Package 'flowCore'

November 12, 2026

Title flowCore: Basic structures for flow cytometry data

Version 2.24.0

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Description Provides S4 data structures and basic functions to deal with flow cytometry data.

Depends R (>= 3.0.2)

Imports Biobase, BiocGenerics (>= 0.29.2), grDevices, graphics, methods, stats, utils, stats4, Rcpp, matrixStats, cytolib (>= 2.13.1), S4Vectors

Suggests Rgraphviz, flowViz, flowStats (>= 3.43.4), testthat, flowWorkspace, flowWorkspaceData, openCyto, knitr, ggcyto, gridExtra

Collate AllGenerics.R AllClasses.R flowFrame-accessors.R flowSet-accessors.R transform_gate-methods.R coerce.R logicalFilterResult-accessors.R summarizeFilter-methods.R filterSummary-accessors.R manyFilterResult-accessors.R summary-methods.R multipleFilterResult-accessors.R on-methods.R transformList-accessors.R identifier-methods.R parameters-methods.R initialize-methods.R filterResult-accessors.R in-methods.R rectangleGate-accessors.R filterResultList-accessors.R IO.R show-methods.R length-methods.R names-methods.R split-methods.R eval-methods.R gatingML.R FCSTransTransform.R median-logicle-transform.R utils.R flowCore.R GvHD.R CytoExploreR_wrappers.R cpp11.R

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biocViews ImmunoOncology, Infrastructure, FlowCytometry, CellBasedAssays

LinkingTo cpp11, BH(>= 1.81.0.0), cytolib, RProtoBufLib

VignetteBuilder knitr

SystemRequirements GNU make, C++17

RoxygenNote 7.2.3

Encoding UTF-8

git_url https://git.bioconductor.org/packages/flowCore

git_branch RELEASE_3_23

git_last_commit a53b880

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-11

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`flowCore-package` *flowCore: Basic structures for flow cytometry data*

Description

Provides S4 data structures and basic infrastructure and functions to deal with flow cytometry data.

Details

Define important flow cytometry data classes: `flowFrame`, `flowSet` and their accessors.

Provide important transformation, filter, gating, workflow, and summary functions for flow cytometry data analysis.

Most of flow cytometry related Bioconductor packages (such as flowStats, flowFP, flowQ, flowViz, flowMerge, flowClust) are heavily dependent on this package.

Package:	flowCore
Type:	Package
Version:	1.11.20
Date:	2009-09-16
License:	Artistic-2.0

Author(s)

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Authors: B. Ellis, P. Haaland, F. Hahne, N. Le Meur, N. Gopalakrishnan

`arcsinhTransform` *Create the definition of an arcsinh transformation function (base specified by user) to be applied on a data set*

Description

Create the definition of the arcsinh Transformation that will be applied on some parameter via the `transform` method. The definition of this function is currently x<-asinh(a+b*x)+c). The transformation would normally be used to convert to a linear valued parameter to the natural logarithm scale. By default a and b are both equal to 1 and c to 0.

Usage

```
arcsinhTransform(transformationId="defaultArcsinhTransform", a=1, b=1, c=0)
```

Arguments

transformationId	character string to identify the transformation
a	positive double that corresponds to a shift about 0.
b	positive double that corresponds to a scale factor.
c	positive double

Value

Returns an object of class `transform`.

Author(s)

B. Ellis

See Also

`transform-class`, `transform`, `asinh`

Other Transform functions: `biexponentialTransform()`, `inverseLogicleTransform()`, `linearTransform()`, `lnTransform()`, `logTransform()`, `logicleTransform()`, `quadraticTransform()`, `scaleTransform()`, `splitScaleTransform()`, `truncateTransform()`

Examples

```
samp <- read.FCS(system.file("extdata",
   "0877408774.B08", package="flowCore"))
  asinhTrans <- arcsinhTransform(transformationId="ln-transformation", a=1, b=1, c=1)
  translist <- transformList('FSC-H', asinhTrans)
  dataTransform <- transform(samp, translist)
```

---

asinht-class *Class "asinht"*

Description

Inverse hyperbolic sine transform class, which represents a transformation defined by the function:

$$f(parameter, a, b) = sinh^{-1}(a * parameter) * b$$

This definition is such that it can function as an inverse of `sinht` using the same definitions of the constants a and b.

Slots

`.Data` Object of class `"function"`.

`a` Object of class `"numeric"` – non-zero constant.

`b` Object of class `"numeric"` – non-zero constant.

`parameters` Object of class `"transformation"` – flow parameter to be transformed

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

Objects from the Class

Objects can be created by calls to the constructor `asinht(parameter,a,b,transformationId)`

Extends

Class `"singleParameterTransform"`, directly.

Class `"transform"`, by class "singleParameterTransform", distance 2.

Class `"transformation"`, by class "singleParameterTransform", distance 3.

Class `"characterOrTransformation"`, by class "singleParameterTransform", distance 4.

Note

The inverse hyperbolic sin transformation object can be evaluated using the eval method by passing the data frame as an argument.The transformed parameters are returned as a matrix with a single column. (See example below)

Author(s)

Gopalakrishnan N, F.Hahne

References

Gating-ML Candidate Recommendation for Gating Description in Flow Cytometry V 1.5

See Also

sinht

Other mathematical transform classes: `EHtrans-class`, `asinhtGml2-class`, `dg1polynomial-class`, `exponential-class`, `hyperlog-class`, `hyperlogtGml2-class`, `invsplitscale-class`, `lintGml2-class`, `logarithm-class`, `logicletGml2-class`, `logtGml2-class`, `quadratic-class`, `ratio-class`, `ratiotGml2-class`, `sinht-class`, `splitscale-class`, `squareroot-class`, `unitytransform-class`

Examples

```
dat <- read.FCS(system.file("extdata","0877408774.B08",  package="flowCore"))
 asinh1<-asinht(parameters="FSC-H",a=2,b=1,transformationId="asinH1")
 transOut<-eval(asinh1)(exprs(dat))
```

`asinhtGml2-class` *Class asinhtGml2*

Description

Inverse hyperbolic sin transformation as parameterized in Gating-ML 2.0.

Details

asinhtGml2 is defined by the following function:

$$bound(f, boundMin, boundMax) = max(min(f, boundMax), boundMin))$$

where

$$f(parameter, T, M, A) = (asinh(parameter{*}sinh(M{*}ln(10))/T){+}A{*}ln(10))/((M{+}A){*}ln(10))$$

This transformation is equivalent to Logicle(T, 0, M, A) (i.e., with W=0). It provides an inverse hyperbolic sine transformation that maps a data value onto the interval [0,1] such that:

- The top of scale value (i.e., T) is mapped to 1.
- Large data values are mapped to locations similar to an (M + A)-decade logarithmic scale.
- A decades of negative data are brought on scale.

In addition, if a boundary is defined by the boundMin and/or boundMax parameters, then the result of this transformation is restricted to the [boundMin,boundMax] interval. Specifically, should the result of the f function be less than boundMin, then let the result of this transformation be boundMin. Analogically, should the result of the f function be more than boundMax, then let the result of this transformation be boundMax. The boundMin parameter shall not be greater than the boundMax parameter.

Slots

`.Data` Object of class `function`.

`T` Object of class `numeric` – positive constant (top of scale value).

`M` Object of class `numeric` – positive constant (desired number of decades).

`A` Object of class `numeric` – non-negative constant that is less than or equal to M (desired number of additional negative decades).

`parameters` Object of class `"transformation"` – flow parameter to be transformed.

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

`boundMin` Object of class `numeric` – lower bound of the transformation, default -Inf.

`boundMax` Object of class `numeric` – upper bound of the transformation, default Inf.

Objects from the Class

Objects can be created by calls to the constructor

`asinhtGml2(parameter, T, M, A, transformationId, boundMin, boundMax)`

Extends

Class singleParameterTransform, directly.

Class transform, by class singleParameterTransform, distance 2.

Class transformation, by class singleParameterTransform, distance 3.

Class characterOrTransformation, by class singleParameterTransform, distance 4.

Note

The inverse hyperbolic sin transformation object can be evaluated using the eval method by passing the data frame as an argument. The transformed parameters are returned as a matrix with a single column. (See example below)

Author(s)

Spidlen, J.

References

Gating-ML 2.0: International Society for Advancement of Cytometry (ISAC) standard for representing gating descriptions in flow cytometry. http://flowcyt.sourceforge.net/gating/20141009.pdf

See Also

asinht, transform-class, transform

Other mathematical transform classes: EHtrans-class, asinht-class, dg1polynomial-class, exponential-class, hyperlog-class, hyperlogtGml2-class, invsplitscale-class, lintGml2-class, logarithm-class, logicletGml2-class, logtGml2-class, quadratic-class, ratio-class, ratiotGml2-class, sinht-class, splitscale-class, squareroot-class, unitytransform-class

Examples

```
myDataIn <- read.FCS(system.file("extdata", "0877408774.B08",
    package="flowCore"))
myASinH1 <- asinhtGml2(parameters = "FSC-H", T = 1000, M = 4.5,
    A = 0, transformationId="myASinH1")
transOut <- eval(myASinH1)(exprs(myDataIn))
```

biexponentialTransform *Compute a transform using the 'biexponential' function*

Description

The 'biexponential' is an over-parameterized inverse of the hyperbolic sine. The function to be inverted takes the form biexp(x) = a*exp(b*(x-w))-c*exp(-d*(x-w))+f with default parameters selected to correspond to the hyperbolic sine.

Usage

```
biexponentialTransform(transformationId="defaultBiexponentialTransform",
                       a = 0.5, b = 1, c = 0.5, d = 1, f = 0, w = 0,
                      tol = .Machine$double.eps^0.25, maxit = as.integer(5000))
```

Arguments

transformationId	A name to assign to the transformation. Used by the transform/filter integration routines.
a	See the function description above. Defaults to 0.5
b	See the function description above. Defaults to 1.0
c	See the function description above. Defaults to 0.5 (the same as a)
d	See the function description above. Defaults to 1 (the same as b)
f	A constant bias for the intercept. Defaults to 0.
w	A constant bias for the 0 point of the data. Defaults to 0.
tol	A tolerance to pass to the inversion routine (uniroot usually)
maxit	A maximum number of iterations to use, also passed to uniroot

Value

Returns values giving the inverse of the biexponential within a certain tolerance. This function should be used with care as numerical inversion routines often have problems with the inversion process due to the large range of values that are essentially 0. Do not be surprised if you end up with population splitting about w and other odd artifacts.

Author(s)

B. Ellis, N Gopalakrishnan

See Also

transform

Other Transform functions: arcsinhTransform(), inverseLogicleTransform(), linearTransform(), lnTransform(), logTransform(), logicleTransform(), quadraticTransform(), scaleTransform(), splitScaleTransform(), truncateTransform()

Examples

```
# Construct some "flow-like" data which tends to be hetereoscedastic.
data(GvHD)
biexp  <- biexponentialTransform("myTransform")

after.1 <- transform(GvHD, transformList('FSC-H', biexp))

biexp  <- biexponentialTransform("myTransform",w=10)
after.2 <- transform(GvHD, transformList('FSC-H', biexp))

opar = par(mfcol=c(3, 1))
plot(density(exprs(GvHD[[1]])[, 1]), main="Original")
plot(density(exprs(after.1[[1]])[, 1]), main="Standard Transform")
plot(density(exprs(after.2[[1]])[, 1]), main="Shifted Zero Point")
```

---

boundaryFilter-class *Class "boundaryFilter"*

Description

Class and constructor for data-driven `filter` objects that discard margin events.

Usage

```
boundaryFilter(x, tolerance=.Machine$double.eps, side=c("both", "lower",
"upper"), filterId="defaultBoundaryFilter")
```

Arguments

`x`	Character giving the name(s) of the measurement parameter(s) on which the filter is supposed to work. Note that all events on the margins of ay of the channels provided by `x` will be discarded, which is often not desired. Such events may not convey much information in the particular channel on which their value falls on the margin, however they may well be informative in other channels.
`tolerance`	Numeric vector, used to set the `tolerance` slot of the object. Can be set separately for each element in `x`. R's recycling rules apply.
`side`	Character vector, used to set the `side` slot of the object. Can be set separately for each element in `x`. R's recycling rules apply.
`filterId`	An optional parameter that sets the `filterId` slot of this filter. The object can later be identified by this name.

Details

Flow cytomtery instruments usually operate on a given data range, and the limits of this range are stored as keywords in the FSC files. Depending on the amplification settings and the dynamic range of the measured signal, values can occur that are outside of the measurement range, and most instruments will simply pile those values at the minimum or maximum range limit. The `boundaryFilter` removes these values, either for a single parameter, or for a combination of parameters. Note that it is often desirable to treat boundary events on a per-parameter basis, since their values might be uninformative for one particular channel, but still be useful in all of the other channels.

The constructor `boundaryFilter` is a convenience function for object instantiation. Evaluating a `boundaryFilter` results in a single sub-populations, an hence in an object of class `filterResult`.

Value

Returns a `boundaryFilter` object for use in filtering `flowFrame`s or other flow cytometry objects.

Slots

`tolerance` Object of class `"numeric"`. The machine tolerance used to decide whether an event is on the measurement boundary. Essentially, this is done by evaluating `x>minRange+tolerance & x<maxRange-tolerance`.

`side` Object of class `"character"`. The margin on which to evaluate the filter. Either `upper` for the upper margin or `lower` for the lower margin or `both` for both margins.

Extends

Class `"parameterFilter"`, directly.

Class `"concreteFilter"`, by class `parameterFilter`, distance 2.

Class `"filter"`, by class `parameterFilter`, distance 3.

Objects from the Class

Objects can be created by calls of the form `new("boundaryFilter",...)` or using the constructor `boundaryFilter`. Using the constructor is the recommended way.

Methods

%in% `signature(x = "flowFrame", table = "boundaryFilter")`: The workhorse used to evaluate the filter on data. This is usually not called directly by the user, but internally by calls to the `filter` methods.

show `signature(object = "boundaryFilter")`: Print information about the filter.

Author(s)

Florian Hahne

See Also

`flowFrame`, `flowSet`, `filter` for evaluation of `boundaryFilters` and `Subset` for subsetting of flow cytometry data sets based on that.

Examples

```
## Loading example data
dat <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))

## Create directly. Most likely from a command line
boundaryFilter("FSC-H", filterId="myBoundaryFilter")

## To facilitate programmatic construction we also have the following
bf <- boundaryFilter(filterId="myBoundaryFilter", x=c("FSC-H"))

## Filtering using boundaryFilter
fres <- filter(dat, bf)
fres
summary(fres)

## We can subset the data with the result from the filtering operation.
Subset(dat, fres)

## A boundaryFilter on the lower margins of several channels
bf2 <- boundaryFilter(x=c("FSC-H", "SSC-H"), side="lower")
```

---

characterOrNumeric-class

Class "characterOrNumeric"

Description

A simple union class of `character` and `numeric`. Objects will be created internally whenever necessary and the user should not need to explicitly interact with this class.

Objects from the Class

A virtual Class: No objects may be created from it.

Examples

```
showClass("characterOrNumeric")
```

`characterOrParameters-class`
Class "characterOrParameters"

Description

A simple union class of `character` and `parameters`. Objects will be created internally whenever necessary and the user should not need to explicitly interact with this class.

Objects from the Class

A virtual Class: No objects may be created from it.

Examples

```
showClass("characterOrParameters")
```

`characterOrTransformation-class`
Class "characterOrTransformation"

Description

A simple union class of `character` and `transformation`. Objects will be created internally whenever necessary and the user should not need to explicitly interact with this class.

Objects from the Class

A virtual Class: No objects may be created from it.

Examples

```
showClass("characterOrTransformation")
```

checkOffset *Fix the offset when its values recorded in header and TEXT don't agree*

Description

Fix the offset when its values recorded in header and TEXT don't agree

Usage

```
checkOffset(offsets, x, ignore.text.offset = FALSE, ...)
```

Arguments

offsets	the named vector returned by findOffsets
x	the text segmented returned by readFCStext
ignore.text.offset	whether to ignore the offset info stored in TEXT segment
...	not used.

Value

the updated offsets

coerce *Convert an object to another class*

Description

These functions manage the relations that allow coercing an object to a given class.

Arguments

from, to	The classes between which def performs coercion. (In the case of the coerce function, these are objects from the classes, not the names of the classes, but you're not expected to call coerce directly.)

Details

The function supplied as the third argument is to be called to implement as(x, to) when x has class from. Need we add that the function should return a suitable object with class to.

Author(s)

F. Hahne, B. Ellis

Examples

```
samp1 <- read.FCS(system.file("extdata","0877408774.E07", package="flowCore"))
samp2 <- read.FCS(system.file("extdata","0877408774.B08",package="flowCore"))
samples <-list("sample1"=samp1,"sample2"=samp2)
experiment <- as(samples,"flowSet")
```

`collapse_desc` *Coerce the list of the keywords into a character Also flatten spillover matrix into a string*

Description

Coerce the list of the keywords into a character Also flatten spillover matrix into a string

Usage

```
collapse_desc(d, collapse.spill = TRUE)
```

Arguments

`d`	a named list of keywords
`collapse.spill`	whether to flatten spillover matrix to a string

Value

a list of strings

Examples

```
data(GvHD)
fr <- GvHD[[1]]
collapse_desc(keyword(fr))
```

`compensatedParameter-class` *Class "compensatedParameter"*

Description

Emission spectral overlap can be corrected by subtracting the amount of spectral overlap from the total detected signals. This compensation process can be described by using spillover matrices.

Details

The compensatedParameter class allows for compensation of specific parameters the user is interested in by creating compensatedParameter objects and evaluating them. This allows for use of compensatedParameter in gate definitions.

Slots

`.Data` Object of class `"function"`.

`parameters` Object of class `"character"` – the flow parameters to be compensated.

`spillRefId` Object of class `"character"` – the name of the compensation object (The compensation object contains the spillover Matrix).

`searchEnv` Object of class `"environment"` -environment in which the compensation object is defined.

`transformationId` Object of class `"character"` – a unique Id to reference the compensatedParameter object.

Objects from the Class

Objects can be created by calls to the constructor of the form `compensatedParameter(parameters,spillRefId,transform`

Extends

Class `"transform"`, directly. Class `"transformation"`, by class "transform", distance 2. Class `"characterOrTransformation"`, by class "transform", distance 3.

Note

The transformation object can be evaluated using the eval method by passing the data frame as an argument. The transformed parameters are returned as a matrix with a single column. (See example below)

Author(s)

Gopalakrishnan N,F.Hahne

See Also

compensation

Examples

```
samp  <- read.flowSet(path=system.file("extdata", "compdata", "data", package="flowCore"))
cfile <- system.file("extdata","compdata","compmatrix", package="flowCore")
comp.mat <- read.table(cfile, header=TRUE, skip=2, check.names = FALSE)
comp.mat

## create a compensation object
comp <- compensation(comp.mat,compensationId="comp1")
## create a compensated parameter object
```

```
cPar1<-compensatedParameter(c("FL1-H","FL3-H"),"comp",searchEnv=.GlobalEnv)
compOut<-eval(cPar1)(exprs(samp[[1]]))
```

`compensation-class` *Class "compensation"*

Description

Class and methods to compensate for spillover between channels by applying a spillover matrix to a `flowSet` or a `flowFrame` assuming a simple linear combination of values.

Usage

```
compensation(..., spillover, compensationId="defaultCompensation")

compensate(x, spillover, ...)
```

Arguments

`spillover`	The spillover or compensation matrix.
`compensationId`	The identifier for the compensation object.
`x`	An object of class `flowFrame` or `flowSet`.
`...`	Further arguments.
	The constructor is designed to be useful in both programmatic and interactive settings, and ... serves as a container for possible arguments. The following combinations of values are allowed:
	Elements in ... are `character` scalars of parameter names or `transform` objects and the colnames in `spillover` match to these parameter names.
	The first element in ... is a `character` vector of parameter names or a list of `character` scalars or `transform` objects and the colnames in `spillover` match to these parameter names.
	Argument `spillover` is missing and the first element in ... is a `matrix`, in which case it is assumed to be the spillover matrix.
	... is missing, in which case all parameter names are taken from the colnames of `spillover`.

Details

The essential premise of compensation is that some fluorochromes may register signals in detectors that do not correspond to their primary detector (usually a photomultiplier tube). To compensate for this fact, some sort of standard is used to obtain the background signal (no dye) and the amount of signal on secondary channels for each fluorochrome relative to the signal on their primary channel.

To calculate the spillover percentage we use either the mean or the median (more often the latter) of the secondary signal minus the background signal for each dye to obtain `n` by `n` matrix, `S`, of

so-called spillover values, expressed as a percentage of the primary channel. The observed values are then considered to be a linear combination of the true fluorescence and the spillover from each other channel so we can obtain the true values by simply multiplying by the inverse of the spillover matrix.

The spillover matrix can be obtained through several means. Some flow cytometers provide a spillover matrix calculated during acquisition, possibly by the operator, that is made available in the metadata of the flowFrame. While there is a theoretical standard keyword `$SPILL` it can also be found in the `SPILLOVER` or `SPILL` keyword depending on the cytometry. More commonly the spillover matrix is calculated using a series of compensation cells or beads collected before the experiment. If you have set of FCS files with one file per fluorochrome as well as an unstained FCS file you can use the `spillover` method for `flowSets` to automatically calculate a spillover matrix.

The `compensation` class is essentially a wrapper around a `matrix` that allows for transformed parameters and method dispatch.

Value

A `compensation` object for the constructor.

A `flowFrame` or `flowSet` for the `compensate` methods.

Slots

`spillover` Object of class `matrix`; the spillover matrix.

`compensationId` Object of class `character`. An identifier for the object.

`parameters` Object of class `parameters`. The flow parameters for which the compensation is defined. This can also be objects of class `transform`, in which case the compensation is performed on the compensated parameters.

Objects from the Class

Objects should be created using the constructor `compensation()`. See the `Usage` and `Arguments` sections for details.

Methods

compensate `signature(x = "flowFrame", spillover = "compensation")`: Apply the compensation defined in a `compensation` object on a `flowFrame`. This returns a compensated `flowFrame`.

Usage:

```
compensate(flowFrame, compensation)
```

compensate `signature(x = "flowFrame", spillover = "matrix")`: Apply a compensation matrix to a `flowFrame`. This returns a compensated `flowFrame`.

Usage:

```
compensate(flowFrame, matrix)
```

compensate `signature(x = "flowFrame", spillover = "data.frame")`:Try to coerce the `data.frame` to a `matrix` and apply that to a `flowFrame`. This returns a compensated `flowFrame`.

