are not yet implemented in this function. If you need extensions, please let us know. The output of the function is an object of class cytoframe.

For specifications of FCS 3.0 see http://www.isac-net.org and the file ../doc/fcs3.html in the doc directory of the package.

The which.lines arguments allow you to read a subset of the record as you might not want to read the thousands of events recorded in the FCS file. It is mainly used when there is not enough memory to read one single FCS (which probably will not happen). It will probably take more time than reading the entire FCS (due to the multiple disk IO).

Value

An object of class cytoframe that contains the data, the parameters monitored, and the keywords and values saved in the header of the FCS file.

See Also

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

truncate_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 a 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()
<table>
<thead>
<tr>
<th>load_meta</th>
<th>Flush/load meta data (keywords, pData, channels/markers) to/from disk (only valid for on-disk cytoset/cytoframe)</th>
</tr>
</thead>
</table>

**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

<table>
<thead>
<tr>
<th>lock</th>
<th>Lock/Unlock the cytoset/cytoframe by turning on/off its read-only flag</th>
</tr>
</thead>
</table>

**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
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  

*logicle transformation.*

**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  

*Gating-ML 2.0 Log transformation.*

**Description**

Used to construct GML 2.0 flog transformer object.

**Usage**

```r
logtGml2_trans(t = 262144, m = 4.5, n = 6, equal.space = FALSE)
```
### Argument

- **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 # fasinb 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**

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

**Usage**

```r
pData(object)
```

```r
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**

```r
plot(x, y, ...)
```

**Arguments**

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

Examples

```r
## 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)
```

---

### pop_add

Add populations to a GatingHierarchy

#### Description

Add populations to a GatingHierarchy

#### Usage

```r
pop_add(gate, gh, ...)
```

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

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

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

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

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

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

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

`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

`prettyAxis(gh, channel)`

### Arguments

- **gh**: `GatingHierarchy`
- **channel**: character channel name

### Value

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

Examples

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

## S3 method for class 'GatingSet'

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

## S3 method for class 'GatingSetList'

```r
recompute(x, ...)
```

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

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

```r
## 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

It is usually used immediately after `add` or `gs_pop_set_gate` calls.
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)
```

---

**sampleNames**  Get/update sample names in a GatingSet

Description

Return a sample names contained in a GatingSet

Usage

```r
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 individual 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 The internal C data structure (gating tree),ncdfFlowSet object(if applicable)
Retrieve sample names by scanning h5 files from a GatingSet folder

Usage

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

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

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

save_gslist(gslist, path, ...)

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

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.

Evaluate“... 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")
G<-load_gs(path="tempFolder")

#G is a GatingSet

save_gslist(gslist1,path="tempFolder")
gslist2<-load_gslist(path="tempFolder")

## End(Not run)

## Not run:

sampleNames(gsdire)

## End(Not run)
scale_gate

Usage

## 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

## 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

```r
## 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)
```

---

**standardize-GatingSet**  The tools to standardize the tree structures and channel names.

**Description**

- `gs_split_by_tree(x)`
- `gs_split_by_channels(x)`
- `gs_check_redundant_nodes(x)`
- `gs_remove_redundant_nodes(x, toRemove)`
- `gs_remove_redundant_channels(gs)`
- `gs_update_channels(gs, map, all = TRUE)`
- `gh_pop_move(gh, node, to)`
- `gs_pop_set_visibility(x, y, FALSE)`
Details

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

- **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. It 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.

---

### 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
computed.MFI <- 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

transform the flow data asssociated 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 underling 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

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

```r
## 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)
```

Brackets operators on `GatingSet` and `GatingSetList` objects

Description

`[` subsets a `GatingSet` or `GatingSetList` using the familiar bracket notation

`[[` extracts a `GatingHierarchy` object from a `GatingSet`.

Usage

```r
## 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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