Usage:

```
compensate(flowFrame, data.frame)
```

identifier, identifier<- `signature(object = "compensation")`: Accessor and replacement methods for the `compensationId` slot.

Usage:

```
identifier(compensation)
identifier(compensation) <- value
```

parameters `signature(object = "compensation")`: Get the parameter names of the `compensation` object. This method also tries to resolve all `transforms` and `transformReferences` before returning the parameters as character vectors. Unresolvable references return `NA`.

Usage:

```
parameters(compensation)
```

show `signature(object = "compensation")`: Print details about the object.

Usage:

This method is automatically called when the object is printed on the screen.

Author(s)

F.Hahne, B. Ellis, N. Le Meur

See Also

`spillover`

Examples

```
## Read sample data and a sample spillover matrix
samp   <- read.flowSet(path=system.file("extdata", "compdata", "data",
          package="flowCore"))
cfile <- system.file("extdata","compdata","compmatrix", package="flowCore")
comp.mat <- read.table(cfile, header=TRUE, skip=2, check.names = FALSE)
comp.mat

## compensate using the spillover matrix directly
summary(samp)
samp <- compensate(samp, comp.mat)
summary(samp)

## create a compensation object and compensate using that
comp <- compensation(comp.mat)
compensate(samp, comp)

## demo the sample-specific compensation
## create a list of comps (each element could be a
## different compensation tailored for the specific sample)
comps <- sapply(sampleNames(samp), function(sn)comp, simplify = FALSE)
# the names of comps must be matched to sample names of the flowset
compensate(samp, comps)
```

complementFilter-class *Class complementFilter*

Description

This class represents the logical complement of a single filter, which is itself a filter that can be incorporated in to further set operations. `complementFilters` are constructed using the prefix unary set operator `"!"` with a single filter operand.

Slots

`filters` Object of class `"list"`, containing the component filters.

`filterId` Object of class `"character"` referencing the filter applied.

Extends

Class `"filter"`, directly.

Author(s)

B. Ellis

See Also

`filter`, `setOperationFilter`

Other setOperationFilter classes: `intersectFilter-class`, `setOperationFilter-class`, `subsetFilter-class`, `unionFilter-class`

concreteFilter-class *Class "concreteFilter"*

Description

The `concreteFilter` serves as a base class for all filters that actually implement a filtering process. At the moment this includes all filters except `filterReference`, the only non-concrete filter at present.

Slots

`filterId` The identifier associated with this class.

Objects from the Class

Objects of this class should never be created directly. It serves only as a point of inheritance.

Extends

Class "filter", directly.

Author(s)

B. Ellis

See Also

parameterFilter

`CytoExploreR_exports` *CytoExploreR exports*

Description

Exported wrappers of internal functions for use by CytoExploreR

Usage

```
CytoExploreR_.estimateLogicle(x, channels, ...)
```

`decompensate` *Decompensate a flowFrame*

Description

Reverse the application of a compensation matrix on a flowFrame

Usage

```
## S4 method for signature 'flowFrame,matrix'
decompensate(x, spillover)

## S4 method for signature 'flowFrame,compensation'
decompensate(x, spillover)
```

Arguments

`x`	flowFrame.
`spillover`	matrix or data.frame or a compensation object

Value

a decompensated flowFrame

Examples

```
library(flowCore)
f = list.files(system.file("extdata",
   "compdata",
   "data",
   package="flowCore"),
 full.name=TRUE)[1]
f = read.FCS(f)
spill = read.csv(system.file("extdata",
       "compdata", "compmatrix",
        package="flowCore"),
        ,sep="\t",skip=2)
colnames(spill) = gsub("\\.","-",colnames(spill))
f.comp = compensate(f,spill)
f.decomp = decompensate(f.comp,as.matrix(spill))
sum(abs(f@exprs-f.decomp@exprs))
all.equal(decompensate(f.comp,spill)@exprs,decompensate(f.comp,as.matrix(spill))@exprs)
all.equal(f@exprs,decompensate(f.comp,spill)@exprs)
```

---

dg1polynomial-class *Class "dg1polynomial"*

Description

dg1polynomial allows for scaling,linear combination and translation within a single transformation defined by the function

$$f(parameter_1, ..., parameter_n, a_1, ..., a_n, b) = b + \Sigma_{i=1}^{n} a_i * parameter_i$$

Slots

`.Data` Object of class `"function"`.

`parameters` Object of class `"parameters"` –the flow parameters that are to be transformed.

`a` Object of class `"numeric"` – coefficients of length equal to the number of flow parameters.

`b` Object of class `"numeric"` – coefficient of length 1 that performs the translation.

`transformationId` Object of class `"character"` unique ID to reference the transformation.

Objects from the Class

Objects can be created by using the constructor `dg1polynomial(parameter,a,b,transformationId)`.

Extends

Class `"transform"`, directly.

Class `"transformation"`, by class "transform", distance 2.

Class `"characterOrTransformation"`, by class "transform", distance 3.

Note

The transformation object can be evaluated using the eval method by passing the data frame as an argument.The transformed parameters are returned as a matrix with a single column.(See example below)

Author(s)

Gopalakrishnan N, F.Hahne

References

Gating-ML Candidate Recommendation for Gating Description in Flow Cytometry V 1.5

See Also

ratio,quadratic,squareroot

Other mathematical transform classes: EHtrans-class, asinht-class, asinhtGml2-class, exponential-class, hyperlog-class, hyperlogtGml2-class, invsplitscale-class, lintGml2-class, logarithm-class, logicletGml2-class, logtGml2-class, quadratic-class, ratio-class, ratiotGml2-class, sinht-class, splitscale-class, squareroot-class, unitytransform-class

Examples

```
dat <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))
dg1<-dg1polynomial(c("FSC-H","SSC-H"),a=c(1,2),b=1,transformationId="dg1")
transOut<-eval(dg1)(exprs(dat))
```

---

each_col *Methods to apply functions over flowFrame margins*

Description

Returns a vector or array of values obtained by applying a function to the margins of a flowFrame. This is equivalent of running apply on the output of exprs(flowFrame).

Usage

```
each_col(x, FUN, ...)
each_row(x, FUN, ...)
```

Arguments

x	Object of class flowFrame.
FUN	the function to be applied. In the case of functions like '+', '%*%', etc., the function name must be backquoted or quoted.
...	optional arguments to 'FUN'.

Author(s)

B. Ellis, N. LeMeur, F. Hahne

See Also

apply

Examples

```
samp <- read.FCS(system.file("extdata", "0877408774.B08", package="flowCore"),
transformation="linearize")
each_col(samp, summary)
```

EHtrans-class *Class "EHtrans"*

Description

EH transformation of a parameter is defined by the function

$$EH(parameter, a, b) = 10^{(\frac{parameter}{a})} + \frac{b * parameter}{a} - 1, parameter >= 0$$

$$-10^{(\frac{-parameter}{a})} + \frac{b * parameter}{a} + 1, parameter < 0$$

Slots

`.Data` Object of class `"function"`.

`a` Object of class `"numeric"` – numeric constant greater than zero.

`b` Object of class `"numeric"` – numeric constant greater than zero.

`parameters` Object of class `"transformation"` – flow parameter to be transformed.

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

Objects from the Class

Objects can be created by calls to the constructor `EHtrans(parameters,a,b,transformationId)`

Extends

Class `"singleParameterTransform"`, directly.

Class `"transform"`, by class "singleParameterTransform", distance 2.

Class `"transformation"`, by class "singleParameterTransform", distance 3.

Class `"characterOrTransformation"`, by class "singleParameterTransform", distance 4.

Note

The transformation object can be evaluated using the eval method by passing the data frame as an argument.The transformed parameters are returned as a matrix with a single column. (See example below)

Author(s)

Gopalakrishnan N, F.Hahne

References

Gating-ML Candidate Recommendation for Gating Description in Flow Cytometry V 1.5

See Also

hyperlog

Other mathematical transform classes: asinht-class, asinhtGml2-class, dg1polynomial-class, exponential-class, hyperlog-class, hyperlogtGml2-class, invsplitscale-class, lintGml2-class, logarithm-class, logicletGml2-class, logtGml2-class, quadratic-class, ratio-class, ratiotGml2-class, sinht-class, splitscale-class, squareroot-class, unitytransform-class

Examples

```
dat <- read.FCS(system.file("extdata","0877408774.B08",
                package="flowCore"))
eh1<-EHtrans("FSC-H",a=1250,b=4,transformationId="eh1")
transOut<-eval(eh1)(exprs(dat))
```

---

ellipsoidGate-class *Class "ellipsoidGate"*

Description

Class and constructor for n-dimensional ellipsoidal filter objects.

Usage

```
ellipsoidGate(..., .gate, mean, distance=1, filterId="defaultEllipsoidGate")
```

Arguments

filterId	An optional parameter that sets the filterId of this gate.
.gate	A definition of the gate via a covariance matrix.
mean	Numeric vector of equal length as dimensions in .gate.

distance	Numeric scalar giving the Mahalanobis distance defining the size of the ellipse. This mostly exists for compliance reasons to the gatingML standard as mean and gate should already uniquely define the ellipse. Essentially, distance is merely a factor that gets applied to the values in the covariance matrix.
...	You can also directly describe the covariance matrix through named arguments, as described below.

Details

A convenience method to facilitate the construction of a ellipsoid filter objects. Ellipsoid gates in n dimensions (n >= 2) are specified by a a covarinace matrix and a vector of mean values giving the center of the ellipse.

This function is designed to be useful in both direct and programmatic usage. In the first case, simply describe the covariance matrix through named arguments. To use this function programmatically, you may pass a covarince matrix and a mean vector directly, in which case the parameter names are the colnames of the matrix.

Value

Returns a ellipsoidGate object for use in filtering flowFrames or other flow cytometry objects.

Slots

mean Objects of class "numeric". Vector giving the location of the center of the ellipse in n dimensions.

cov Objects of class "matrix". The covariance matrix defining the shape of the ellipse.

distance Objects of class "numeric". The Mahalanobis distance defining the size of the ellipse.

parameters Object of class "character", describing the parameter used to filter the flowFrame.

filterId Object of class "character", referencing the filter.

Extends

Class "parameterFilter", directly.

Class "concreteFilter", by class parameterFilter, distance 2.

Class "filter", by class parameterFilter, distance 3.

Objects from the Class

Objects can be created by calls of the form new("ellipsoidGate",...) or by using the constructor ellipsoidGate. Using the constructor is the recommended way.

Methods

%in% signature(x = "flowFrame", table = "ellipsoidGate"): The workhorse used to evaluate the filter on data. This is usually not called directly by the user, but internally by calls to the filter methods.

show signature(object = "ellipsoidGate"): Print information about the filter.

Note

See the documentation in the flowViz package for plotting of ellipsoidGates.

Author(s)

F.Hahne, B. Ellis, N. LeMeur

See Also

flowFrame, polygonGate, rectangleGate, polytopeGate, filter for evaluation of rectangleGates and split and Subsetfor splitting and subsetting of flow cytometry data sets based on that.

Other Gate classes: polygonGate-class, polytopeGate-class, quadGate-class, rectangleGate-class

Examples

```
## Loading example data
dat <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))

## Defining the gate
cov <- matrix(c(6879, 3612, 3612, 5215), ncol=2,
dimnames=list(c("FSC-H", "SSC-H"), c("FSC-H", "SSC-H")))
mean <- c("FSC-H"=430, "SSC-H"=175)
eg <- ellipsoidGate(filterId= "myEllipsoidGate", .gate=cov, mean=mean)

## Filtering using ellipsoidGates
fres <- filter(dat, eg)
fres
summary(fres)

## The result of ellipsoid filtering is a logical subset
Subset(dat, fres)

## We can also split, in which case we get those events in and those
## not in the gate as separate populations
split(dat, fres)

##ellipsoidGate can be converted to polygonGate by interpolation
pg <- as(eg, "polygonGate")
pg
```

---

estimateMedianLogicle *Estimates a common logicle transformation for a flowSet.*

Description

Of the negative values for each channel specified, the median of the specified quantiles are used.

Usage

```
estimateMedianLogicle(flow_set, channels, m = 4.5, q = 0.05)
```

Arguments

flow_set	object of class 'flowSet'
channels	character vector of channels to transform
m	TODO – default value from .lgclTrans
q	quantile

Value

TODO

---

exponential-class *Class "exponential"*

Description

Exponential transform class, which represents a transformation given by the function

$$f(parameter, a, b) = e^{parameter/b} * \frac{1}{a}$$

Slots

`.Data` Object of class `"function"`.

`a` Object of class `"numeric"` – non-zero constant.

`b` Object of class `"numeric"`- non-zero constant.

`parameters` Object of class `"transformation"` – flow parameter to be transformed.

`transformationId` Object of class `"character"` – unique ID to reference the transformation

Objects from the Class

Objects can be created by calls to the constructor`exponential(parameters,a,b)`.

Extends

Class `"singleParameterTransform"`, directly.

Class `"transform"`, by class "singleParameterTransform", distance 2.

Class `"transformation"`, by class "singleParameterTransform", distance 3.

Class `"characterOrTransformation"`, by class "singleParameterTransform", distance 4.

Note

The exponential transformation object can be evaluated using the eval method by passing the data frame as an argument.The transformed parameters are returned as a matrix with a single column

Author(s)

Gopalakrishnan N, F.Hahne

References

Gating-ML Candidate Recommendation for Gating Description in Flow Cytometry V 1.5

See Also

logarithm

Other mathematical transform classes: EHtrans-class, asinht-class, asinhtGml2-class, dg1polynomial-class, hyperlog-class, hyperlogtGml2-class, invsplitscale-class, lintGml2-class, logarithm-class, logicletGml2-class, logtGml2-class, quadratic-class, ratio-class, ratiotGml2-class, sinht-class, splitscale-class, squareroot-class, unitytransform-class

Examples

```
dat <- read.FCS(system.file("extdata","0877408774.B08",
 package="flowCore"))
 exp1<-exponential(parameters="FSC-H",a=1,b=37,transformationId="exp1")
 transOut<-eval(exp1)(exprs(dat))
```

---

expressionFilter-class

Class "expressionFilter"

Description

A filter holding an expression that can be evaluated to a logical vector or a vector of factors.

Usage

```
expressionFilter(expr, ..., filterId="defaultExpressionFilter")
char2ExpressionFilter(expr, ..., filterId="defaultExpressionFilter")
```

Arguments

filterId	An optional parameter that sets the filterId of this filter. The object can later be identified by this name.
expr	A valid R expression or a character vector that can be parsed into an expression.
...	Additional arguments that are passed to the evaluation environment of the expression.

Details

The expression is evaluated in the environment of the flow cytometry values, hence the parameters of a flowFrame can be accessed through regular R symbols. The convenience function char2ExpressionFilter exists to programmatically construct expressions.

Value

Returns a expressionFilter object for use in filtering flowFrames or other flow cytometry objects.

Slots

expr The expression that will be evaluated in the context of the flow cytometry values.

args An environment providing additional parameters.

deparse A character scalar of the deparsed expression.

filterId The identifier of the filter.

Extends

Class "concreteFilter", directly.

Class "filter", by class concreteFilter, distance 2.

Objects from the Class

Objects can be created by calls of the form new("expressionFilter", ...), using the expressionFilter constructor or, programmatically, from a character string using the char2ExpressionFilter function.

Methods

%in% signature(x = "flowFrame", table = "expressionFilter"): The workhorse used to evaluate the gate on data. This is usually not called directly by the user, but internally by calls to the filter methods.

show signature(object = "expressionFilter"): Print information about the gate.

Author(s)

F. Hahne, B. Ellis

See Also

flowFrame, filter for evaluation of sampleFilters and split and Subsetfor splitting and subsetting of flow cytometry data sets based on that.

Examples

```
## Loading example data
dat <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))

#Create the filter
ef <- expressionFilter(`FSC-H` > 200, filterId="myExpressionFilter")
ef

## Filtering using sampeFilters
fres <- filter(dat, ef)
fres
summary(fres)

## The result of sample filtering is a logical subset
newDat <- Subset(dat, fres)
all(exprs(newDat)[,"FSC-H"] > 200)

## We can also split, in which case we get those events in and those
## not in the gate as separate populations
split(dat, fres)

## Programmatically construct an expression
dat <- dat[,-8]
r <- range(dat)
cn <- paste("`", colnames(dat), "`", sep="")
exp <- paste(cn, ">", r[1,], "&", cn, "<", r[2,], collapse=" & ")
ef2 <- char2ExpressionFilter(exp, filterId="myExpressionFilter")
ef2
fres2 <- filter(dat, ef2)
fres2
summary(fres2)
```

FCSTransTransform *Computes a transform using the 'iplogicle' function*

Description

Transforms FCS data using the iplogicle function from FCSTrans by Quian et al. The core functionality of FCSTrans has been imported to produce transformed FCS data rescaled and truncated as produced by FCSTrans. The `w` parameter is estimated by `iplogicle` automatically, then makes a call to `iplogicore` which in turn uses the logicle transform code of Wayne Moore.

Usage

```
FCSTransTransform(transformationId = "defaultFCSTransTransform",
                  channelrange = 2^18, channeldecade = 4.5,
                  range = 4096, cutoff = -111, w = NULL, rescale = TRUE)
```

Arguments

transformationId	A name to assign to the transformation. Used by the transform/filter routines.
channelrange	is the range of the data. By default, 2^18 = 262144.
channeldecade	is the number of logarithmic decades. By default, it is set to 4.5.
range	the target resolution. The default value is 2^12 = 4096.
cutoff	a threshold below which the logicle transformation maps values to 0.
w	the logicle width. This is estimated by iplogicle by default. Details can be found in the Supplementary File from Quian et al.
rescale	logical parameter whether or not the data should be rescaled to the number of channels specified in range. By default, the value is TRUE but can be set to FALSE if you want to work on the transformed scale.

Details

For the details of the FCSTrans transformation, we recommend the excellent Supplementary File that accompanies Quian et al. (2012): http://onlinelibrary.wiley.com/doi/10.1002/cyto.a.22037/suppinfo

Author(s)

Wayne Moore, N Gopalakrishnan

References

Y Quian, Y Liu, J Campbell, E Thompson, YM Kong, RH Scheuermann; FCSTrans: An open source software system for FCS file conversion and data transformation. Cytometry A, 2012

See Also

inverseLogicleTransform, estimateLogicle , logicleTransform

Examples

```
data(GvHD)
samp <- GvHD[[1]]
## User defined logicle function
lgcl <- transformList(c('FL1-H', 'FL2-H'), FCSTransTransform())
after <- transform(samp, lgcl)
```

filter-and-methods *Take the intersection of two filters*

Description

There are two notions of intersection in flowCore. First, there is the usual intersection boolean operator & that has been overridden to allow the intersection of two filters or of a filter and a list for convenience. There is also the %&% or %subset% operator that takes an intersection, but with subset semantics rather than simple intersection semantics. In other words, when taking a subset, calculations from summary and other methods are taken with respect to the right hand filter. This primarily affects calculations, which are ordinarily calculated with respect to the entire population as well as data-driven gating procedures which will operate only on elements contained by the right hand filter. This becomes especially important when using filters such as norm2Filter

Usage

```
e1 %&% e2
e1 %subset% e2
```

Arguments

e1, e2	filter objects or lists of filter objects

Author(s)

B. Ellis

filter-class *A class for representing filtering operations to be applied to flow data.*

Description

The filter class is the virtual base class for all filter/gating objects in flowCore. In general you will want to subclass or create a more specific filter.

Slots

filterId A character vector that identifies this filter. This is typically user specified but can be automatically deduced by certain filter operations, particularly boolean and set operations.

Objects from the Class

All filter objects in flowCore should be instantiated through their constructors. These are functions that share the same name with the respective filter classes. E.g., rectangleGate() is the constructor function for rectangular gates, and kmeansFilter() creates objects of class kmeansFilter. Usually these constructors can deal with various different inputs, allowing to utilize the same function in different programmatic or interactive settings. For all filters that operate on specific flow parameters (i.e., those inheriting from parameterFilter), the parameters need to be passed to the constructor, either as names or colnames of additional input arguments or explicitly as separate arguments. See the documentation of the respective filter classes for details. If parameters are explicitly defined as separate arguments, they may be of class character, in which case they will be evaluated literally as colnames in a flowFrame, or of class transform, in which case the filtering is performed on a temporarily transformed copy of the input data. See here for details.

Methods

%in% Used in the usual way this returns a vector of values that identify which events were accepted by the filter. A single filter may encode several populations so this can return either a logical vector, a factor vector or a numeric vector of probabilities that the event is accepted by the filter. Minimally, you must implement this method when creating a new type of filter

&, |, ! Two filters can be composed using the usual boolean operations returning a filter class of a type appropriate for handling the operation. These methods attempt to guess an appropriate filterId for the new filter

%subset%, %&% Defines a filter as being a subset of another filter. For deterministic filters the results will typically be equivalent to using an \& operation to compose the two filters, though summary methods will use subset semantics when calculating proportions. Additionally, when the filter is data driven, such as norm2Filter, the subset semantics are applied to the data used to fit the filter possibly resulting in quite different, and usually more desirable, results.

%on% Used in conjunction with a transformList to create a transformFilter. This filter is similar to the subset filter in that the filtering operation takes place on transformed values rather than the original values.

filter A more formal version of %in%, this method returns a filterResult object that can be used in subsequent filter operations as well as providing more metadata about the results of the filtering operation. See the documenation for filter methods for details.

summarizeFilter When implementing a new filter this method is used to update the filterDetails slot of a filterResult. It is optional and typically only needs to be implemented for data-driven filters.

Author(s)

B. Ellis, P.D. Haaland and N. LeMeur

See Also

transform, filter

filter-in-methods *Filter-specific membership methods*

Description

Membership methods must be defined for every object of type `filter` with respect to a `flowFrame` object. The operation is considered to be general and may return a `logical`, `numeric` or `factor` vector that will be handled appropriately. The ability to handle logical matrices as well as vectors is also planned but not yet implemented.

Usage

```
x %in% table
```

Arguments

`x`	a `flowFrame`
`table`	an object of type `filter` or `filterResult` or one of their derived classes, representing a gate, filter, or result to check for the membership of x

Value

Vector of type `logical`, `numeric` or `factor` depending on the arguments

Author(s)

F.Hahne, B. Ellis

filter-methods *Filter FCS files*

Description

These methods link filter descriptions to a particular set of flow cytometry data allowing for the lightweight calculation of summary statistics common to flow cytometry analysis.

Usage

```
filter(x, filter, method = c("convolution", "recursive"),
sides = 2L, circular = FALSE, init = NULL)
```

Arguments

`x`	Object of class `flowFrame` or `flowSet`.
`filter`	An object of class `filter` or a named list `filters`.
`method, sides, circular, init`	These arguments are not used.

Details

The `filter` method conceptually links a filter description, represented by a `filter` object, to a particular `flowFrame`. This is accomplished via the `filterResult` object, which tracks the linked frame as well as caching the results of the filtering operation itself, allowing for fast calculation of certain summary statistics such as the percentage of events accepted by the `filter`. This method exists chiefly to allow the calculation of these statistics without the need to first `Subset` a `flowFrame`, which can be quite large.

When applying on a `flowSet`, the `filter` argument can either be a single `filter` object, in which case it is recycled for all frames in the set, or a named list of `filter` objects. The names are supposed to match the frame identifiers (i.e., the output of `sampleNames(x)` of the `flowSet`. If some frames identifiers are missing, the particular frames are skipped during filtering. Accordingly, all `filters` in the filter list that can't be mapped to the `flowSet` are ignored. Note that all `filter` objects in the list must be of the same type, e.g. `rectangleGates`.

Value

A `filterResult` object or a `filterResultList` object if x is a `flowSet`. Note that `filterResult` objects are themselves filters, allowing them to be used in filter expressions or `Subset` operations.

Author(s)

F Hahne, B. Ellis, N. Le Meur

See Also

`Subset`, `filter`, `filterResult`

Examples

```
## Filtering a flowFrame
samp <- read.FCS(system.file("extdata","0877408774.B08", package="flowCore"))
rectGate <- rectangleGate(filterId="nonDebris","FSC-H"=c(200,Inf))
fr <- filter(samp,rectGate)
class(fr)
summary(fr)

## filtering a flowSet
data(GvHD)
foo <- GvHD[1:3]
fr2 <- filter(foo, rectGate)
class(fr2)
summary(fr2)

## filtering a flowSet using different filters for each frame
rg2 <- rectangleGate(filterId="nonDebris","FSC-H"=c(300,Inf))
rg3 <- rectangleGate(filterId="nonDebris","FSC-H"=c(400,Inf))
flist <- list(rectGate, rg2, rg3)
names(flist) <- sampleNames(foo)
fr3 <- filter(foo, flist)
```

filter-on-methods *Methods for Function %on% in Package 'flowCore'*

Description

This operator is used to construct a `transformFilter` that first applies a `transformList` to the data before applying the `filter` operation. You may also apply the operator to a `flowFrame` or `flowSet` to obtain transformed values specified in the list.

Usage

```
e1 %on% e2
```

Arguments

e1	a `filter`, `transform`, or `transformList` object
e2	a `transform`, `transformList`, `flowFrame`, or `flowSet` object

Author(s)

B. Ellis

Examples

```
samp <- read.FCS(system.file("extdata","0877408774.B08", package="flowCore"))
plot(transform("FSC-H"=log, "SSC-H"=log) %on% samp)


rectangle <- rectangleGate(filterId="rectangleGateI","FSC-H"=c(4.5, 5.5))
sampFiltered <- filter(samp, rectangle %on% transform("FSC-H"=log, "SSC-H"=log))
res <- Subset(samp, sampFiltered)

plot(transform("FSC-H"=log, "SSC-H"=log) %on% res)
```

filterDetails-methods *Obtain details about a filter operation*

Description

A filtering operation captures details about its metadata and stores it in a `filterDetails` slot in a `filterResult` object that is accessed using the `filterDetails` method. Each set of metadata is indexed by the `filterId` of the filter allowing for all the metadata in a complex filtering operation to be recovered after the final filtering.

Methods

filterDetails(result = "filterResult", filterId = "missing") When no particular `filterId` is specified all the details are returned

filterDetails(result = "filterResult", filterId = "ANY") You can also obtain a particular subset of details

Author(s)

B. Ellis, P.D. Haaland and N. LeMeur

`filterList-class` *Class "filterList"*

Description

Container for a list of `filter` objects. The class mainly exists for method dispatch.

Usage

```
filterList(x, filterId=identifier(x[[1]]))
```

Arguments

`x`	A list of `filter` objects.
`filterId`	The global identifier of the filter list. As default, we take the filterId of the first `filter` object in `x`.

Value

A `filterList` object for the constructor.

Slots

`.Data` Object of class `"list"`. The class directly extends `list`, and this slot holds the list data.

`filterId` Object of class `"character"`. The identifier for the object.

Objects from the Class

Objects are created from regular lists using the constructor `filterList`.

Extends

Class `"list"`, from data part.

Methods

show `signature(object = "filterList")`: Print details about the object.

identifier, identifier<- `signature(object = "filterList")`: Accessor and replacement method for the object's filterId slot.

Author(s)

Florian Hahne

See Also

`filter`,

Examples

```
f1 <- rectangleGate(FSC=c(100,200), filterId="testFilter")
f2 <- rectangleGate(FSC=c(200,400))
fl <- filterList(list(a=f1, b=f2))
fl
identifier(fl)
```

---

filterReference-class *Class filterReference*

Description

A reference to another filter inside a reference. Users should generally not be aware that they are using this class.

Slots

`name` The R name of the referenced filter.

`env` The environment where the filter must live.

`filterId` The filterId, not really used since you always resolve.

Objects from the Class

Objects are generally not created by users so there is no constructor function.

Extends

Class `"filter"`, directly.

Author(s)

B. Ellis

filterResult-class *Class "filterResult"*

Description

Container to store the result of applying a `filter` on a `flowFrame` object

Slots

`frameId` Object of class `"character"` referencing the `flowFrame` object filtered. Used for sanity checking.

`filterDetails` Object of class `"list"` describing the filter applied.

`filterId` Object of class `"character"` referencing the filter applied.

Extends

Class `"filter"`, directly.

Methods

== test equality

Author(s)

B. Ellis, N. LeMeur

See Also

`filter`, `"logicalFilterResult"`, `"multipleFilterResult"`, `"randomFilterResult"`

Examples

```
showClass("filterResult")
```

filterResultList-class *Class "filterResultList"*

Description

Container to store the result of applying a `filter` on a `flowSet` object

Slots

`.Data` Object of class `"list"`. The class directly extends `list`, and this slot holds the list data.

`frameId` Object of class `"character"` The IDs of the `flowFrames` in the filtered `flowSet`.

`filterDetails` Object of class `"list"`. Since `filterResultList` inherits from `filterResult`, this slot has to be set. It contains only the input filter.

`filterId` Object of class `"character"`. The identifier for the object.

Objects from the Class

Objects are created by applying a `filter` on a `flowSet`. The user doesn't have to deal with manual object instantiation.

Extends

Class `"list"`, from data part. Class `"filterResult"`, directly. Class `"concreteFilter"`, by class "filterResult", distance 2. Class `"filter"`, by class "filterResult", distance 3.

Methods

[`signature(x = "filterResultList", i = "ANY")`: Subset to `filterResultList`.

[[`signature(x = "filterResultList", i = "ANY")`: Subset to individual `filterResult`.

names `signature(x = "filterResultList")`: Accessor to the frameId slot.

parameters `signature(object = "filterResultList")`: Return parameters on which data has been filtered.

show `signature(object = "filterResultList")`: Print details about the object.

split `signature(x = "flowSet", f = "filterResultList")`: Split a `flowSet` based on the results in the `filterResultlIst`. See `split` for details.

summary `signature(object = "filterResultList")`: Summarize the filtering operation. This creates a `filterSummaryList` object.

Author(s)

Florian Hahne

See Also

`filter`, `filterResult`, `logicalFilterResult`, `multipleFilterResult`, `randomFilterResult`

Examples

```
library(flowStats)
## Loading example data and creating a curv1Filter
data(GvHD)
dat <- GvHD[1:3]
c1f <- curv1Filter(filterId="myCurv1Filter", x=list("FSC-H"), bwFac=2)

## applying the filter
```

```
fres <- filter(dat, c1f)
fres

## subsetting the list
fres[[1]]
fres[1:2]

## details about the object
parameters(fres)
names(fres)
summary(fres)

## splitting based on the filterResults
split(dat, fres)
```

`filters-class` *Class "filters" and "filtersList"*

Description

The `filters` class is the container for a list of `filter` objects.

The `filtersList` class is the container for a list of `filters` objects.

Usage

```
filters(x)

filtersList(x)
```

Arguments

x	A list of `filter` or `filters` objects.

Details

The `filters` class mainly exists for displaying multiple filters/gates on one single panel(flowFrame) of `xyplot`. Note that it is different from `filterList` class which is to be applied to a flowSet. In other words, `filter` objects of a `fliterList` are to be applied to different flowFrames. However,all of `filter` objects of a `filters` object are for one single flowFrame, more specifically for one pair of projections(parameters).So these filters should share the common parameters.

And `filtersList` is a list of `filters` objects, which are to be applied to a flowSet.

Value

A `filters` or `filtersList` object from the constructor

Slots

`.Data` Object of class `"list"`. The class directly extends `list`, and this slot holds the list data.

Extends

Class `"list"`

Objects from the Class

Objects are created from regular lists using the constructors `filters` and `filtersList`:

```
filters(x)
filtersList(x)
```

Author(s)

Mike Jiang

See Also

`filter`, `filterList`

`filterSummary-class` *Class "filterSummary"*

Description

Class and methods to handle the summary information of a gating operation.

Usage

```
## S4 method for signature 'filterResult'
summary(object, ...)
```

Arguments

`object`	An object inheriting from class `filterResult` which is to be summarized.
`...`	Further arguments that are passed to the generic.

Details

Calling `summary` on a `filterResult` object prints summary information on the screen, but also creates objects of class `filterSummary` for computational access.

Value

An object of class `filterSummary` for the `summary` constructor, a named list for the subsetting operators. The `$` operator returns a named vector of the respective value, where each named element corresponds to one sub-population.

Slots

`name` Object of class `"character"` The name(s) of the populations created in the filtering operation. For a `logicalFilterResult` this is just a single value; the name of the `link{filter}`.

`true` Object of class `"numeric"`. The number of events within the population(s).

`count` Object of class `"numeric"`. The total number of events in the gated `flowFrame`.

`p` Object of class `"numeric"` The percentage of cells in the population(s).

Objects from the Class

Objects are created by calling `summary` on a `link{filterResult}` object. The user doesn't have to deal with manual object instantiation.

Methods

[[`signature(x = "filterSummary", i = "numeric")`: Subset the `filterSummary` to a single population. This only makes sense for `multipleFilterResults`. The output is a list of summary statistics.

[[`signature(x = "filterSummary", i = "character")`: see above

$ `signature(x = "filterSummary", name = "ANY")`: A list-like accessor to the slots and more. Valid values are `n` and `count` (those are identical), `true` and `in` (identical), `false` and `out` (identical), `name`, `p` and `q` (`1-p`).

coerce `signature(from = "filterSummary", to = "data.frame")`: Coerce object to `data.frame`.

length `signature(x = "filterSummary")`: The number of populations in the `fitlerSummary`.

names `signature(x = "filterSummary")`: The names of the populations in the `filterSummary`.

print `signature(x = "filterSummary")`: Print details about the object.

show `signature(object = "filterSummary")`: Print details about the object.

toTable `signature(x = "filterSummary")`: Coerce object to `data.frame`.

Author(s)

Florian Hahne, Byron Ellis

See Also

`filterResult`, `logicalFilterResult`, `multipleFilterResult`, `flowFrame` `filterSummaryList`

Examples

```
library(flowStats)

## Loading example data, creating and applying a curv1Filter
dat <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))
c1f <- curv1Filter(filterId="myCurv1Filter", x=list("FSC-H"), bwFac=2)
fres <- filter(dat, c1f)
```

```
## creating and showing the summary
summary(fres)
s <- summary(fres)

## subsetting
s[[1]]
s[["peak 2"]]

##accessing details
s$true
s$n
toTable(s)
```

---

filterSummaryList-class

Class "filterSummaryList"

Description

Class and methods to handle summary statistics for from filtering operations on whole flowSets.

Arguments

object	An object of class. filterResultList which is to be summarized.
...	Further arguments that are passed to the generic.

Details

Calling summary on a filterResultList object prints summary information on the screen, but also creates objects of class filterSummaryList for computational access.

Value

An object of class filterSummaryList.

Slots

.Data Object of class "list". The class directly extends list, and this slot holds the list data.

Usage

summary(object, ...)

Objects from the Class

Objects are created by calling summary on a link{filterResultList} object. The user doesn't have to deal with manual object instantiation.

Extends

Class "list", from .Data part.

Methods

toTable signature(x = "filterSummaryList"): Coerce object to data.frame. Additional factors are added to indicate list items in the original object.

Author(s)

Florian Hahne

See Also

filterResult, filterResultList, logicalFilterResult, multipleFilterResult, flowFrame filterSummary

Examples

```
library(flowStats)

## Loading example data, creating and applying a curv1Filter
data(GvHD)
dat <- GvHD[1:3]
c1f <- curv1Filter(filterId="myCurv1Filter", x=list("FSC-H"), bwFac=2)
fres <- filter(dat, c1f)

## creating and showing the summary
summary(fres)
s <- summary(fres)

## subsetting
s[[1]]

##accessing details
toTable(s)
```

---

flowFrame-class *'flowFrame': a class for storing observed quantitative properties for a population of cells from a FACS run*

Description

This class represents the data contained in a FCS file or similar data structure. There are three parts of the data:

1. a numeric matrix of the raw measurement values with rows=events and columns=parameters

2. annotation for the parameters (e.g., the measurement channels, stains, dynamic range)
3. additional annotation provided through keywords in the FCS file

Details

Objects of class `flowFrame` can be used to hold arbitrary data of cell populations, acquired in flow-cytometry.

FCS is the Data File Standard for Flow Cytometry, the current version is FCS 3.0. See the vignette of this package for additional information on using the object system for handling of flow-cytometry data.

Slots

`exprs` Object of class `matrix` containing the measured intensities. Rows correspond to cells, columns to the different measurement channels. The `colnames` attribute of the matrix is supposed to hold the names or identifiers for the channels. The `rownames` attribute would usually not be set.

`parameters` An `AnnotatedDataFrame` containing information about each column of the `flowFrame`. This will generally be filled in by `read.FCS` or similar functions using data from the FCS keywords describing the parameters.

`description` A list containing the meta data included in the FCS file.

Creating Objects

Objects can be created using

```
new("flowFrame",
exprs = ...., Object of class matrix
parameters = ...., Object of class AnnotatedDataFrame
description = ...., Object of class list
)
```

or the constructor `flowFrame`, with mandatory arguments `exprs` and optional arguments `parameters` and `description`.

```
flowFrame(exprs, parameters, description=list())
```

To create a `flowFrame` directly from an FCS file, use function `read.FCS`. This is the recommended and safest way of object creation, since `read.FCS` will perform basic data quality checks upon import. Unless you know exactly what you are doing, creating objects using `new` or the constructor is discouraged.

Methods

There are separate documentation pages for most of the methods listed here which should be consulted for more details.

`[` Subsetting. Returns an object of class `flowFrame`. The subsetting is applied to the `exprs` slot, while the `description` slot is unchanged. 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), `flowFrames` can be subset via `filterResult` and `filter` objects.

Usage:

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

Note that the value of argument drop is ignored when subsetting flowFrames.

**$** Subsetting by channel name. This is similar to subsetting of columns of data.frames, i.e., frame$FSC.H is equivalent to frame[, "FSC.H"]. Note that column names may have to be quoted if they are no valid R symbols (e.g. frame$"FSC-H").

exprs, exprs<- Extract or replace 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 flowFrame, but all have to be defined there).

Usage:

```
exprs(flowFrame)
exprs(flowFrame) <- value
```

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

Usage:

```
head(flowFrame)
tail(flowFrame)
```

description, description<- Extract the whole list of annotation keywords and their corresponding values or replace values by keyword (description<- is equivalent to keyword<-). Usually one would only be interested in a subset of keywords, in which case the keyword method is more appropriate. The optional hideInternal parameter can be used to exclude internal FCS parameters starting with $.

Usage:

```
description(flowFrame)
description(flowFrame) <- value
```

keyword, keyword<- Extract ore replace one or more entries from the description slot by keyword. Methods are defined for character vectors (select a keyword by name), functions (select a keyword by evaluating a function on their content) and for lists (a combination of the above). See keyword for details.

Usage:

```
keyword(flowFrame)
keyword(flowFrame, character)
keyword(flowFrame, list)
keyword(flowFrame) <- list(value)
```

parameters, parameters<- Extract parameters and return an object of class AnnotatedDataFrame, or replace such an object. To access the actual parameter annotation, use pData(parameters(frame)). 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(flowFrame)
parameters(flowFrame) <- value
```

show Display details about the `flowFrame` object.

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

Usage:

```
summary(flowFrame)
```

plot Basic plots for `flowFrame` 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. This simple method still uses the legacy `flowViz` package. For far more sophisticated plotting of flow cytometry data, see the `ggcyto` package.

Usage:

```
plot(flowFrame, ...)
plot(flowFrame, character, ...)
plot(flowFrame, smooth=FALSE, ...)
```

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

Usage:

```
ncol(flowFrame)
nrow(flowFrame)
dim(flowFrame)
```

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(flowFrame)
colnames(flowFrame)
colnames(flowFrame) <- value
```

names Extract pretty formated names of the parameters including parameter descriptions.

Usage:

```
names(flowFrame)
```

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

Usage:

```
identifier(flowFrame)
```

range Get instrument or actual data range of the `flowFame`. 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`flowFrames`.

parameters:

x: flowFrame 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(flowFrame, function, ...)
each_col(flowFrame, function, ...)
```

transform Apply a transformation function on a flowFrame object. This uses R's transform function by treating the flowFrame 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(flowFrame, translist, ...)
```

filter Apply a filter object on a flowFrame 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(flowFrame, filter)
```

split Split flowFrame 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(flowFrame, filter, flowSet=FALSE, ...)
split(flowFrame, filterResult, flowSet=FALSE, ...)
split(flowFrame, factor, flowSet=FALSE, ...)
```

Subset Subset a flowFrame 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(flowFrame, filter)
Subset(flowFrame, logical)
```

cbind2 Expand a flowFrame by the data in a numeric matrix of the same length. The matrix must have column names different from those of the flowFrame. The additional method for numerics only raises a useful error message.

Usage:

```
cbind2(flowFrame, matrix)
cbind2(flowFrame, numeric)
```

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

Usage:

```
compensate(flowFrame, matrix) compensate(flowFrame, data.frame)
```

decompensate Reverse the application of a compensation matrix (or a compensation object) on a flowFrame object. This returns a decompensated flowFrame.

Usage:

```
decompensate(flowFrame, matrix) decompensate(flowFrame, data.frame)
```

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

Usage:

```
spillover(flowFrame)
```

== Test equality between two `flowFrames`

<, >, <=, >= These operators basically treat the `flowFrame` as a numeric matrix.

`initialize(flowFrame)`**:** Object instantiation, used by `new`; not to be called directly by the user.

Author(s)

F. Hahne, B. Ellis, P. Haaland and N. Le Meur

See Also

`flowSet`, `read.FCS`

Examples

```
## load example data
data(GvHD)
frame <- GvHD[[1]]

## subsetting
frame[1:4,]
frame[,3]
frame[,"FSC-H"]
frame$"SSC-H"

## accessing and replacing raw values
head(exprs(frame))
exprs(frame) <- exprs(frame)[1:3000,]
frame
exprs(frame) <- exprs(frame)[,1:6]
frame

## access FCS keywords
head(keyword(frame))
keyword(frame, c("FILENAME", "$FIL"))

## parameter annotation
parameters(frame)
pData(parameters(frame))

## summarize frame data
summary(frame)

## plotting
plot(frame)
if(require(flowViz)){
plot(frame)
```

```
plot(frame, c("FSC-H", "SSC-H"))
plot(frame[,1])
plot(frame, c("FSC-H", "SSC-H"), smooth=FALSE)
}

## frame dimensions
ncol(frame)
nrow(frame)
dim(frame)

## accessing and replacing parameter names
featureNames(frame)
all(featureNames(frame) == colnames(frame))
colnames(frame) <- make.names(colnames(frame))
colnames(frame)
parameters(frame)$name
names(frame)

## accessing a GUID
identifier(frame)
identifier(frame) <- "test"

##  range of a frame
range(frame) #instrument range
range(frame, type = "data") #actual data range
range(frame)$FSC.H

## iterators
head(each_row(frame, mean))
head(each_col(frame, mean))

## transformation
opar <- par(mfcol=c(1:2))
if(require(flowViz))
plot(frame, c("FL1.H", "FL2.H"))
frame <- transform(frame, transformList(c("FL1.H", "FL2.H"), log))
if(require(flowViz))
plot(frame, c("FL1.H", "FL2.H"))
par(opar)
range(frame)

## filtering of flowFrames
rectGate <- rectangleGate(filterId="nonDebris","FSC.H"=c(200,Inf))
fres <- filter(frame, rectGate)
summary(fres)

## splitting of flowFrames
split(frame, rectGate)
split(frame, rectGate, flowSet=TRUE)
split(frame, fres)
f <- cut(exprs(frame$FSC.H), 3)
split(frame, f)
```

```
## subsetting according to filters and filter results
Subset(frame, rectGate)
Subset(frame, fres)
Subset(frame, as.logical(exprs(frame$FSC.H) < 300))
frame[rectGate,]
frame[fres,]

## accessing the spillover matrix
try(spillover(frame))

## check equality
frame2 <- frame
frame == frame2
exprs(frame2) <- exprs(frame)*2
frame == frame2
```

`flowSet-class` *'flowSet': a class for storing flow cytometry raw data from quantitative cell-based assays*

Description

This class is a container for a set of `flowFrame` objects

Slots

`frames` An `environment` containing one or more `flowFrame` objects.

`phenoData` An `AnnotatedDataFrame` containing the phenotypic data for the whole data set. Each row corresponds to one of the `flowFrame`s in the `frames` slot. The `sampleNames` of `phenoData` (see below) must match the names of the `flowFrame` in the `frames` environment.

Creating Objects

Objects can be created using

```
new('flowSet',
frames = ...., # environment with flowFrames
phenoData = .... # object of class AnnotatedDataFrame
colnames = .... # object of class character
)
```

or via the constructor `flowSet`, which takes arbitrary numbers of flowFrames, either as a list or directly as arguments, along with an optional `AnnotatedDataFrame` for the `phenoData` slot and a `character` scalar for the `name` by which the object can be referenced.

```
flowSet(..., phenoData)
```

Alternatively, `flowSets` can be coerced from `list` and `environment` objects.

```
as(list("A"=frameA,"B"=frameB),"flowSet")
```

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

Methods

[, [[Subsetting. x[i] where i is a scalar, returns a flowSet object, and x[[i]] a flowFrame object. In this respect the semantics are similar to the behavior of the subsetting operators for lists. x[i, j] returns a flowSet for which the parameters of each flowFrame have been subset according to j, x[[i,j]] returns the subset of a single flowFrame for all parameters in j. Similar to data frames, valid values for i and j are logicals, integers and characters.

Usage:

```
flowSet[i]
flowSet[i,j]
flowSet[[i]]
```

**$** Subsetting by frame name. This will return a single flowFrame object. Note that names may have to be quoted if they are no valid R symbols (e.g. flowSet$"sample 1"

colnames, colnames<- Extract or replace the colnames slot.

Usage:

```
colnames(flowSet)
colnames(flowSet) <- value
```

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

Usage:

```
identifier(flowSet)
identifier(flowSet) <- value
```

phenoData, phenoData<- Extract or replace the AnnotatedDataFrame from the phenoData slot.

Usage:

```
phenoData(flowSet)
phenoData(flowSet) <- value
```

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

Usage:

```
pData(flowSet)
pData(flowSet)$someColumn <- value
```

varLabels, varLabels<- Extract and set varLabels in the AnnotatedDataFrame of the phenoData slot.

Usage:

```
varLabels(flowSet)
varLabels(flowSet) <- value
```

sampleNames Extract and replace sample names from the phenoData object. Sample names correspond to frame identifiers, and replacing them will also replace the GUID slot for each frame. Note that sampleName need to be unique.

Usage:

```
sampleNames(flowSet)
sampleNames(flowSet) <- 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:

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

length number of `flowFrame` objects in the set.

Usage:

```
length(flowSet)
```

show display object summary.

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

Usage:

```
summary(flowSet)
```

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

Usage:

```
fsApply(flowSet, function, ...)
fsApply(flowSet, function, use.exprs=TRUE, ...)
```

compensate Apply a compensation matrix on all frames in a `flowSet` object. See separate documentation for details.

Usage:

```
compensate(flowSet, matrix)
```

transform Apply a transformation function on all frames of a `flowSet` object. See separate documentation for details.

Usage:

```
transform(flowSet, ...)
```

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

Usage:

```
filter(flowSet, filter)
filter(flowSet, list(filters))
```

split Split all `flowSet` 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 `flowSet`. This returns a list of `flowFrame`s or an object of class `flowSet` if the `flowSet` argument is set to `TRUE`. Alternatively, a `flowSet` can be split into separate subsets according to a factor (or any vector that can be coerced into factors), similar to the behaviour of `split` for lists. This will return a list of `flowSet`s. See `split` for details.

Usage:

```
split(flowSet, filter)
split(flowSet, filterResult)
split(flowSet, list(filters))
split(flowSet, factor)
```

Subset Returns a `flowSet` of `flowFrame`s that have been subset according to a `filter` or `filterResult`, or according to a list of such items of equal length as the `flowSet`.

Usage:

```
Subset(flowSet, filter)
Subset(flowSet, filterResult)
Subset(flowSet, list(filters))
```

rbind2 Combine two `flowSet` objects, or one `flowSet` and one `flowFrame` object.

Usage:

```
rbind2(flowSet, flowSet)
rbind2(flowSet, flowFrame)
```

spillover Compute spillover matrix from a compensation set. See separate documentation for details.

Important note on storage and performance

The bulk of the data in a `flowSet` object is stored in an `environment`, and is therefore not automatically copied when the `flowSet` object is copied. If `x` is an object of class `flowSet`, then the code

```
y <- x
```

will create an object `y` that contains copies of the `phenoData` and administrative data in `x`, but refers to the *same* environment with the actual fluorescence data. See below for how to create proper copies.

The reason for this is performance. The pass-by-value semantics of function calls in `R` can result in numerous copies of the same data object being made in the course of a series of nested function calls. If the data object is large, this can result in considerable cost of memory and performance. `flowSet` objects are intended to contain experimental data in the order of hundreds of Megabytes, which can effectively be treated as read-only: typical tasks are the extraction of subsets and the calculation of summary statistics. This is afforded by the design of the `flowSet` class: an object of that class contains a `phenoData` slot, some administrative information, and a *reference* to an environment with the fluorescence data; when it is copied, only the reference is copied, but not the potentially large set of fluorescence data themselves.

However, note that subsetting operations, such as `y <- x[i]` do create proper copies, including a copy of the appropriate part of the fluorescence data, as it should be expected. Thus, to make a proper copy of a `flowSet` `x`, use `y <- x[seq(along=x)]`

Author(s)

F. Hahne, B. Ellis, P. Haaland and N. Le Meur

See Also

flowFrame, read.flowSet

Examples

```
## load example data and object creation
data(GvHD)

## subsetting to flowSet
set <- GvHD[1:4]
GvHD[1:4,1:2]
sel <- sampleNames(GvHD)[1:2]
GvHD[sel, "FSC-H"]
GvHD[sampleNames(GvHD) == sel[1], colnames(GvHD[1]) == "SSC-H"]

## subsetting to flowFrame
GvHD[[1]]
GvHD[[1, 1:3]]
GvHD[[1, "FSC-H"]]
GvHD[[1, colnames(GvHD[1]) == "SSC-H"]]
GvHD$s5a02

## constructor
flowSet(GvHD[[1]], GvHD[[2]])
pd <- phenoData(GvHD)[1:2,]
flowSet(s5a01=GvHD[[1]], s5a02=GvHD[[2]],phenoData=pd)

## colnames
colnames(set)
colnames(set) <- make.names(colnames(set))

## object name
identifier(set)
identifier(set) <- "test"

## phenoData
pd <- phenoData(set)
pd
pd$test <- "test"
phenoData(set) <- pd
pData(set)
varLabels(set)
varLabels(set)[6] <- "Foo"
varLabels(set)

## sampleNames
sampleNames(set)
sampleNames(set) <- LETTERS[1:length(set)]
sampleNames(set)

## keywords
keyword(set, list("transformation"))
```

```
## length
length(set)

## compensation
samp <- read.flowSet(path=system.file("extdata","compdata","data",
package="flowCore"))
cfile <- system.file("extdata","compdata","compmatrix", package="flowCore")
comp.mat <- read.table(cfile, header=TRUE, skip=2, check.names = FALSE)
comp.mat
summary(samp[[1]])
samp <- compensate(samp, as.matrix(comp.mat))
summary(samp[[1]])

## transformation
opar <- par(mfcol=c(1:2))
plot(set[[1]], c("FL1.H", "FL2.H"))
set <- transform(set, transformList(c("FL1.H", "FL2.H"), log))
plot(set[[1]], c("FL1.H", "FL2.H"))
par(opar)

## filtering of flowSets
rectGate <- rectangleGate(filterId="nonDebris", FSC.H=c(200,Inf))
fres <- filter(set, rectGate)
class(fres)
summary(fres[[1]])
rectGate2 <- rectangleGate(filterId="nonDebris2", SSC.H=c(300,Inf))
fres2 <- filter(set, list(A=rectGate, B=rectGate2, C=rectGate, D=rectGate2))

## Splitting frames of a flowSet
split(set, rectGate)
split(set[1:2], rectGate, populatiuon="nonDebris2+")
split(set, c(1,1,2,2))

## subsetting according to filters and filter results
Subset(set, rectGate)
Subset(set, filter(set, rectGate))
Subset(set, list(A=rectGate, B=rectGate2, C=rectGate, D=rectGate2))

## combining flowSets
rbind2(set[1:2], set[3:4])
rbind2(set[1:3], set[[4]])
rbind2(set[[4]], set[1:2])
```

`flowSet_to_list` *Convert a flowSet to a list of flowFrames*

Description

This is a simple helper function for splitting a `flowSet` in to a list of its constituent `flowFrames`.

Usage

```
flowSet_to_list(fs)
```

Arguments

fs	a flowSet

Value

a list of flowFrames

---

fr_append_cols *Append data columns to a flowFrame*

Description

Append data columns to a flowFrame

Usage

```
fr_append_cols(fr, cols)
```

Arguments

fr	A flowFrame.
cols	A numeric matrix containing the new data columns to be added. Must have unique 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 .

Value

A flowFrame

Author(s)

Mike Jiang

Examples

```
data(GvHD)
tmp <- GvHD[[1]]

kf <- kmeansFilter("FSC-H"=c("Pop1","Pop2","Pop3"), filterId="myKmFilter")
fres <- filter(tmp, kf)
cols <- as.integer(fres@subSet)
cols <- matrix(cols, dimnames = list(NULL, "km"))
tmp <- fr_append_cols(tmp, cols)

tmpfile <- tempfile()
write.FCS(tmp, tmpfile)
```

`fsApply` *Apply a Function over values in a flowSet*

Description

`fsApply`, like many of the `apply`-style functions in R, acts as an iterator for `flowSet` objects, allowing the application of a function to either the `flowFrame` or the data matrix itself. The output can then be reconstructed as either a `flowSet`, a list, or a matrix depending on options and the type of objects returned.

Usage

```
fsApply(x, FUN, ..., simplify=TRUE, use.exprs=FALSE)
```

Arguments

`x`	`flowSet` to be used
`FUN`	the function to be applied to each element of `x`
`...`	optional arguments to `FUN`.
`simplify`	logical (default: TRUE); if all true and all objects are `flowFrame` objects, a `flowSet` object will be constructed. If all of the values are of the same type there will be an attempt to construct a vector or matrix of the appropriate type (e.g. all numeric results will return a matrix).
`use.exprs`	logical (default: FALSE); should the `FUN` be applied on the `flowFrame` object or the expression values.

Author(s)

B. Ellis

See Also

`apply`, `sapply`

Examples

```
fcs.loc <- system.file("extdata",package="flowCore")
file.location <- paste(fcs.loc, dir(fcs.loc), sep="/")
samp <- read.flowSet(file.location[1:3])

#Get summary information about each sample.
fsApply(samp,summary)

#Obtain the median of each parameter in each frame.
fsApply(samp,each_col,median)
```

---

getChannelMarker *get channel and marker information from a* flowFrame *that matches to the given keyword*

Description

This function tries best to guess the flow parameter based on the keyword supplied by name It first does a complete word match(case insensitive) between name and flow channels and markers. If there are duplcated matches, throw the error. If no matches, it will try the partial match.

Usage

```
getChannelMarker(frm, name, ...)
```

Arguments

frm	flowFrame object
name	character the keyword to match
...	other arguments: not used.

Value

an one-row data.frame that contains "name"(i.e. channel) and "desc"(i.e. stained marker) columns.

getIndexSort *Extract Index Sorted Data from an FCS File*

Description

Retrieve a data frame of index sorted data and sort indices from an FCS file.

Details

The input FCS file should already be compensated. Index sorting permits association of cell-level fluorescence intensities with downstream data collection on the sorted cells. Cells are sorted into a plate with `X,Y` coordinates, and those coordinates are stored in the FCS file.

This function will extract the data frame of flow data and the `X,Y` coordinates for the cell-level data, which can be written to a text file, or concatenated with sample-level information and analyzed in R. The coordinates are names 'XLoc','YLoc', and a 'name' column is also prepended with the FCS file name.

Value

Matrix of fluorescence intensities and sort indices for plate location. When no index sorting data is available, invisibly returns 0. Test for 0 to check success.

Methods

getIndexSort(x = "flowFrame") Return a matrix of fluorescence intensities and indices into the sorting plate for each cell.

Author(s)

G. Finak

Examples

```
samp <- read.FCS(system.file("extdata","0877408774.B08", package="flowCore"))
# This will return a message that no index sorting data is available
getIndexSort(samp)
```

GvHD *Extract of a Graft versus Host Disease monitoring experiment (Rizzieri et al., 2007)*

Description

A flow cytometry high throughput screening was used to identify biomarkers that would predict the development of GvHD. The GvHD dataset is an extract of a collection of weekly peripheral blood samples obtained from patients following allogenic blood and marrow transplant. Samples were taken at various time points before and after graft.

Usage

```
data(GvHD)
```

Format

The format is an object of class `flowSet` composed of 35 `flowFrames`. Each `flowFrame` corresponds to one sample at one time point. The `phenodata` lists:

Patient The patient Id code

Visit The number of visits to the hospital

Days The number of days since the graft. Negative values correpond to days before the graft.

Grade Grade of the cancer

Details

This GvHD dataset represents the measurements of one biomarker (leukocyte) for 5 patients over 7 visits (7 time points). The blood samples were labeled with four different fluorescent probes to identify the biomarker and the fluorescent intensity was determined for at least ten thousand cells per sample.

Source

Complete dataset available at http://www.ficcs.org/software.html#Data_Files, the Flow Informatics and Computational Cytometry Society website (FICCS)

References

Rizzieri DA et al. J Clin Oncol. 2007 Jan 16; [Epub ahead of print] PMID: 17228020

`hyperlog-class` *Class "hyperlog"*

Description

Hyperlog transformation of a parameter is defined by the function

$$f(parameter, a, b) = rootEH(y, a, b) - parameter$$

where EH is a function defined by

$$EH(y, a, b) = 10^{(\frac{y}{a})} + \frac{b * y}{a} - 1, y >= 0$$

$$EH(y, a, b) = -10^{(\frac{-y}{a})} + \frac{b * y}{a} + 1, y < 0$$

Slots

`.Data` Object of class `"function"`.

`a` Object of class `"numeric"` – numeric constant treater than zero.

`b` Object of class `"numeric"` numeric constant greater than zero.

`parameters` Object of class `"transformation"` – flow parameter to be transformed.

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

Objects from the Class

Objects can be created by calls to the constructor `hyperlog(parameter,a,b,transformationId)`

Extends

Class `"singleParameterTransform"`, directly.

Class `"transform"`, by class "singleParameterTransform", distance 2.

Class `"transformation"`, by class "singleParameterTransform", distance 3.

Class `"characterOrTransformation"`, by class "singleParameterTransform", distance 4.

Note

The transformation object can be evaluated using the eval method by passing the data frame as an argument.The transformed parameters are returned as a matrix with a single column. (See example below)

Author(s)

Gopalakrishnan N, F.Hahne

References

Gating-ML Candidate Recommendation for Gating Description in Flow Cytometry V 1.5

See Also

EHtrans

Other mathematical transform classes: EHtrans-class, asinht-class, asinhtGml2-class, dg1polynomial-class, exponential-class, hyperlogtGml2-class, invsplitscale-class, lintGml2-class, logarithm-class, logicletGml2-class, logtGml2-class, quadratic-class, ratio-class, ratiotGml2-class, sinht-class, splitscale-class, squareroot-class, unitytransform-class

Examples

```
dat <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))
hlog1<-hyperlog("FSC-H",a=1,b=1,transformationId="hlog1")
transOut<-eval(hlog1)(exprs(dat))
```

---

hyperlogtGml2-class *Class hyperlogtGml2*

Description

Hyperlog transformation parameterized according to Gating-ML 2.0.

Details

hyperlogtGml2 is defined by the following function:

$$bound(hyperlog, boundMin, boundMax) = max(min(hyperlog, boundMax), boundMin))$$

where

$$hyperlog(x, T, W, M, A) = root(EH(y, T, W, M, A) - x)$$

and EH is defined as:

$$EH(y, T, W, M, A) = ae^{by} + cy - f$$

where

- x is the value that is being transformed (an FCS dimension value). Typically, x is less than or equal to T, although the transformation function is also defined for x greater than T.
- y is the result of the transformation.
- T is greater than zero and represents the top of scale value.
- M is greater than zero and represents the number of decades that the true logarithmic scale approached at the high end of the Hyperlog scale would cover in the plot range.
- W is positive and not greater than half of M and represents the number of such decades in the approximately linear region.

- A is the number of additional decades of negative data values to be included. A shall be greater than or equal to $-W$, and less than or equal to $M - 2W$
- root is a standard root finding algorithm (e.g., Newton's method) that finds y such as $B(y, T, W, M, A) = x$.

and a, b, c and f are defined by means of T, W, M, A, w, $x0$, $x1$, $x2$, $e0$, ca and fa as:

$$w = W/(M + A)$$

$$x2 = A/(M + A)$$

$$x1 = x2 + w$$

$$x0 = x2 + 2 * w$$

$$b = (M + A) * ln(10)$$

$$e0 = e^{b*x0}$$

$$ca = e0/w$$

$$fa = e^{b*x1} + ca * x1$$

$$a = T/(e^b + ca - fa)$$

$$c = ca * a$$

$$f = fa * a$$

In addition, if a boundary is defined by the boundMin and/or boundMax parameters, then the result of this transformation is restricted to the [boundMin,boundMax] interval. Specifically, should the result of the hyperlog function be less than boundMin, then let the result of this transformation be boundMin. Analogically, should the result of the hyperlog function be more than boundMax, then let the result of this transformation be boundMax. The boundMin parameter shall not be greater than the boundMax parameter.

Slots

`.Data` Object of class `function`.

`T` Object of class `numeric` – positive constant (top of scale value).

`M` Object of class `numeric` – positive constant (desired number of decades).

`W` Object of class `numeric` – positive constant that is not greater than half of M (the number of such decades in the approximately linear region)

`A` Object of class `numeric` – a constant that is greater than or equal to -W, and also less than or equal to M-2W. (A represents the number of additional decades of negative data values to be included.)

`parameters` Object of class `"transformation"` – flow parameter to be transformed.

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

`boundMin` Object of class `numeric` – lower bound of the transformation, default -Inf.

`boundMax` Object of class `numeric` – upper bound of the transformation, default Inf.

Objects from the Class

Objects can be created by calls to the constructor

`hyperlogtGml2(parameter, T, M, W, A, transformationId, boundMin,boundMax)`

Extends

Class singleParameterTransform, directly.

Class transform, by class singleParameterTransform, distance 2.

Class transformation, by class singleParameterTransform, distance 3.

Class characterOrTransformation, by class singleParameterTransform, distance 4.

Note

That hyperlogtGml2 transformation brings "reasonable" data values to the scale of $[0, 1]$. The transformation is somewhat similar to logicletGml2. (See Gating-ML 2.0 for detailed comparison)

The hyperlog transformation object can be evaluated using the eval method by passing the data frame as an argument. The transformed parameters are returned as a matrix with a single column. (See example below)

Author(s)

Spidlen, J., Moore, W.

References

Gating-ML 2.0: International Society for Advancement of Cytometry (ISAC) standard for representing gating descriptions in flow cytometry. http://flowcyt.sourceforge.net/gating/20141009.pdf

See Also

hyperlog, logicleTransform, transform-class, transform

Other mathematical transform classes: EHtrans-class, asinht-class, asinhtGml2-class, dg1polynomial-class, exponential-class, hyperlog-class, invsplitscale-class, lintGml2-class, logarithm-class, logicletGml2-class, logtGml2-class, quadratic-class, ratio-class, ratiotGml2-class, sinht-class, splitscale-class, squareroot-class, unitytransform-class

Examples

```
myDataIn  <- read.FCS(system.file("extdata", "0877408774.B08",
    package="flowCore"))
myHyperLg <- hyperlogtGml2(parameters = "FSC-H", T = 1023, M = 4.5,
    W = 0.5, A = 0, transformationId="myHyperLg")
transOut  <- eval(myHyperLg)(exprs(myDataIn))
```

identifier-methods *Retrieve the GUID of flowCore objects*

Description

Retrieve the GUID (globally unique identifier) of a flowFrame that was generated by the cytometer or the identifier of a filter or filterResult given by the analyst.

Usage

```
identifier(object)
```

Arguments

object	Object of class flowFrame, filter or filterResult.

Details

GUID or Globally Unique Identifier is a pseudo-random number used in software applications. While each generated GUID is not guaranteed to be unique, the total number of unique keys (2\^128) is so large that the probability of the same number being generated twice is very small.

Note that if no GUID has been recorded along with the FCS file, the name of the file is returned.

Value

Character vector representing the GUID or the name of the file.

Methods

identifier(object = "filter") Return identifier of a filter object.

identifier(object = "filterReference") Return identifier of a filterReference object.

identifier(object = "filterResult") Return identifier of a filterResult object.

identifier(object = "transform") Return identifier of a transform object.

identifier(object = "flowFrame") Return GUID from the description slot of a flowFrame object or, alternatively, the name of the input FCS file in case none can be found. For flowFrame objects there also exists a replacement method.

Author(s)

N. LeMeur

Examples

```
samp <- read.FCS(system.file("extdata","0877408774.B08", package="flowCore"))
identifier(samp)
```

intersectFilter-class *Class intersectFilter*

Description

This class represents the intersection of two filters, which is itself a filter that can be incorporated in to further set operations. `intersectFilters` are constructed using the binary set operator `"&"` with operands consisting of a single filter or list of filters.

Slots

`filters` Object of class `"list"`, containing the component filters.

`filterId` Object of class `"character"` referencing the filter applied.

Extends

Class `"filter"`, directly.

Author(s)

B. Ellis

See Also

`filter`, `setOperationFilter`

Other setOperationFilter classes: `complementFilter-class`, `setOperationFilter-class`, `subsetFilter-class`, `unionFilter-class`

inverseLogicleTransform

Computes the inverse of the transform defined by the 'logicleTransform' function or the transformList generated by 'estimateLogicle' function

Description

inverseLogicleTransform can be use to compute the inverse of the Logicle transformation. The parameters w, t, m, a for calculating the inverse are obtained from the 'trans' input passed to the 'inverseLogicleTransform' function. (The inverseLogicleTransform method makes use of the C++ implementation of the inverse logicle transform contributed by Wayne Moore et al.)

Usage

```
inverseLogicleTransform(trans,transformationId,...)
```

Arguments

trans	An object of class 'transform' created using the 'logicleTransform' function or class 'transformList' created by 'estimateLogicle'. The parameters w, t, m, a for calculating the inverse are obtained from the 'trans' input passed to the 'inverseLogicleTransform' function.
transformationId	A name to assigned to the inverse transformation. Used by the transform routines.
...	not used.

Author(s)

Wayne Moore, N. Gopalakrishnan

References

Parks D.R., Roederer M., Moore W.A.(2006) A new "logicle" display method avoids deceptive effects of logarithmic scaling for low signals and compensated data. CytometryA, 96(6):541-51.

See Also

logicleTransform

Other Transform functions: arcsinhTransform(), biexponentialTransform(), linearTransform(), lnTransform(), logTransform(), logicleTransform(), quadraticTransform(), scaleTransform(), splitScaleTransform(), truncateTransform()

Examples

```
data(GvHD)
samp <- GvHD[[1]]

#########inverse the transform object###############
logicle  <- logicleTransform(t = 10000, w = 0.5, m = 4.5 , a =0 ,"logicle")
## transform FL1-H parameter using logicle transformation
after <- transform(samp, transformList('FL1-H', logicle))

## Inverse transform the logicle transformed data to retrieve the original data
invLogicle <- inverseLogicleTransform(trans = logicle)
before <- transform (after, transformList('FL1-H', invLogicle))

#########inverse the transformList object###############
translist <- estimateLogicle(samp, c("FL1-H", "FL2-H"))
after <- transform(samp, translist)
## Inverse
invLogicle <- inverseLogicleTransform(translist)
before <- transform (after, invLogicle)
```

`invsplitscale-class` *Class "invsplitscale"*

Description

As its name suggests, the inverse split scale transformation class represents the inverse transformation of a split scale transformation that has a logarithmic scale at high values and a linear scale at low values.

Details

The inverse split scale transformation is defined by the function

$$f(parameter, r, maxValue, transitionChannel)\frac{(parameter - b)}{a}, parameter <= t * a + b$$

$$f(parameter, r, maxValue, transitionChannel) = \frac{10^{parameter * \frac{d}{r}}}{c}, parameter > t * a + b$$

where

$$b = \frac{transitionChannel}{2}$$

$$d = \frac{2 * log_{10}(e) * r}{transitionChannel} + log_{10}(maxValue)$$

$$t = 10^{log_{10}t}$$

$$a = \frac{transitionChannel}{2 * t}$$

$$log_{10}ct = \frac{(a * t + b) * d}{r}$$

$$c = 10^{log_{10}ct}$$

Slots

`.Data` Object of class `"function"`.

`r` Object of class `"numeric"` – a positive value indicating the range of the logarithmic part of the dispmlay.

`maxValue` Object of class `"numeric"` – a positive value indicating the maximum value the transformation is applied to.

`transitionChannel` Object of class `"numeric"` – non negative value that indicates where to split the linear vs. logarithmic transformation.

`parameters` Object of class `"transformation"` – flow parameter to be transformed.

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

Objects from the Class

Objects can be created by calls to the constructor `invsplitscale(parameters,r,maxValue,transitionChannel,transfo`

Extends

Class "singleParameterTransform", directly.

Class "transform", by class "singleParameterTransform", distance 2.

Class "transformation", by class "singleParameterTransform", distance 3.

Class "characterOrTransformation", by class "singleParameterTransform", distance 4.

Note

The transformation object can be evaluated using the eval method by passing the data frame as an argument.The transformed parameters are returned as a matrix with a single column. (See example below)

Author(s)

Gopalakrishnan N,F.Hahne

References

Gating-ML Candidate Recommendation for Gating Description in Flow Cytometry

See Also

splitscale

Other mathematical transform classes: EHtrans-class, asinht-class, asinhtGml2-class, dg1polynomial-class, exponential-class, hyperlog-class, hyperlogtGml2-class, lintGml2-class, logarithm-class, logicletGml2-class, logtGml2-class, quadratic-class, ratio-class, ratiotGml2-class, sinht-class, splitscale-class, squareroot-class, unitytransform-class

Examples

```
dat <- read.FCS(system.file("extdata","0877408774.B08",package="flowCore"))
sp1<-invsplitscale("FSC-H",r=512,maxValue=2000,transitionChannel=512)
transOut<-eval(sp1)(exprs(dat))
```

---

keyword-methods *Methods to retrieve keywords of a flowFrame*

Description

Accessor and replacement methods for items in the description slot (usually read in from a FCS file header). It lists the keywords and its values for a flowFrame specified by a character vector. Additional methods for function and lists exists for more programmatic access to the keywords.

Usage

```
keyword(object, keyword, ...)
```

Arguments

object	Object of class flowFrame.
keyword	Character vector or list of potential keywords or function. If missing all keywords are returned.
...	compact: logical scaler to indicate whether to hide all the cytometer instrument and laser settings from keywords.

Details

The keyword methods allow access to the keywords stored in the FCS files, either for a flowFrame or for a list of frames in a flowSet. The most simple use case is to provide a character vector or a list of character strings of keyword names. A more sophisticated version is to provide a function which has to take one mandatory argument, the value of this is the flowFrame. This can be used to query arbitrary information from the flowFrames description slot or even the raw data. The function has to return a single character string. The list methods allow to combine functional and direct keyword access. The replacement method takes a named character vector or a named list as input.

Methods

keyword(object = "flowFrame", keyword = "character") Return values for all keywords from the description slot in object that match the character vector keyword.

keyword(object = "flowFrame", keyword = "function") Apply the function in keyword on the flowFrame object. The function needs to be able to cope with a single argument and it needs to return a single character string. A typical use case is for instance to paste together values from several different keywords or to compute some statistic on the flowFrame and combine it with one or several other keywords.

keyword(object = "flowFrame", keyword = "list") Combine characters and functions in a list to select keyword values.

keyword(object = "flowFrame", keyword = "missing") This is essentially an alias for description and returns all keyword-value pairs.

keyword(object = "flowSet", keyword = "list") This is a wrapper around fsApply(object, keyword, keyword) which essentially iterates over the frames in the flowSet.

keyword(object = "flowSet", keyword = "ANY") This first coerces the keyword (mostly a character vector) to a list and then calls the next applicable method.

Author(s)

N LeMeur,F Hahne,B Ellis

See Also

description

Examples

```
samp <- read.FCS(system.file("extdata","0877408774.B08", package="flowCore"))
keyword(samp)
keyword(samp, compact = TRUE)

keyword(samp, "FCSversion")

keyword(samp, function(x,...) paste(keyword(x, "SAMPLE ID"), keyword(x,
"GUID"), sep="_"))

keyword(samp)[["foo"]] <- "bar"

data(GvHD)
keyword(GvHD, list("GUID", cellnumber=function(x) nrow(x)))
```

---

kmeansFilter-class *Class "kmeansFilter"*

Description

A filter that performs one-dimensional k-means (Lloyd-Max) clustering on a single flow parameter.

Usage

```
kmeansFilter(..., filterId="defaultKmeansFilter")
```

Arguments

`...`	`kmeansFilter` are defined by a single flow parameter and an associated list of `k` population names. They can be given as a character vector via a named argument, or as a list with a single named argument. In both cases the name will be used as the flow parameter and the content of the list or of the argument will be used as population names, after coercing to character. For example
	`kmeansFilter(FSC=c("a", "b", "c"))`
	or
	`kmeansFilter(list(SSC=1:3))`
	If the parameter is not fully realized, but instead is the result of a `transformation` operation, two arguments need to be passed to the constructor: the first one being the `transform` object and the second being a vector of population names which can be coerced to a character. For example
	`kmeansFilter(tf, c("D", "E"))`

`filterId`	An optional parameter that sets the `filterId` of the object. The filter can later be identified by this name.

Details

The one-dimensional k-means filter is a multiple population filter capable of operating on a single flow parameter. It takes a parameter argument associated with two or more populations and results in the generation of an object of class `multipleFilterResult`. Populations are considered to be ordered such that the population with the smallest mean intensity will be the first population in the list and the population with the highest mean intensity will be the last population listed.

Value

Returns a `kmeansFilter` object for use in filtering `flowFrames` or other flow cytometry objects.

Slots

`populations` Object of class `character`. The names of the `k` populations (or clusters) that will be created by the `kmeansFilter`. These names will later be used for the respective subpopulations in `split` operations and for the summary of the `filterResult`.

`parameters` Object of class `parameters`, defining a single parameter for which the data in the `flowFrame` is to be clustered. This may also be a `transformation` object.

`filterId` Object of class `character`, an identifier or name to reference the `kmeansFilter` object later on.

Extends

Class `parameterFilter`, directly.

Class `concreteFilter`, by class `parameterFilter`, distance 2.

Class `filter`, by class `parameterFilter`, distance3.

Objects from the Class

Like all other `filter` objects in `flowCore`, `kmeansFilter` objects should be instantiated through their constructor `kmeansFilter()`. See the `Usage` section for details.

Methods

%in% `signature(x = "flowFrame", table = "kmeansFilter")`: The workhorse used to evaluate the filter on data.

Usage:

This is usually not called directly by the user, but internally by the `filter` methods.

show `signature(object = "kmeansFilter")`: Print information about the filter.

Usage:

The method is called automatically whenever the object is printed on the screen.

Note

See the documentation in the `flowViz` package for plotting of `kmeansFilters`.

Author(s)

F. Hahne, B. Ellis, N. LeMeur

See Also

flowFrame, flowSet, filter for evaluation of kmeansFilters and split for splitting of flow cytometry data sets based on the result of the filtering operation.

Examples

```
## Loading example data
dat <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))

## Create the filter
kf <- kmeansFilter("FSC-H"=c("Pop1","Pop2","Pop3"), filterId="myKmFilter")

## Filtering using kmeansFilters
fres <- filter(dat, kf)
fres
summary(fres)
names(fres)

## The result of quadGate filtering are multiple sub-populations
## and we can split our data set accordingly
split(dat, fres)

## We can limit the splitting to one or several sub-populations
split(dat, fres, population="Pop1")
split(dat, fres, population=list(keep=c("Pop1","Pop2")))
```

---

linearTransform *Create the definition of a linear transformation function to be applied on a data set*

Description

Create the definition of the linear Transformation that will be applied on some parameter via the transform method. The definition of this function is currently x <- a*x+b

Usage

```
linearTransform(transformationId="defaultLinearTransform", a = 1, b = 0)
```

Arguments

transformationId	character string to identify the transformation
a	double that corresponds to the multiplicative factor in the equation
b	double that corresponds to the additive factor in the equation

Value

Returns an object of class transform.

Author(s)

N. LeMeur

See Also

transform-class, transform

Other Transform functions: arcsinhTransform(), biexponentialTransform(), inverseLogicleTransform(), lnTransform(), logTransform(), logicleTransform(), quadraticTransform(), scaleTransform(), splitScaleTransform(), truncateTransform()

Examples

```
samp <- read.FCS(system.file("extdata",
   "0877408774.B08", package="flowCore"))
  linearTrans <- linearTransform(transformationId="Linear-transformation", a=2, b=0)
  dataTransform <- transform(samp, transformList('FSC-H' ,linearTrans))
```

---

lintGml2-class *Class lintGml2*

Description

Linear transformation as parameterized in Gating-ML 2.0.

Details

lintGml2 is defined by the following function:

$$bound(f, boundMin, boundMax) = max(min(f, boundMax), boundMin))$$

where

$$f(parameter, T, A) = (parameter + A)/(T + A)$$

This transformation provides a linear display that maps scale values from the $[-A, T]$ interval to the $[0, 1]$ interval. However, it is defined for all $xinR$ including outside of the $[-A, T]$ interval.

In addition, if a boundary is defined by the boundMin and/or boundMax parameters, then the result of this transformation is restricted to the [boundMin,boundMax] interval. Specifically, should the result of the f function be less than boundMin, then let the result of this transformation be boundMin. Analogically, should the result of the f function be more than boundMax, then let the result of this transformation be boundMax. The boundMin parameter shall not be greater than the boundMax parameter.

Slots

`.Data` Object of class `function`.

`T` Object of class `numeric` – positive constant (top of scale value).

`A` Object of class `numeric` – non-negative constant that is less than or equal to T; it is determining the bottom end of the transformation.

`parameters` Object of class `"transformation"` – flow parameter to be transformed.

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

`boundMin` Object of class `numeric` – lower bound of the transformation, default -Inf.

`boundMax` Object of class `numeric` – upper bound of the transformation, default Inf.

Objects from the Class

Objects can be created by calls to the constructor

```
lintGml2(parameter, T, A, transformationId, boundMin, boundMax)
```

Extends

Class `singleParameterTransform`, directly.

Class `transform`, by class singleParameterTransform, distance 2.

Class `transformation`, by class singleParameterTransform, distance 3.

Class `characterOrTransformation`, by class singleParameterTransform, distance 4.

Note

The linear transformation object can be evaluated using the eval method by passing the data frame as an argument. The transformed parameters are returned as a matrix with a single column. (See example below)

Author(s)

Spidlen, J.

References

Gating-ML 2.0: International Society for Advancement of Cytometry (ISAC) standard for representing gating descriptions in flow cytometry. http://flowcyt.sourceforge.net/gating/20141009.pdf

See Also

linearTransform, transform-class, transform

Other mathematical transform classes: EHtrans-class, asinht-class, asinhtGml2-class, dg1polynomial-class, exponential-class, hyperlog-class, hyperlogtGml2-class, invsplitscale-class, logarithm-class, logicletGml2-class, logtGml2-class, quadratic-class, ratio-class, ratiotGml2-class, sinht-class, splitscale-class, squareroot-class, unitytransform-class

Examples

```
myDataIn <- read.FCS(system.file("extdata", "0877408774.B08",
    package="flowCore"))
myLinTr1 <- lintGml2(parameters = "FSC-H", T = 1000, A = 0,
    transformationId="myLinTr1")
transOut <- eval(myLinTr1)(exprs(myDataIn))
```

---

lnTransform *Create the definition of a ln transformation function (natural logarithim) to be applied on a data set*

Description

Create the definition of the ln Transformation that will be applied on some parameter via the transform method. The definition of this function is currently x<-log(x)*(r/d). The transformation would normally be used to convert to a linear valued parameter to the natural logarithm scale. Typically r and d are both equal to 1.0. Both must be positive.

Usage

```
lnTransform(transformationId="defaultLnTransform", r=1, d=1)
```

Arguments

transformationId	character string to identify the transformation
r	positive double that corresponds to a scale factor.
d	positive double that corresponds to a scale factor

Value

Returns an object of class transform.

Author(s)

B. Ellis and N. LeMeur

See Also

transform-class, transform

Other Transform functions: arcsinhTransform(), biexponentialTransform(), inverseLogicleTransform(), linearTransform(), logTransform(), logicleTransform(), quadraticTransform(), scaleTransform(), splitScaleTransform(), truncateTransform()

Examples

```
  data(GvHD)
  lnTrans <- lnTransform(transformationId="ln-transformation", r=1, d=1)
  ln1 <- transform(GvHD, transformList('FSC-H', lnTrans))

opar = par(mfcol=c(2, 1))
plot(density(exprs(GvHD[[1]])[ ,1]), main="Original")
plot(density(exprs(ln1[[1]])[ ,1]), main="Ln Transform")
```

---

logarithm-class *Class "logarithm"*

Description

Logartithmic transform class, which represents a transformation defined by the function

Details

$$f(parameter, a, b) = ln(a * prarameter) * b \quad a * parameter > 0$$

$$0 \quad a * parameter <= 0$$

Slots

`.Data` Object of class `"function"`

`a` Object of class `"numeric"` – non-zero multiplicative constant.

`b` Object of class `"numeric"` – non-zero multiplicative constant.

`parameters` Object of class `"transformation"` – flow parameters to be transformed.

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

Objects from the Class

Objects can be created by calls to the constructor `logarithm(parameters,a,b,transformationId)`

Extends

Class "singleParameterTransform", directly.

Class "transform", by class "singleParameterTransform", distance 2.

Class "transformation", by class "singleParameterTransform", distance 3.

Class "characterOrTransformation", by class "singleParameterTransform", distance 4.

Note

The logarithm transformation object can be evaluated using the eval method by passing the data frame as an argument.The transformed parameters are returned as a matrix with a single column. (See example below)

Author(s)

Gopalakrishnan N, F.Hahne

References

Gating-ML Candidate Recommendation for Gating Description in Flow Cytometry V 1.5

See Also

exponential, quadratic

Other mathematical transform classes: EHtrans-class, asinht-class, asinhtGml2-class, dg1polynomial-class, exponential-class, hyperlog-class, hyperlogtGml2-class, invsplitscale-class, lintGml2-class, logicletGml2-class, logtGml2-class, quadratic-class, ratio-class, ratiotGml2-class, sinht-class, splitscale-class, squareroot-class, unitytransform-class

Examples

```
dat <- read.FCS(system.file("extdata","0877408774.B08",
 package="flowCore"))
 lg1<-logarithm(parameters="FSC-H",a=2,b=1,transformationId="lg1")
 transOut<-eval(lg1)(exprs(dat))
```

---

logicalFilterResult-class

Class "logicalFilterResult"

Description

Container to store the result of applying a filter on a flowFrame object

Slots

`subSet` Object of class `"numeric"`, which is a logical vector indicating the population membership of the data in the gated flowFrame.

`frameId` Object of class `"character"` referencing the `flowFrame` object filtered. Used for sanity checking.

`filterDetails` Object of class `"list"` describing the filter applied.

`filterId` Object of class `"character"` referencing the filter applied.

Extends

Class `"filterResult"`, directly. Class `"filter"`, by class "filterResult", distance 2.

Author(s)

B. Ellis

See Also

`filter`

Examples

```
showClass("logicalFilterResult")
```

`logicletGml2-class` *Class logicletGml2*

Description

Logicle transformation as published by Moore and Parks.

Details

logicletGml2 is defined by the following function:

$$bound(logicle, boundMin, boundMax) = max(min(logicle, boundMax), boundMin))$$

where

$$logicle(x, T, W, M, A) = root(B(y, T, W, M, A) - x)$$

and B is a modified biexponential function:

$$B(y, T, W, M, A) = ae^{by} - ce^{-dy} - f$$

where

- x is the value that is being transformed (an FCS dimension value). Typically, x is less than or equal to T, although the transformation function is also defined for x greater than T.

- y is the result of the transformation.
- T is greater than zero and represents the top of scale value.
- M is greater than zero and represents the number of decades that the true logarithmic scale approached at the high end of the Logicle scale would cover in the plot range.
- W is non-negative and not greater than half of M and represents the number of such decades in the approximately linear region. The choice of $W = M/2$ specifies a scale that is essentially linear over the whole range except for a small region of large data values. For situations in which values of W approaching $M/2$ might be chosen, ordinary linear display scales will usually be more appropriate. The choice of $W = 0$ gives essentially the hyperbolic sine function.
- A is the number of additional decades of negative data values to be included. A shall be greater than or equal to $-W$, and less than or equal to $M - 2W$
- root is a standard root finding algorithm (e.g., Newton's method) that finds y such as $B(y, T, W, M, A) = x$.

and a, b, c, d and f are defined by means of T, W, M, A, w, $x0$, $x1$, $x2$, ca and fa as:

$$w = W/(M + A)$$

$$x2 = A/(M + A)$$

$$x1 = x2 + w$$

$$x0 = x2 + 2 * w$$

$$b = (M + A) * ln(10)$$

and d is a constant so that

$$2 * (ln(d) - ln(b)) + w * (d + b) = 0$$

given b and w, and

$$ca = e^{x0*(b+d)}$$

$$fa = e^{b*x1} - (ca/(e^{d*x1}))$$

$$a = T/(e^b - fa - (ca/e^d))$$

$$c = ca * a$$

$$f = fa * a$$

The Logicle scale is the inverse of a modified biexponential function. It provides a Logicle display that maps scale values onto the $[0, 1]$ interval such that the data value T is mapped to 1, large data values are mapped to locations similar to an (M + A)-decade logarithmic scale, and A decades of negative data are brought on scale. For implementation purposes, it is recommended to follow guidance in Moore and Parks publication.

In addition, if a boundary is defined by the boundMin and/or boundMax parameters, then the result of this transformation is restricted to the [boundMin,boundMax] interval. Specifically, should the result of the logicle function be less than boundMin, then let the result of this transformation be boundMin. Analogically, should the result of the logicle function be more than boundMax, then let the result of this transformation be boundMax. The boundMin parameter shall not be greater than the boundMax parameter.

Slots

`.Data` Object of class `function`.

`T` Object of class `numeric` – positive constant (top of scale value).

`M` Object of class `numeric` – positive constant (desired number of decades).

`W` Object of class `numeric` – non-negative constant that is not greater than half of M (the number of such decades in the approximately linear region).

`A` Object of class `numeric` – a constant that is greater than or equal to -W, and also less than or equal to M-2W. (A represents the number of additional decades of negative data values to be included.)

`parameters` Object of class `"transformation"` – flow parameter to be transformed.

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

`boundMin` Object of class `numeric` – lower bound of the transformation, default -Inf.

`boundMax` Object of class `numeric` – upper bound of the transformation, default Inf.

Objects from the Class

Objects can be created by calls to the constructor

```
logicletGml2(parameter, T, M, W, A, transformationId, boundMin,boundMax)
```

Extends

Class `singleParameterTransform`, directly.

Class `transform`, by class singleParameterTransform, distance 2.

Class `transformation`, by class singleParameterTransform, distance 3.

Class `characterOrTransformation`, by class singleParameterTransform, distance 4.

Note

Please note that `logicletGml2` and `logicleTransform` are similar transformations; however, the Gating-ML 2.0 compliant `logicletGml2` brings "reasonable" data values to the scale of $[0, 1]$ while the `logicleTransform` scales these values to $[0, M]$.

The logicle transformation object can be evaluated using the eval method by passing the data frame as an argument. The transformed parameters are returned as a matrix with a single column. (See example below)

Author(s)

Spidlen, J., Moore, W.

References

Gating-ML 2.0: International Society for Advancement of Cytometry (ISAC) standard for representing gating descriptions in flow cytometry. http://flowcyt.sourceforge.net/gating/20141009.pdf

Moore, WA and Parks, DR. Update for the logicle data scale including operational code implementations. Cytometry A., 2012:81A(4):273-277.

Parks, DR and Roederer, M and Moore, WA. A new "Logicle" display method avoids deceptive effects of logarithmic scaling for low signals and compensated data. Cytometry A., 2006:69(6):541-551.

See Also

logicleTransform, transform-class, transform

Other mathematical transform classes: EHtrans-class, asinht-class, asinhtGml2-class, dg1polynomial-class, exponential-class, hyperlog-class, hyperlogtGml2-class, invsplitscale-class, lintGml2-class, logarithm-class, logtGml2-class, quadratic-class, ratio-class, ratiotGml2-class, sinht-class, splitscale-class, squareroot-class, unitytransform-class

Examples

```
myDataIn  <- read.FCS(system.file("extdata", "0877408774.B08",
    package="flowCore"))
myLogicle <- logicletGml2(parameters = "FSC-H", T = 1023, M = 4.5,
    W = 0.5, A = 0, transformationId="myLogicle")
transOut  <- eval(myLogicle)(exprs(myDataIn))
```

---

logicleTransform *Computes a transform using the 'logicle_transform' function*

Description

Logicle transformation creates a subset of biexponentialTransform hyperbolic sine transformation functions that provides several advantages over linear/log transformations for display of flow cytometry data. (The logicleTransform method makes use of the C++ implementation of the logicle transform contributed by Wayne Moore et al.)

Usage

```
logicleTransform(transformationId="defaultLogicleTransform", w = 0.5, t = 262144,
                 m = 4.5, a = 0)
                 estimateLogicle(x, channels,...)
```

Arguments

transformationId	A name to assign to the transformation. Used by the transform/filter routines.
w	w is the linearization width in asymptotic decades. w should be > 0 and determines the slope of transformation at zero. w can be estimated using the equation w=(m-log10(t/abs(r)))/2, where r is the most negative value to be included in the display
t	Top of the scale data value, e.g, 10000 for common 4 decade data or 262144 for a 18 bit data range. t should be greater than zero
m	m is the full width of the transformed display in asymptotic decades. m should be greater than zero
a	Additional negative range to be included in the display in asymptotic decades. Positive values of the argument brings additional negative input values into the transformed display viewing area. Default value is zero corresponding to a Standard logicle function.
x	Input flow frame for which the logicle transformations are to be estimated.
channels	channels or markers for which the logicle transformation is to be estimated.
...	other arguments: q: a numeric type specifying quantile value, default is 0.05

Author(s)

Wayne Moore, N Gopalakrishnan

References

Parks D.R., Roederer M., Moore W.A.(2006) A new "logicle" display method avoids deceptive effects of logarithmic scaling for low signals and compensated data. CytometryA, 96(6):541-51.

See Also

inverseLogicleTransform, estimateLogicle

Other Transform functions: arcsinhTransform(), biexponentialTransform(), inverseLogicleTransform(), linearTransform(), lnTransform(), logTransform(), quadraticTransform(), scaleTransform(), splitScaleTransform(), truncateTransform()

Examples

```
data(GvHD)
samp <- GvHD[[1]]
## User defined logicle function
lgcl <- logicleTransform( w = 0.5, t= 10000, m =4.5)
trans <- transformList(c("FL1-H", "FL2-H"), lgcl)
after <- transform(samp, trans)
invLgcl <- inverseLogicleTransform(trans = lgcl)
trans <- transformList(c("FL1-H", "FL2-H"), invLgcl)
before <- transform (after,  trans)
```

```
## Automatically estimate the logicle transformation based on the data
lgcl <- estimateLogicle(samp, channels = c("FL1-H", "FL2-H", "FL3-H", "FL2-A", "FL4-H"))
## transform  parameters using the estimated logicle transformation
after <- transform(samp, lgcl)
```

`logtGml2-class` *Class logtGml2*

Description

Log transformation as parameterized in Gating-ML 2.0.

Details

logtGml2 is defined by the following function:

$$bound(f, boundMin, boundMax) = max(min(f, boundMax), boundMin))$$

where

$$f(parameter, T, M) = (1/M) * log10(x/T) + 1$$

This transformation provides a logarithmic display that maps scale values from the $(0, T]$ interval to the $(-Inf, 1]$ interval such that the data value T is mapped to 1 and M decades of data are mapped into the interval. Also, the limit for x going to 0 is -Inf.

In addition, if a boundary is defined by the boundMin and/or boundMax parameters, then the result of this transformation is restricted to the [boundMin,boundMax] interval. Specifically, should the result of the f function be less than boundMin, then let the result of this transformation be boundMin. Analogically, should the result of the f function be more than boundMax, then let the result of this transformation be boundMax. The boundMin parameter shall not be greater than the boundMax parameter.

Slots

`.Data` Object of class `function`.

`T` Object of class `numeric` – positive constant (top of scale value).

`M` Object of class `numeric` – positive constant (number of decades).

`parameters` Object of class `"transformation"` – flow parameter to be transformed.

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

`boundMin` Object of class `numeric` – lower bound of the transformation, default -Inf.

`boundMax` Object of class `numeric` – upper bound of the transformation, default Inf.

Objects from the Class

Objects can be created by calls to the constructor

`logtGml2(parameter, T, M, transformationId, boundMin, boundMax)`

Extends

Class singleParameterTransform, directly.

Class transform, by class singleParameterTransform, distance 2.

Class transformation, by class singleParameterTransform, distance 3.

Class characterOrTransformation, by class singleParameterTransform, distance 4.

Note

The log transformation object can be evaluated using the eval method by passing the data frame as an argument. The transformed parameters are returned as a matrix with a single column. (See example below)

Author(s)

Spidlen, J.

References

Gating-ML 2.0: International Society for Advancement of Cytometry (ISAC) standard for representing gating descriptions in flow cytometry. http://flowcyt.sourceforge.net/gating/20141009.pdf

See Also

logTransform, transform-class, transform

Other mathematical transform classes: EHtrans-class, asinht-class, asinhtGml2-class, dg1polynomial-class, exponential-class, hyperlog-class, hyperlogtGml2-class, invsplitscale-class, lintGml2-class, logarithm-class, logicletGml2-class, quadratic-class, ratio-class, ratiotGml2-class, sinht-class, splitscale-class, squareroot-class, unitytransform-class

Examples

```
myDataIn <- read.FCS(system.file("extdata", "0877408774.B08",
    package="flowCore"))
myLogTr1 <- logtGml2(parameters = "FSC-H", T = 1023, M = 4.5,
    transformationId="myLogTr1")
transOut <- eval(myLogTr1)(exprs(myDataIn))
```

`logTransform` *Create the definition of a log transformation function (base specified by user) to be applied on a data set*

Description

Create the definition of the log Transformation that will be applied on some parameter via the `transform` method. The definition of this function is currently x<-log(x,logbase)*(r/d). The transformation would normally be used to convert to a linear valued parameter to the natural logarithm scale. Typically r and d are both equal to 1.0. Both must be positive. logbase = 10 corresponds to base 10 logarithm.

Usage

```
logTransform(transformationId="defaultLogTransform", logbase=10, r=1, d=1)
```

Arguments

`transformationId`	character string to identify the transformation
`logbase`	positive double that corresponds to the base of the logarithm.
`r`	positive double that corresponds to a scale factor.
`d`	positive double that corresponds to a scale factor

Value

Returns an object of class `transform`.

Author(s)

B. Ellis, N. LeMeur

See Also

`transform-class`, `transform`

Other Transform functions: `arcsinhTransform()`, `biexponentialTransform()`, `inverseLogicleTransform()`, `linearTransform()`, `lnTransform()`, `logicleTransform()`, `quadraticTransform()`, `scaleTransform()`, `splitScaleTransform()`, `truncateTransform()`

Examples

```
samp <- read.FCS(system.file("extdata",
   "0877408774.B08", package="flowCore"))
 logTrans <- logTransform(transformationId="log10-transformation", logbase=10, r=1, d=1)
 trans <- transformList('FSC-H', logTrans)
 dataTransform <- transform(samp, trans)
```

manyFilterResult-class *Class "manyFilterResult"*

Description

The result of a several related, but possibly overlapping filter results. The usual creator of this object will usually be a `filter` operation on a `flowFrame` object.

Slots

`subSet` Object of class `"matrix"`.

`frameId` Object of class `"character"` referencing the `flowFrame` object filtered. Used for sanity checking.

`filterDetails` Object of class `"list"` describing the filter applied.

`filterId` Object of class `"character"` referencing the filter applied.

`dependency` Any dependencies between the filters. Currently not used.

Extends

Class `"filterResult"`, directly. Class `"filter"`, by class "filterResult", distance 2.

Methods

[, [[subsetting. If `x` is `manyFilterResult`, then `x[[i]]` a `filterResult` object. The semantics is similar to the behavior of the subsetting operators for lists.

length number of `filterResult` objects in the set.

names names of the `filterResult` objects in the set.

summary summary `filterResult` objects in the set.

Author(s)

B. Ellis

See Also

`filterResult`

Examples

```
showClass("manyFilterResult")
```

`markernames` *get or update the marker names*

Description

marker names corresponds to the 'desc' column of the phenoData of the flowFrame.

Usage

```
markernames(object, ...)

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

markernames(object) <- value

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

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

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

Arguments

`object`	flowFrame or flowSet
`...`	not used
`value`	a named list or character vector. the names corresponds to the name(channel) and actual values are the desc(marker).

Details

When extract marker names from a flowSet, it throws the warning if the marker names are not all the same across samples.

Value

marker names as a character vector. The marker names for FSC,SSC and Time channels are automatically excluded in the returned value. When object is a flowSet and the marker names are not consistent across flowFrames, it returns a list of unique marker sets.

Examples

```
data(GvHD)
fr <- GvHD[[1]]
markernames(fr)

chnls <- c("FL1-H", "FL3-H")
markers <- c("CD15", "CD14")
names(markers) <- chnls
markernames(fr) <- markers
markernames(fr)

fs <- GvHD[1:3]
markernames(fs)
```

---

multipleFilterResult-class

Class "multipleFilterResult"

Description

Container to store the result of applying `filter` on set of `flowFrame` objects

Slots

`subSet` Object of class `"factor"` indicating the population membership of the data in the gated flowFrame.

`frameId` Object of class `"character"` referencing the `flowFrame` object filtered. Used for sanity checking.

`filterDetails` Object of class `"list"` describing the filter applied.

`filterId` Object of class `"character"` referencing the filter applied.

Extends

Class `"filterResult"`, directly. Class `"filter"`, by class "filterResult", distance 2.

Methods

[, [[subsetting. If `x` is `multipleFilterResult`, then `x[[i]]` a `FilterResult` object. The semantics is similar to the behavior of the subsetting operators for lists.

length number of `FilterResult` objects in the set.

names names of the `FilterResult` objects in the set.

summary summary `FilterResult` objects in the set.

Author(s)

B. Ellis

See Also

filterResult

Examples

```
showClass("multipleFilterResult")
```

---

normalization-class *Class "normalization"*

Description

Class and methods to normalize a a flowSet using a potentially complex normalization function.

Usage

```
normalization(parameters, normalizationId="defaultNormalization",
              normFunction, arguments=list())

normalize(data, x,...)
```

Arguments

parameters	Character vector of parameter names.
normalizationId	The identifier for the normalization object.
x	An object of class flowSet.
normFunction	The normalization function
arguments	The list of additional arguments to normFunction
data	The flowSet to normalize.
...	other arguments: see normalize-methodsfor details.

Details

Data normalization of a flowSet is a rather fuzzy concept. The idea is to have a rather general function that takes a flowSet and a list of parameter names as input and applies any kind of normalization to the respective data columns. The output of the function has to be a flowSet again. Although we don't formally check for it, the dimensions of the input and of the output set should remain the same. Additional arguments may be passed to the normalization function via the arguments list. Internally we evaluate the function using do.call and one should check its documentation for details.

Currently, the most prominent example for a normalization function is warping, as provided by the flowStats package.

Value

A `normalization` object for the constructor.

A `flowSet` for the `normalize` methods.

Slots

`parameters` Object of class `"character"`. The flow parameters that are supposed to be normalized by the normalization function.

`normalizationId` Object of class `"character"`. An identifier for the object.

`normFunction` Object of class `"function"` The normalization function. It has to take two mandatory arguments: `x`, the `flowSet`, and `parameters`, a character of parameter names that are to be normalized by the function. Additional arguments have to be passed in via `arguments`.

`arguments` Object of class `"list"` A names list of additional arguments. Can be `NULL`.

Objects from the Class

Objects should be created using the constructor `normalization()`. See the `Usage` and `Arguments` sections for details.

Methods

identifier<- `signature(object = "normalization", value = "character")`: Set method for the identifier slot.

identifier `signature(object = "normalization")`: Get method for the identifier slot.

normalize `signature(data = "flowSet", x = "normalization")`: Apply a normalization to a `flowSet`.

parameters `signature(object = "normalization")`: The more generic constructor.

Author(s)

F. Hahne

`nullParameter-class` *Class "nullParameter"*

Description

A class used internally for coercing transforms to characters for a return value when a coercion cannot be performed. The user should never need to interact with this class.

Objects from the Class

Objects will be created internally whenever necessary and this should not be of any concern to the user.

parameterFilter-class *Class "parameterFilter"*

Description

A concrete filter that acts on a set of parameters.

Slots

`parameters` The names of the parameters employed by this filter.

`filterId` The filter identifier.

Objects from the Class

`parameterFilter` objects are never created directly. This class serves as an inheritance point for filters that depends on particular parameters.

Extends

Class "concreteFilter", directly. Class "filter", by class "concreteFilter", distance 2.

Author(s)

B. Ellis

parameters-class *Class "parameters"*

Description

A representation of flow parameters that allows for referencing.

Slots

`.Data` A list of the individual parameters.

Objects from the Class

Objects will be created internally whenever necessary and this should not be of any concern to the user.

Extends

Class "list", from data part. Class "vector", by class "list", distance 2.

Author(s)

Nishant Gopalakrishnan

parameters-methods *Obtain information about parameters for flow cytometry objects.*

Description

Many different objects in flowCore are associated with one or more parameters. This includes filter, flowFrame and parameterFilter objects that all either describe or use parameters.

Usage

```
parameters(object, ...)
```

Arguments

object	Object of class filter, flowFrame or parameterFilter.
...	Further arguments that get passed on to the methods.

Value

When applied to a flowFrame object, the result is an AnnotatedDataFrame describing the parameters recorded by the cytometer. For other objects it will usually return a vector of names used by the object for its calculations.

Methods

parameters(object = "filter") Returns for all objects that inherit from filter a vector of parameters on which a gate is defined.

parameters(object = "parameterFilter") see above

parameters(object = "setOperationFilter") see above

parameters(object = "filterReference") see above

parameters(object = "flowFrame") Returns an AnnotatedDataFrame containing detailed descriptions about the measurement parameters of the flowFrame. For flowFrame objects there also exists a replacement method.

Author(s)

B. Ellis, N. Le Meur, F. Hahne

Examples

```
samp <- read.FCS(system.file("extdata","0877408774.B08", package="flowCore"))
parameters(samp)
print(samp@parameters@data)
```

parameterTransform-class *Class "parameterTransform"*

Description

Link a transformation to particular flow parameters

Slots

`.Data` Object of class `"function"`, the transformation function.

`parameters` Object of class `"character"` The parameters the transformation is applied to.

`transformationId` Object of class `"character"`. The identifier for the object.

Objects from the Class

Objects are created by using the `%on%` operator and are usually not directly instantiated by the user.

Extends

Class `"transform"`, directly. Class `"function"`, by class "transform", distance 2.

Methods

%on% `signature(e1 = "filter", e2 = "parameterTransform")`: Apply the transformation.

%on% `signature(e1 = "parameterTransform", e2 = "flowFrame")`: see above

parameters `signature(object = "parameterTransform")`: Accessor to the parameters slot

Author(s)

Byron Ellis

polygonGate-class *Class "polygonGate"*

Description

Class and constructor for 2-dimensional polygonal `filter` objects.

Usage

```
polygonGate(..., .gate, boundaries, filterId="defaultPolygonGate")
```

Arguments

filterId	An optional parameter that sets the filterId of this gate.
.gate, boundaries	A definition of the gate. This can be either a list or a named matrix as described below. Note the argument boundaries is deprecated and will go away in the next release.
...	You can also directly describe a gate without wrapping it in a list or matrix, as described below.

Details

Polygons are specified by the coordinates of their vertices in two dimensions. The constructor is designed to be useful in both direct and programmatic usage. It takes either a list or a named matrix with 2 columns and at least 3 rows containing these coordinates. Alternatively, vertices can be given as named arguments, in which case the function tries to convert the values into a matrix.

Value

Returns a polygonGate object for use in filtering flowFrames or other flow cytometry objects.

Slots

boundaries Object of class "matrix". The vertices of the polygon in two dimensions. There need to be at least 3 vertices specified for a valid polygon.

parameters Object of class "character", describing the parameter used to filter the flowFrame.

filterId Object of class "character", referencing the filter.

Extends

Class "parameterFilter", directly.

Class "concreteFilter", by class parameterFilter, distance 2.

Class "filter", by class parameterFilter, distance 3.

Objects from the Class

Objects can be created by calls of the form new("polygonGate", ...) or by using the constructor polygonGate. Using the constructor is the recommended way.

Methods

%in% signature(x = "flowFrame", table = "polygonGate"): The workhorse used to evaluate the filter on data. This is usually not called directly by the user, but internally by calls to the filter methods.

show signature(object = "polygonGate"): Print information about the filter.

Note

See the documentation in the flowViz package for plotting of polygonGates.

Author(s)

F.Hahne, B. Ellis N. Le Meur

See Also

flowFrame, rectangleGate, ellipsoidGate, polytopeGate, filter for evaluation of rectangleGates and split and Subsetfor splitting and subsetting of flow cytometry data sets based on that.

Other Gate classes: ellipsoidGate-class, polytopeGate-class, quadGate-class, rectangleGate-class

Examples

```
## Loading example data
dat <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))

## Defining the gate
sqrcut <- matrix(c(300,300,600,600,50,300,300,50),ncol=2,nrow=4)
colnames(sqrcut) <- c("FSC-H","SSC-H")
pg <- polygonGate(filterId="nonDebris", boundaries= sqrcut)
pg

## Filtering using polygonGates
fres <- filter(dat, pg)
fres
summary(fres)

## The result of polygon filtering is a logical subset
Subset(dat, fres)

## We can also split, in which case we get those events in and those
## not in the gate as separate populations
split(dat, fres)
```

---

polytopeGate-class *Define filter boundaries*

Description

Convenience methods to facilitate the construction of filter objects

Usage

```
polytopeGate(..., .gate, b, filterId="defaultPolytopeGate")
```

Arguments

filterId	An optional parameter that sets the filterId of this gate.
.gate	A definition of the gate. This can be either a list, vector or matrix, described below.
b	Need documentation
...	You can also directly describe a gate without wrapping it in a list or matrix, as described below.

Details

These functions are designed to be useful in both direct and programmatic usage.

For rectangle gate in n dimensions, if n=1 the gate correspond to a range gate. If n=2, the gate is a rectangle gate. To use this function programmatically, you may either construct a list or you may construct a matrix with n columns and 2 rows. The first row corresponds to the minimal value for each parameter while the second row corresponds to the maximal value for each parameter. The names of the parameters are taken from the column names as in the third example.

Rectangle gate objects can also be multiplied together using the * operator, provided that both gate have orthogonal axes.

For polygon gate, the boundaries are specified as vertices in 2 dimensions, for polytope gate objects as vertices in n dimensions.

Polytope gate objects will represent the convex polytope determined by the vertices and parameter b which together specify the polytope as an intersection of half-spaces represented as a system of linear inequalities, $Ax \leq b$

For quadrant gates, the boundaries are specified as a named list or vector of length two.

Value

Returns a rectangleGate or polygonGate object for use in filtering flowFrames or other flow cytometry objects.

Author(s)

F.Hahne, B. Ellis N. Le Meur

See Also

flowFrame, filter

Other Gate classes: ellipsoidGate-class, polygonGate-class, quadGate-class, rectangleGate-class

quadGate-class *Class "quadGate"*

Description

Class and constructors for quadrant-type filter objects.

Usage

```
quadGate(..., .gate, filterId="defaultQuadGate")
```

Arguments

filterId	An optional parameter that sets the filterId of this filter. The object can later be identified by this name.
.gate	A definition of the gate for programmatic access. This can be either a named list or a named numeric vector, as described below.
...	The parameters of quadGates can also be directly described using named function arguments, as described below.

Details

quadGates are defined by two parameters, which specify a separation of a two-dimensional parameter space into four quadrants. The quadGate function is designed to be useful in both direct and programmatic usage.

For the interactive use, these parameters can be given as additional named function arguments, where the names correspond to valid parameter names in a flowFrame or flowSet. For a more programmatic approach, a named list or numeric vector of the gate boundaries can be passed on to the function as argument .gate.

Evaluating a quadGate results in four sub-populations, and hence in an object of class multipleFilterResult. Accordingly, quadGates can be used to split flow cytometry data sets.

Value

Returns a quadGate object for use in filtering flowFrames or other flow cytometry objects.

Slots

boundary Object of class "numeric", length 2. The boundaries of the quadrant regions.

parameters Object of class "character", describing the parameter used to filter the flowFrame.

filterId Object of class "character", referencing the gate.

Extends

Class "parameterFilter", directly.

Class "concreteFilter", by class parameterFilter, distance 2.

Class "filter", by class parameterFilter, distance 3.

Objects from the Class

Objects can be created by calls of the form `new("quadGate", ...)` or using the constructor `quadGate`. The latter is the recommended way.

Methods

%in% `signature(x = "flowFrame", table = "quadGate")`: The workhorse used to evaluate the gate on data. This is usually not called directly by the user, but internally by calls to the `filter` methods.

show `signature(object = "quadGate")`: Print information about the gate.

Note

See the documentation in the `flowViz` package for plotting of `quadGates`.

Author(s)

F.Hahne, B. Ellis N. Le Meur

See Also

`flowFrame`, `flowSet`, `filter` for evaluation of `quadGates` and `split` for splitting of flow cytometry data sets based on that.

Other Gate classes: `ellipsoidGate-class`, `polygonGate-class`, `polytopeGate-class`, `rectangleGate-class`

Examples

```
## Loading example data
dat <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))

## Create directly. Most likely from a command line
quadGate(filterId="myQuadGate1", "FSC-H"=100, "SSC-H"=400)

## To facilitate programmatic construction we also have the following
quadGate(filterId="myQuadGate2", list("FSC-H"=100, "SSC-H"=400))
## FIXME: Do we want this?
##quadGate(filterId="myQuadGate3", .gate=c("FSC-H"=100, "SSC-H"=400))

## Filtering using quadGates
qg <- quadGate(filterId="quad", "FSC-H"=600, "SSC-H"=400)
fres <- filter(dat, qg)
fres
summary(fres)
names(fres)

## The result of quadGate filtering are multiple sub-populations
## and we can split our data set accordingly
split(dat, fres)
```

```
## We can limit the splitting to one or several sub-populations
split(dat, fres, population="FSC-H-SSC-H-")
split(dat, fres, population=list(keep=c("FSC-H-SSC-H-",
"FSC-H-SSC-H+")))
```

---

quadratic-class *Class "quadratic"*

Description

Quadratic transform class which represents a transformation defined by the function

$$f(parameter, a) = a * parameter^2$$

Slots

`.Data` Object of class `"function"`.

`a` Object of class `"numeric"` – non-zero multiplicative constant.

`parameters` Object of class `"transformation"` – flow parameter to be transformed.

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

Objects from the Class

Objects can be created by calls to the constructor `quadratic(parameters,a,transformationId)`

Extends

Class `"singleParameterTransform"`, directly.

Class `"transform"`, by class "singleParameterTransform", distance 2.

Class `"transformation"`, by class "singleParameterTransform", distance 3.

Class `"characterOrTransformation"`, by class "singleParameterTransform", distance 4.

Note

The quadratic transformation object can be evaluated using the eval method by passing the data frame as an argument.The transformed parameters are returned as a column vector. (See example below)

Author(s)

Gopalakrishnan N, F.Hahne

References

Gating-ML Candidate Recommendation for Gating Description in Flow Cytometry V 1.5

See Also

dg1polynomial,ratio,squareroot

Other mathematical transform classes: EHtrans-class, asinht-class, asinhtGml2-class, dg1polynomial-class, exponential-class, hyperlog-class, hyperlogtGml2-class, invsplitscale-class, lintGml2-class, logarithm-class, logicletGml2-class, logtGml2-class, ratio-class, ratiotGml2-class, sinht-class, splitscale-class, squareroot-class, unitytransform-class

Examples

```
dat <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))
quad1<-quadratic(parameters="FSC-H",a=2,transformationId="quad1")
transOut<-eval(quad1)(exprs(dat))
```

---

quadraticTransform *Create the definition of a quadratic transformation function to be applied on a data set*

Description

Create the definition of the quadratic Transformation that will be applied on some parameter via the `transform` method. The definition of this function is currently x <- a*x\^2 + b*x + c

Usage

```
quadraticTransform(transformationId="defaultQuadraticTransform", a = 1, b = 1, c = 0)
```

Arguments

`transformationId`	character string to identify the transformation
`a`	double that corresponds to the quadratic coefficient in the equation
`b`	double that corresponds to the linear coefficient in the equation
`c`	double that corresponds to the intercept in the equation

Value

Returns an object of class `transform`.

Author(s)

N. Le Meur

See Also

transform-class, transform

Other Transform functions: arcsinhTransform(), biexponentialTransform(), inverseLogicleTransform(), linearTransform(), lnTransform(), logTransform(), logicleTransform(), scaleTransform(), splitScaleTransform(), truncateTransform()

Examples

```
samp <- read.FCS(system.file("extdata",
   "0877408774.B08", package="flowCore"))
 quadTrans <- quadraticTransform(transformationId="Quadratic-transformation", a=1, b=1, c=0)
  dataTransform <- transform(samp, transformList('FSC-H', quadTrans))
```

---

randomFilterResult-class

Class "randomFilterResult"

Description

Container to store the result of applying a filter on a flowFrame object, with the population membership considered to be stochastic rather than absolute. Currently not utilized.

Slots

subSet Object of class "numeric", which is a logical vector indicating the population membership of the data in the gated flowFrame.

frameId Object of class "character" referencing the flowFrame object filtered. Used for sanity checking.

filterDetails Object of class "list" describing the filter applied.

filterId Object of class "character" referencing the filter applied.

Extends

Class "filterResult", directly. Class "filter", by class "filterResult", distance 2.

Author(s)

B. Ellis

See Also

filter

ratio-class *Class "ratio"*

Description

ratio transform calculates the ratio of two parameters defined by the function

$$f(parameter_1, parameter_2) = \frac{parameter_1}{parameter_2}$$

Slots

`.Data` Object of class `"function"`.

`numerator` Object of class `"transformation"` – flow parameter to be transformed

`denominator` Object of class `"transformation"` – flow parameter to be transformed.

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

Objects from the Class

Objects can be created by calls to the constructor `ratio(parameter1,parameter2,transformationId)` .

Extends

Class `"transform"`, directly.

Class `"transformation"`, by class "transform", distance 2.

Class `"characterOrTransformation"`, by class "transform", distance 3.

Note

The ratio transformation object can be evaluated using the eval method by passing the data frame as an argument.The transformed parameters are returned as matrix with one column. (See example below)

Author(s)

Gopalakrishnan N, F.Hahne

References

Gating-ML Candidate Recommendation for Gating Description in Flow Cytometry V 1.5

See Also

dg1polynomial,quadratic,squareroot

Other mathematical transform classes: `EHtrans-class`, `asinht-class`, `asinhtGml2-class`, `dg1polynomial-class`, `exponential-class`, `hyperlog-class`, `hyperlogtGml2-class`, `invsplitscale-class`, `lintGml2-class`, `logarithm-class`, `logicletGml2-class`, `logtGml2-class`, `quadratic-class`, `ratiotGml2-class`, `sinht-class`, `splitscale-class`, `squareroot-class`, `unitytransform-class`

Examples

```
dat <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))
rat1<-ratio("FSC-H","SSC-H",transformationId="rat1")
transOut<-eval(rat1)(exprs(dat))
```

`ratiotGml2-class` *Class "ratiotGml2"*

Description

Ratio transformation as parameterized in Gating-ML 2.0.

Details

ratiotGml2 is defined by the following function:

$$bound(f, boundMin, boundMax) = max(min(f, boundMax), boundMin))$$

where

$$f(p1, p2, A, B, C) = A * (p1 - B)/(p2 - C)$$

If a boundary is defined by the boundMin and/or boundMax parameters, then the result of this transformation is restricted to the [boundMin,boundMax] interval. Specifically, should the result of the f function be less than boundMin, then let the result of this transformation be boundMin. Analogically, should the result of the f function be more than boundMax, then let the result of this transformation be boundMax. The boundMin parameter shall not be greater than the boundMax parameter.

Slots

`.Data` Object of class `function`.

`numerator` Object of class `"transformation"` – flow parameter to be used as numerator in the transformation function.

`denominator` Object of class `"transformation"` – flow parameter to be used as denominator in the transformation function.

`pA` Object of class `numeric` constant A.

`pB` Object of class `numeric` constant B.

`pC` Object of class `numeric` constant C.

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

`boundMin` Object of class `numeric` – lower bound of the transformation, default -Inf.

`boundMax` Object of class `numeric` – upper bound of the transformation, default Inf.

Objects from the Class

Objects can be created by calls to the constructor

`ratiotGml2(p1, p2, A, B, C, transformationId, boundMin, boundMax)`

Extends

Class "transform", directly.

Class "transformation", by class "transform", distance 2.

Class "characterOrTransformation", by class "transform", distance 3.

Note

The ratiotGml2 transformation object can be evaluated using the eval method by passing the data frame as an argument. The transformed parameters are returned as matrix with one column. (See example below)

Author(s)

Spidlen, J.

References

Gating-ML 2.0: International Society for Advancement of Cytometry (ISAC) standard for representing gating descriptions in flow cytometry. http://flowcyt.sourceforge.net/gating/20141009.pdf

See Also

ratio, transform-class, transform

Other mathematical transform classes: EHtrans-class, asinht-class, asinhtGml2-class, dg1polynomial-class, exponential-class, hyperlog-class, hyperlogtGml2-class, invsplitscale-class, lintGml2-class, logarithm-class, logicletGml2-class, logtGml2-class, quadratic-class, ratio-class, sinht-class, splitscale-class, squareroot-class, unitytransform-class

Examples

```
myDataIn <- read.FCS(system.file("extdata", "0877408774.B08",
    package="flowCore"))
myRatioT <- ratiotGml2("FSC-H", "SSC-H", pA = 2, pB = 3,
    pC = -10, transformationId = "myRatioT")
transOut <- eval(myRatioT)(exprs(myDataIn))
```

read.FCS *Read an FCS file*

Description

Check validity and Read Data File Standard for Flow Cytometry

Usage

```
isFCSfile(files)

read.FCS(filename, transformation="linearize", which.lines=NULL,
         alter.names=FALSE, column.pattern=NULL, invert.pattern = FALSE,
         decades=0, ncdf = FALSE, min.limit=NULL,
         truncate_max_range = TRUE, dataset=NULL, emptyValue=TRUE,
         channel_alias = NULL, ...)
```

Arguments

filename	Character of length 1: filename
transformation	An 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^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 NULL all the records are read, if of length 1, a random sample of the size indicated by which.lines is read in. It's used to achieve partial disk IO for the large FCS that can't fit the full data into memory. Be aware the potential slow read (especially for the large size of random sampling) due to the frequent disk seek operations.
alter.names	boolean indicating whether or not we should rename the columns to valid R names using make.names. The default is FALSE.
column.pattern	An optional regular expression defining parameters we should keep when loading the file. The default is NULL.
invert.pattern	logical. By default, FALSE. If TRUE, inverts the regular expression specified in column.pattern. This is useful for indicating the channel names that we do not want to read. If column.pattern is set to NULL, this argument is ignored.
decades	When scaling is activated, the number of decades to use for the output.

ncdf — Deprecated. Please use 'ncdfFlow' package for cdf based storage.

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. When the transformation keyword of the FCS header is set (typically to "custom" or "applied"), no shift up to min.limit will occur.

truncate_max_range — logical type. Default is TRUE. can be optionally turned off to avoid truncating the extreme positive value to the instrument measurement range .i.e.'$PnR'. When the transformation keyword of the FCS header is set (typically to "custom" or "applied"), no truncation will occur.

dataset — The FCS file specification allows for multiple data segments in a single file. Since the output of read.FCS is a single flowFrame we can't automatically read in all available sets. This parameter allows to chose one of the subsets for import. Its value is supposed to 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 — boolean indicating whether or not we allow empty value for keyword values in TEXT segment. It affects how the double delimiters are treated. IF TRUE, The double delimiters are parsed as a pair of start and end single delimiter for an empty value. Otherwise, double delimiters are parsed one part of string as the keyword value. default is TRUE.

channel_alias — an optional data.frame used to provide the alias of the channels to standardize and solve the discrepancy across FCS files. It is expected to contain 'alias' and 'channels' column of 'channel_alias'. Each row/entry specifies the common alias name for a collection of channels (comma separated). See examples for details.

For each channel in the FCS file, read.FCS will first attempt to find an exact match in the 'channels' column. If no exact match is found, it will check for partial matches. That is, if "V545" is in the 'channels' column of 'channel_alias' and "V545-A" is present in the FCS file, this partial match will allow the corresponding 'alias' to be assigned. This partial matching only works in this direction ("V545-A" in the 'channels' column will not match "V545" in the FCS file) and care should be exercised to ensure no unintended partial matching of other channel names. If no exact or partial match is found, the channel is unchanged in the resulting flowFrame.

... — ignore.text.offset: 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 discrepancy is found. User can turn it on to ignore TEXT segment when he is sure of the accuracy of HEADER so that the file still can be read.

files — A vector of filenames

Details

The function isFCSfile determines whether its arguments are valid FCS files.

The function read.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 me know. The output of the function is an object of class flowFrame.

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

isFCSfile returns a logical vector.

read.FCS returns an object of class flowFrame that contains the data in the exprs slot, the parameters monitored in the parameters slot and the keywords and value saved in the header of the FCS file.

Author(s)

F. Hahne, N.Le Meur

See Also

read.flowSet

Examples

```
## a sample file
fcsFile <- system.file("extdata", "0877408774.B08", package="flowCore")

## read file and linearize values
samp <-  read.FCS(fcsFile, transformation="linearize")
exprs(samp[1:3,])
keyword(samp)[3:6]
class(samp)

## Only read in lines 2 to 5
subset <- read.FCS(fcsFile, which.lines=2:5, transformation="linearize")
exprs(subset)

## Read in a random sample of 100 lines
subset <- read.FCS(fcsFile, which.lines=100, transformation="linearize")
nrow(subset)

#manually supply the alias vs channel options mapping as a data.frame
map <- data.frame(alias = c("A", "B")
                  , channels = c("FL2", "FL4")
)
fr <- read.FCS(fcsFile, channel_alias = map)
```

```
fr
```

`read.FCSheader` *Read the TEXT section of a FCS file*

Description

Read (part of) the TEXT section of a Data File Standard for Flow Cytometry that contains FACS keywords.

Usage

```
read.FCSheader(files, path = ".", keyword = NULL, ...)
```

Arguments

`files`	Character vector of filenames.
`path`	Directory where to look for the files.
`keyword`	An optional character vector that specifies the FCS keyword to read.
`...`	other arguments passed to `link[flowCore]{read.FCS}`

Details

The function `read.FCSheader` 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). The output of the function is the TEXT section of the FCS files. The user can specify some keywords to limit the output to the information of interest.

Value

A list of character vectors. Each element of the list correspond to one FCS file.

Author(s)

N.Le Meur

See Also

`link[flowCore]{read.flowSet}`, `link[flowCore]{read.FCS}`

Examples

```
samp <- read.FCSheader(system.file("extdata",
   "0877408774.B08", package="flowCore"))
samp

samp <- read.FCSheader(system.file("extdata",
   "0877408774.B08", package="flowCore"), keyword=c("$DATE", "$FIL"))
samp
```

`read.flowSet` *Read a set of FCS files*

Description

Read one or several FCS files: Data File Standard for Flow Cytometry

Usage

```
read.flowSet(files=NULL, path=".", pattern=NULL, phenoData,
             descriptions,name.keyword, alter.names=FALSE,
             transformation = "linearize", which.lines=NULL,
            column.pattern = NULL, invert.pattern = FALSE, decades=0, sep="\t",
             as.is=TRUE, name, ncdf=FALSE, dataset=NULL, min.limit=NULL,
             truncate_max_range = TRUE, emptyValue=TRUE,
             ignore.text.offset = FALSE, channel_alias = 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 `flowFrame` object, see details.
`descriptions`	Character vector to annotate the object of class `flowSet`.
`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 sampleNames, and if that is not present (or not unique), then the file names are used.
`alter.names`	see `read.FCS` for details.
`transformation`	see `read.FCS` for details.
`which.lines`	see `read.FCS` for details.
`column.pattern`	see `read.FCS` for details.
`invert.pattern`	see `read.FCS` for details.
`decades`	see `read.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 phenoDataslot.
name	An optional character scalar used as name of the object.
ncdf	Deprecated. Please refer to 'ncdfFlow' package for cdf based storage.
dataset	see read.FCS for details.
min.limit	see read.FCS for details.
truncate_max_range	see read.FCS for details.
emptyValue	see read.FCS for details.
ignore.text.offset	see read.FCS for details.
channel_alias	see read.FCS for details.
...	Further arguments that get passed on to read.AnnotatedDataFrame, see details.

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 flowSet.

Author(s)

F. Hahne, N.Le Meur, B. Ellis

Examples

```
fcs.loc <- system.file("extdata",package="flowCore")
file.location <- paste(fcs.loc, dir(fcs.loc), sep="/")

samp <- read.flowSet(file.location[1:3])
```

`rectangleGate-class` *Class "rectangleGate"*

Description

Class and constructor for n-dimensional rectangular `filter` objects.

Usage

```
rectangleGate(..., .gate, filterId="defaultRectangleGate")
```

Arguments

`filterId`	An optional parameter that sets the `filterId` of this gate. The object can later be identified by this name.
`.gate`	A definition of the gate. This can be either a list, or a matrix, as described below.
`...`	You can also directly provide the boundaries of a `rectangleGate` as additional named arguments, as described below.

Details

This class describes a rectangular region in `n` dimensions, which is a Cartesian product of `n` orthogonal intervals in these dimensions. `n=1` corresponds to a range gate, `n=2` to a rectangle gate, `n=3` corresponds to a box region and `n>3` to a hyper-rectangular regions. Intervals may be open on one side, in which case the value for the boundary is supposed to be `Inf` or `-Inf`, respectively. `rectangleGates` are inclusive, that means that events on the boundaries are considered to be in the gate.

The constructor is designed to be useful in both direct and programmatic usage. To use it programmatically, you may either construct a named list or you may construct a matrix with `n` columns and 2 rows. The first row corresponds to the minimal value for each parameter while the second row corresponds to the maximal value for each parameter. The names of the parameters are taken from the column names or from the list names, respectively. Alternatively, the boundaries of the `rectangleGate` can be given as additional named arguments, where each of these arguments should be a numeric vector of length 2; the function tries to collapse these boundary values into a matrix.

Note that boundaries of `rectangleGates` where `min > max` are syntactically valid, however when evaluated they will always be empty.

rectangleGate objects can also be multiplied using the * operator, provided that both gates have orthogonal axes. This results in higher-dimensional rectangleGates. The inverse operation of subsetting by parameter name(s) is also available.

Evaluating a rectangleGate generates an object of class logicalFilterResult. Accordingly, rectangleGates can be used to subset and to split flow cytometry data sets.

Value

Returns a rectangleGate object for use in filtering flowFrames or other flow cytometry objects.

Slots

min,max Objects of class "numeric". The minimum and maximum values of the n-dimensional rectangular region.

parameters Object of class "character", indicating the parameters for which the rectangleGate is defined.

filterId Object of class "character", referencing the filter.

Extends

Class "parameterFilter", directly.

Class "concreteFilter", by class parameterFilter, distance 2.

Class "filter", by class parameterFilter, distance 3.

Objects from the Class

Objects can be created by calls of the form new("rectangleGate",...), by using the constructor rectangleGate or by combining existing rectangleGates using the * method. Using the constructor is the recommended way of object instantiation.

Methods

%in% signature(x = "flowFrame", table = "rectangleGate"): The workhorse used to evaluate the filter on data. This is usually not called directly by the user, but internally by calls to the filter methods.

show signature(object = "rectangleGate"): Print information about the filter.

* signature(e1 = "rectangleGate", e2 = "rectangleGate"): combining two rectangleGates into one higher dimensional representation.

[signature(x = "rectangleGate", i = "character"): Subsetting of a rectangleGate by parameter name(s). This is essentially the inverse to *.

Note

See the documentation in the flowViz package for details on plotting of rectangleGates.

Author(s)

F.Hahne, B. Ellis N. Le Meur

See Also

flowFrame, polygonGate, ellipsoidGate, polytopeGate, filter for evaluation of rectangleGates and split and Subsetfor splitting and subsetting of flow cytometry data sets based on that.

Other Gate classes: ellipsoidGate-class, polygonGate-class, polytopeGate-class, quadGate-class

Examples

```
## Loading example data
dat <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))

#Create directly. Most likely from a command line
rectangleGate(filterId="myRectGate", "FSC-H"=c(200, 600), "SSC-H"=c(0, 400))

#To facilitate programmatic construction we also have the following
rg <- rectangleGate(filterId="myRectGate", list("FSC-H"=c(200, 600),
"SSC-H"=c(0, 400)))
mat <- matrix(c(200, 600, 0, 400), ncol=2, dimnames=list(c("min", "max"),
c("FSC-H", "SSC-H")))
rg <- rectangleGate(filterId="myRectGate", .gate=mat)

## Filtering using rectangleGates
fres <- filter(dat, rg)
fres
summary(fres)

## The result of rectangle filtering is a logical subset
Subset(dat, fres)

## We can also split, in which case we get those events in and those
## not in the gate as separate populations
split(dat, fres)

## Multiply rectangle gates
rg1 <- rectangleGate(filterId="FSC-", "FSC-H"=c(-Inf, 50))
rg2 <- rectangleGate(filterId="SSC+", "SSC-H"=c(50, Inf))
rg1 * rg2

## Subset rectangle gates
rg["FSC-H"]

##2d rectangleGate can be coerced to polygonGate
as(rg, "polygonGate")
```

---

rotate_gate *Simplified geometric rotation of gates*

Description

Rotate a Gate-type filter object through a specified angle

Usage

```
## Default S3 method:
rotate_gate(obj, deg = NULL, rot_center = NULL, ...)
```

Arguments

obj	An ellipsoidGate or polygonGate
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.
...	Additional arguments not used

Details

This method allows for 2-dimensional 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. Further, keep in mind that the 2-dimensional rotation takes place in the plane where the dimensions of the two variables are evenly linearly scaled. Displaying a rotated ellipse in a plot where the axes are not scaled evenly may make it appear that the ellipse has been distorted even though this is not the case.

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.

Value

A Gate-type filter object of the same type as gate, with the rotation applied

Examples

```
## Not run:
#' # Rotates the original gate 15 degrees counter-clockwise
rotated_gate <- rotate_gate(original_gate, deg = 15)
# Rotates the original gate 270 degrees counter-clockwise
rotated_gate <- rotate_gate(original_gate, 270)

## End(Not run)
```

sampleFilter-class *Class "sampleFilter"*

Description

This non-parameter filter selects a number of events from the primary flowFrame.

Usage

```
sampleFilter(size, filterId="defaultSampleFilter")
```

Arguments

filterId	An optional parameter that sets the filterId of this filter. The object can later be identified by this name.
size	The number of events to select.

Details

Selects a number of events without replacement from a flowFrame.

Value

Returns a sampleFilter object for use in filtering flowFrames or other flow cytometry objects.

Slots

size Object of class "numeric". Then number of events that are to be selected.

filterId A character vector that identifies this filter.

Extends

Class "concreteFilter", directly.

Class "filter", by class concreteFilter, distance 2.

Objects from the Class

Objects can be created by calls of the form new("sampleFilter",...) or using the constructor sampleFilter. The latter is the recommended way.

Methods

%in% signature(x = "flowFrame", table = "sampleFilter"): The workhorse used to evaluate the gate on data. This is usually not called directly by the user, but internally by calls to the filter methods.

show signature(object = "sampleFilter"): Print information about the gate.

Author(s)

B. Ellis, F.Hahne

See Also

flowFrame, filter for evaluation of sampleFilters and split and Subsetfor splitting and subsetting of flow cytometry data sets based on that.

Examples

```
## Loading example data
dat <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))

#Create the filter
sf <- sampleFilter(filterId="mySampleFilter", size=500)
sf

## Filtering using sampleFilters
fres <- filter(dat, sf)
fres
summary(fres)

## The result of sample filtering is a logical subset
Subset(dat, fres)

## We can also split, in which case we get those events in and those
## not in the gate as separate populations
split(dat, fres)
```

---

scaleTransform — *Create the definition of a scale transformation function to be applied on a data set*

Description

Create the definition of the scale Transformation that will be applied on some parameter via the transform method. The definition of this function is currently x = (x-a)/(b-a). The transformation would normally be used to convert to a 0-1 scale. In this case, b would be the maximum possible value and a would be the minimum possible value.

Usage

```
scaleTransform(transformationId="defaultScaleTransform", a, b)
```

Arguments

transformationId	character string to identify the transformation
a	double that corresponds to the value that will be transformed to 0
b	double that corresponds to the value that will be transformed to 1

Value

Returns an object of class transform.

Author(s)

P. Haaland

See Also

transform-class, transform

Other Transform functions: arcsinhTransform(), biexponentialTransform(), inverseLogicleTransform(), linearTransform(), lnTransform(), logTransform(), logicleTransform(), quadraticTransform(), splitScaleTransform(), truncateTransform()

Examples

```
samp <- read.FCS(system.file("extdata",
   "0877408774.B08", package="flowCore"))
  scaleTrans <- scaleTransform(transformationId="Truncate-transformation", a=1, b=10^4)
  dataTransform <- transform(samp, transformList('FSC-H', scaleTrans))
```

---

scale_gate *Simplified geometric scaling of gates*

Description

Scale a Gate-type filter object in one or more dimensions

Usage

```
## Default S3 method:
scale_gate(obj, scale = NULL, ...)
```

Arguments

obj	A Gate-type filter object (quadGate, rectangleGate, ellipsoidGate, or polygonGate)
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.
...	Additional arguments 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 accompanyging scale transformation applied to its underlying data, see 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.

Value

A Gate-type filter object of the same type as gate, with the scaling applied

Examples

```
## Not run:
# Scales both dimensions by a factor of 5
scaled_gate <- scale_gate(original_gate, 5)

# Shrinks the gate in the first dimension by factor of 1/2
# and expands it in the other dimension by factor of 3
scaled_gate <- scale_gate(original_gate, c(0.5,3))

## End(Not run)
```

setOperationFilter-class *Class "setOperationFilter"*

Description

This is a Superclass for the unionFilter, intersectFilter, complementFilter and subsetFilter classes, which all consist of two or more component filters and are constructed using set operators (`&`, `|`, `!`, and `%&%` or `%subset%` respectively).

Slots

`filters` Object of class `"list"`, containing the component filters.

`filterId` Object of class `"character"` referencing the filter applied.

Extends

Class `"filter"`, directly.

Author(s)

B. Ellis

See Also

`filter`

Other setOperationFilter classes: `complementFilter-class`, `intersectFilter-class`, `subsetFilter-class`, `unionFilter-class`

shift_gate *Simplified geometric translation of gates*

Description

Shift a Gate-type filter object in one or more dimensions

Usage

```
## Default S3 method:
shift_gate(obj, dx = NULL, dy = NULL, center = NULL, ...)
```

Arguments

obj	A Gate-type filter object (quadGate, rectangleGate, ellipsoidGate, or polygonGate)
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 specifiying dx and/or dy)
...	Additional arguments 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 divinding boundary in each dimension. For ellipsoidGate objects, this will shift the center (and therefore all points of the ellipse). For polgonGate 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.

Value

A Gate-type filter object of the same type as gate, with the translation applied

Examples

```
## Not run:
# Moves the entire gate +500 in its first dimension and 0 in its second dimension
shifted_gate <- shift_gate(original_gate, dx = 500)

#Moves the entire gate +250 in its first dimension and +700 in its second dimension
shifted_gate <- shift_gate(original_gate, dx = 500, dy = 700)

# Same as previous
shifted_gate <- shift_gate(original_gate, c(500,700))

# Move the gate based on shifting its center to (700, 1000)
```

```
shifted_gate <- shift_gate(original_gate, center = c(700, 1000))

## End(Not run)
```

---

singleParameterTransform-class
Class "singleParameterTransform"

Description

A transformation that operates on a single parameter

Slots

`.Data` Object of class `"function"`. The transformation.

`parameters` Object of class `"transformation"`. The parameter to transform. Can be a derived parameter from another transformation.

`transformationId` Object of class `"character"`. An identifier for the object.

Objects from the Class

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

Extends

Class `"transform"`, directly. Class `"transformation"`, by class "transform", distance 2. Class `"characterOrTransformation"`, by class "transform", distance 3.

Author(s)

F Hahne

Examples

```
showClass("singleParameterTransform")
```

sinht-class *Class "sinht"*

Description

Hyperbolic sin transform class, which represents a transformation defined by the function:

$$f(parameter, a, b) = sinh(parameter/b)/a$$

This definition is such that it can function as an inverse of asinht using the same definitions of the constants a and b.

Slots

`.Data` Object of class `"function"`.

`a` Object of class `"numeric"` – non-zero constant.

`b` Object of class `"numeric"` – non-zero constant.

`parameters` Object of class `"transformation"` – flow parameter to be transformed

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

Objects from the Class

Objects can be created by calls to the constructor `sinht(parameter,a,b,transformationId)`.

Extends

Class "singleParameterTransform", directly.

Class "transform", by class "singleParameterTransform", distance 2.

Class "transformation", by class "singleParameterTransform", distance 3.

Class "characterOrTransformation", by class "singleParameterTransform", distance 4.

Note

The transformation object can be evaluated using the eval method by passing the data frame as an argument.The transformed parameters are returned as a matrix with a single column.(See example below)

Author(s)

Gopalakrishnan N, F.Hahne

References

Gating-ML Candidate Recommendation for Gating Description in Flow Cytometry V 1.5

See Also

asinht

Other mathematical transform classes: EHtrans-class, asinht-class, asinhtGml2-class, dg1polynomial-class, exponential-class, hyperlog-class, hyperlogtGml2-class, invsplitscale-class, lintGml2-class, logarithm-class, logicletGml2-class, logtGml2-class, quadratic-class, ratio-class, ratiotGml2-class, splitscale-class, squareroot-class, unitytransform-class

Examples

```
dat <- read.FCS(system.file("extdata","0877408774.B08",  package="flowCore"))
sinh1<-sinht(parameters="FSC-H",a=1,b=2000,transformationId="sinH1")
transOut<-eval(sinh1)(exprs(dat))
```

---

split-methods *Methods to split flowFrames and flowSets according to filters*

Description

Divide a flow cytometry data set into several subset according to the results of a filtering operation. There are also methods available to split according to a factor variable.

Details

The splitting operation in the context of flowFrames and flowSets is the logical extension of subsetting. While the latter only returns the events contained within a gate, the former splits the data into the groups of events contained within and those not contained within a particular gate. This concept is extremely useful in applications where gates describe the distinction between positivity and negativity for a particular marker.

The flow data structures in flowCore can be split into subsets on various levels:

flowFrame: row-wise splitting of the raw data. In most cases, this will be done according to the outcome of a filtering operation, either using a filter that identifiers more than one sub-population or by a logical filter, in which case the data is split into two populations: "in the filter" and "not in the filter". In addition, the data can be split according to a factor (or a numeric or character vector that can be coerced into a factor).

flowSet: can be either split into subsets of flowFrames according to a factor or a vector that can be coerced into a factor, or each individual flowFrame into subpopulations based on the filters or filterResults provided as a list of equal length.

Splitting has a special meaning for filters that result in multipleFilterResults or manyFilterResults, in which case simple subsetting doesn't make much sense (there are multiple populations that are defined by the gate and it is not clear which of those should be used for the subsetting operation). Accordingly, splitting of multipleFilterResults creates multiple subsets. The argument population can be used to limit the output to only one or some of the resulting subsets. It takes as values a character vector of names of the populations of interest. See the documentation of the different filter classes on how population names can be defined and the respective default values. For splitting of

logicalFilterResults, the population argument can be used to set the population names since there is no reasonable default other than the name of the gate. The content of the argument prefix will be prepended to the population names and '+' or '-' are finally appended allowing for more flexible naming schemes.

The default return value for any of the split methods is a list, but the optional logical argument flowSet can be used to return a flowSet instead. This only applies when splitting flowFrames, splitting of flowSets always results in lists of flowSet objects.

Methods

flowFrame methods:

split(x = "flowFrame", f = "ANY", drop = "ANY") Catch all input and cast an error if there is no method for f to dispatch to.

split(x = "flowFrame", f = "factor", drop = "ANY") Split a flowFrame by a factor variable. Length of f should be the same as nrow(x), otherwise it will be recycled, possibly leading to undesired outcomes. The optional argument drop works in the usual way, in that it removes empty levels from the factor before splitting.

split(x = "flowFrame", f = "character", drop = "ANY") Coerce f to a factor and split on that.

split(x = "flowFrame", f = "numeric", drop = "ANY") Coerce f to a factor and split on that.

split(x = "flowFrame", f = "filter", drop = "ANY") First applies the filter to the flowFrame and then splits on the resulting filterResult object.

split(x = "flowFrame", f = "logicalFilterResult", drop = "ANY") Split into the two subpopulations (in and out of the gate). The optional argument population can be used to control the names of the results.

split(x = "flowFrame", f = "manyFilterResult", drop = "ANY") Split into the several subpopulations identified by the filtering operation. Instead of returning a list, the additional logical argument codeflowSet makes the method return an object of class flowSet. The optional population argument takes a character vector indicating the subpopulations to use for splitting (as identified by the population name in the filterDetails slot).

split(x = "flowFrame", f = "multipleFilterResult", drop = "ANY") Split into the several subpopulations identified by the filtering operation. Instead of returning a list, the additional logical argument codeflowSet makes the method return an object of class flowSet. The optional population argument takes a character vector indicating the subpopulations to use for splitting (as identified by the population name in the filterDetails slot). Alternatively, this can be a list of characters, in which case the populations for each list item are collapsed into one flowFrame.

flowSet methods:

split(x = "flowSet", f = "ANY", drop = "ANY") Catch all input and cast an error if there is no method for f to dispatch to.

split(x = "flowSet", f = "factor", drop = "ANY") Split a flowSet by a factor variable. Length of f needs to be the same as length(x). The optional argument drop works in the usual way, in that it removes empty levels from the factor before splitting.

split(x = "flowSet", f = "character", drop = "ANY") Coerce f to a factor and split on that.

split(x = "flowSet", f = "numeric", drop = "ANY") Coerce `f` to a factor and split on that.

split(x = "flowSet", f = "list", drop = "ANY") Split a `flowSet` by a list of `filterResult`s (as typically returned by filtering operations on a `flowSet`). The length of the list has to be equal to the length of the `flowSet` and every list item needs to be a `filterResult` of equal class with the same parameters. Instead of returning a list, the additional logical argument codeflowSet makes the method return an object of class `flowSet`. The optional `population` argument takes a character vector indicating the subpopulations to use for splitting (as identified by the population name in the `filterDetails` slot). Alternatively, this can be a list of characters, in which case the populations for each list item are collapsed into one `flowFrame`. Note that using the `population` argument implies common population names for all`filterResult`s in the list and there will be an error if this is not the case.

Author(s)

F Hahne, B. Ellis, N. Le Meur

Examples

```
data(GvHD)
qGate <- quadGate(filterId="qg", "FSC-H"=200, "SSC-H"=400)

## split a flowFrame by a filter that creates
## a multipleFilterResult
samp <- GvHD[[1]]
fres <- filter(samp, qGate)
split(samp, qGate)

## return a flowSet rather than a list
split(samp, fres, flowSet=TRUE)

## only keep one population
names(fres)
##split(samp, fres, population="FSC-Height+SSC-Height+")


## split the whole set, only keep two populations
##split(GvHD, qGate, population=c("FSC-Height+SSC-Height+",
##"FSC-Height-SSC-Height+"))

## now split the flowSet according to a factor
split(GvHD, pData(GvHD)$Patient)
```

`splitscale-class` *Class "splitscale"*

Description

The split scale transformation class defines a transformation that has a logarithmic scale at high values and a linear scale at low values. The transition points are chosen so that the slope of the transformation is continuous at the transition points.

Details

The split scale transformation is defined by the function

$$f(parameter, r, maxValue, transitionChannel) = a * parameter + b, parameter <= t$$

$$(parameter, r, maxValue, transitionChannel) = log_{10}(c * parameter) * \frac{r}{d}, parameter > t$$

where,

$$b = \frac{transitionChannel}{2}$$

$$d = \frac{2 * log_{10}(e) * r}{transitionChannel} + log_{10}(maxValue)$$

$$t = 10^{log_{10}t}$$

$$a = \frac{transitionChannel}{2 * t}$$

$$log_{10}ct = \frac{(a * t + b) * d}{r}$$

$$c = 10^{log_{10}ct}$$

Slots

`.Data` Object of class `"function"`.

`r` Object of class `"numeric"` – a positive value indicating the range of the logarithmic part of the display.

`maxValue` Object of class `"numeric"` – a positive value indicating the maximum value the transformation is applied to.

`transitionChannel` Object of class `"numeric"` – non negative value that indicates where to split the linear vs. logarithmic transformation.

`parameters` Object of class `"transformation"` – flow parameter to be transformed.

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

Objects from the Class

Objects can be created by calls to the constructor `splitscale(parameters,r,maxValue,transitionChannel,transforma`

Extends

Class `"singleParameterTransform"`, directly. Class `"transform"`, by class "singleParameterTransform", distance 2. Class `"transformation"`, by class "singleParameterTransform", distance 3. Class `"characterOrTransformation"`, by class "singleParameterTransform", distance 4.

Note

The transformation object can be evaluated using the eval method by passing the data frame as an argument.The transformed parameters are returned as a matrix with a single column. (See example below)

Author(s)

Gopalakrishnan N, F.Hahne

References

Gating-ML Candidate Recommendation for Gating Description in Flow Cytometry

See Also

invsplitscale

Other mathematical transform classes: EHtrans-class, asinht-class, asinhtGml2-class, dg1polynomial-class, exponential-class, hyperlog-class, hyperlogtGml2-class, invsplitscale-class, lintGml2-class, logarithm-class, logicletGml2-class, logtGml2-class, quadratic-class, ratio-class, ratiotGml2-class, sinht-class, squareroot-class, unitytransform-class

Examples

```
dat <- read.FCS(system.file("extdata","0877408774.B08",package="flowCore"))
sp1<-splitscale("FSC-H",r=768,maxValue=10000,transitionChannel=256)
transOut<-eval(sp1)(exprs(dat))
```

`splitScaleTransform` *Compute the split-scale transformation describe by FL. Battye*

Description

The split scale transformation described by Francis L. Battye [B15] (Figure 13) consists of a logarithmic scale at high values and a linear scale at low values with a fixed transition point chosen so that the slope (first derivative) of the transform is continuous at that point. The scale extends to the negative of the transition value that is reached at the bottom of the display.

Usage

```
splitScaleTransform(transformationId="defaultSplitscaleTransform",
                    maxValue=1023, transitionChannel=64, r=192)
```

Arguments

transformationId	A name to assign to the transformation. Used by the transform/filter integration routines.
maxValue	Maximum value the transformation is applied to, e.g., 1023
transitionChannel	Where to split the linear versus the logarithmic transformation, e.g., 64
r	Range of the logarithm part of the display, ie. it may be expressed as the maxChannel - transitionChannel considering the maxChannel as the maximum value to be obtained after the transformation.

Value

Returns values giving the inverse of the biexponential within a certain tolerance. This function should be used with care as numerical inversion routines often have problems with the inversion process due to the large range of values that are essentially 0. Do not be surprised if you end up with population splitting about w and other odd artifacts.

Author(s)

N. LeMeur

References

Battye F.L. A Mathematically Simple Alternative to the Logarithmic Transform for Flow Cytometric Fluorescence Data Displays. http://www.wehi.edu.au/cytometry/Abstracts/AFCG05B.html.

See Also

transform

Other Transform functions: arcsinhTransform(), biexponentialTransform(), inverseLogicleTransform(), linearTransform(), lnTransform(), logTransform(), logicleTransform(), quadraticTransform(), scaleTransform(), truncateTransform()

Examples

```
data(GvHD)
ssTransform  <- splitScaleTransform("mySplitTransform")
after.1 <- transform(GvHD, transformList('FSC-H', ssTransform))

opar = par(mfcol=c(2, 1))
plot(density(exprs(GvHD[[1]])[, 1]), main="Original")
plot(density(exprs(after.1[[1]])[, 1]), main="Split-scale Transform")
```

squareroot-class *Class "squareroot"*

Description

Square root transform class, which represents a transformation defined by the function

$$f(parameter, a) = \sqrt{|\frac{parameter}{a}|}$$

Slots

`.Data` Object of class `"function"`

`a` Object of class `"numeric"` – non-zero multiplicative constant

`parameters` Object of class `"transformation"` – flow parameter to be transformed.

`transformationId` Object of class `"character"` – unique ID to reference the transformation.

Objects from the Class

Objects can be created by calls to the constructor `squareroot(parameters,a,transformationId)`

Extends

Class `"singleParameterTransform"`, directly.

Class `"transform"`, by class "singleParameterTransform", distance 2.

Class `"transformation"`, by class "singleParameterTransform", distance 3.

Class `"characterOrTransformation"`, by class "singleParameterTransform", distance 4.

Note

The squareroot transformation object can be evaluated using the eval method by passing the data frame as an argument.The transformed parameters are returned as a column vector. (See example below)

Author(s)

Gopalakrishnan N, F.Hahne

References

Gating-ML Candidate Recommendation for Gating Description in Flow Cytometry

See Also

dg1polynomial, ratio, quadratic

Other mathematical transform classes: EHtrans-class, asinht-class, asinhtGml2-class, dg1polynomial-class, exponential-class, hyperlog-class, hyperlogtGml2-class, invsplitscale-class, lintGml2-class, logarithm-class, logicletGml2-class, logtGml2-class, quadratic-class, ratio-class, ratiotGml2-class, sinht-class, splitscale-class, unitytransform-class

Examples

```
dat <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))
sqrt1<-squareroot(parameters="FSC-H",a=2,transformationId="sqrt1")
transOut<-eval(sqrt1)(exprs(dat))
```

Subset-methods *Subset a flowFrame or a flowSet*

Description

An equivalent of a subset function for flowFrame or a flowSet object. Alternatively, the regular subsetting operators can be used for most of the topics documented here.

Usage

```
Subset(x, subset, ...)
```

Arguments

x	The flow object, frame or set, to subset.
subset	A filter object or, in the case of flowSet subsetting, a named list of filters.
...	Like the original subset function, you can also select columns.

Details

The Subset method is the recommended method for obtaining a flowFrame that only contains events consistent with a particular filter. It is functionally equivalent to frame[as(filter(frame,subset),"logical"),] when used in the flowFrame context. Used in the flowSet context, it is equivalent to using fsApply to apply the filtering operation to each flowFrame.

Additionally, using Subset on a flowSet can also take a named list as the subset. In this case, the names of the list object should correspond to the sampleNames of the flowSet, allowing a different filter to be applied to each frame. If not all of the names are used or excess names are present, a warning will be generated but the valid filters will be applied for the rare instances where this is the intended operation. Note that a filter operation will generate a list of filterResult objects that can be used directly with Subset in this manner.

Value

Depending on the original context, either a flowFrame or a flowSet.

Author(s)

B. Ellis

See Also

split, subset

Examples

```
sample <- read.flowSet(path=system.file("extdata", package="flowCore"),
pattern="0877408774")
result <- filter(sample, rectangleGate("FSC-H"=c(-Inf, 1024)))
result
Subset(sample,result)
```

---

subsetFilter-class *Class subsetFilter*

Description

This class represents the action of applying a filter on the subset of data resulting from another filter. This is itself a filter that can be incorporated in to further set operations. This is similar to an intersectFilter, with behavior only differing if the component filters are data-driven.

Details

subsetFilters are constructed using the equivalent binary set operators "%&%" or "%subset%". The operator is not symmetric, as the filter on the right-hand side will take the subset of the filter on the left-hand side as input. Left-hand side operands can be a filter or list of filters, while the right-hand side operand must be a single filter.

Slots

filters Object of class "list", containing the component filters.

filterId Object of class "character" referencing the filter applied.

Extends

Class "filter", directly.

Author(s)

B. Ellis

See Also

filter, setOperationFilter

Other setOperationFilter classes: complementFilter-class, intersectFilter-class, setOperationFilter-class, unionFilter-class

---

summarizeFilter-methods

Methods for function summarizeFilter

Description

Internal methods to populate the filterDetails slot of a filterResult object.

Usage

```
summarizeFilter(result, filter)
```

Arguments

result	A filterResult (or one of its derived classes) representing the result of a filtering operation in whose filterDetails slot the information will be stored.
filter	The corresponding filter (or one of its derived classes).

Methods

summarizeFilter(result = "filterResult", filter = "filter") summarizeFilter methods are called during the process of filtering. Their output is a list, and it can be arbitrary data that should be stored along with the results of a filtering operation.

summarizeFilter(result = "filterResult", filter = "filterReference") see above

summarizeFilter(result = "filterResult", filter = "parameterFilter") see above

summarizeFilter(result = "filterResult", filter = "subsetFilter") see above

summarizeFilter(result = "logicalFilterResult", filter = "norm2Filter") see above

summarizeFilter(result = "logicalFilterResult", filter = "parameterFilter") see above

summarizeFilter(result = "multipleFilterResult", filter = "parameterFilter") see above

`timeFilter-class` *Class "timeFilter"*

Description

Define a `filter` that removes stretches of unusual data distribution within a single parameter over time. This can be used to correct for problems during data acquisition like air bubbles or clods.

Usage

```
timeFilter(..., bandwidth=0.75, binSize, timeParameter,
filterId="defaultTimeFilter")
```

Arguments

`...`	The names of the parameters on which the filter is supposed to work on. Names can either be given as individual arguments, or as a list or a character vector.
`filterId`	An optional parameter that sets the `filterId` slot of this gate. The object can later be identified by this name.
`bandwidth, binSize`	Numerics used to set the `bandwidth` and `binSize` slots of the object.
`timeParameter`	Character used to set the `timeParameter` slot of the object.

Details

Clods and disturbances in the laminar flow of a FACS instrument can cause temporal aberrations in the data acquisition that lead to artifactual values. `timeFilters` try to identify such stretches of disturbance by computing local variance and location estimates and to remove them from the data.

Value

Returns a timeFilter object for use in filtering `flowFrame`s or other flow cytometry objects.

Slots

`bandwidth` Object of class `"numeric"`. The sensitivity of the filter, i.e., the amount of local variance of the signal we want to allow.

`binSize` Object of class `"numeric"`. The size of the bins used for the local variance and location estimation. If `NULL`, a reasonable default is used when evaluating the filter.

`timeParameter` Object of class `"character"`, used to define the time domain parameter. If `NULL`, the filter tries to guess the time domain from the `flowFrame`.

`parameters` Object of class `"character"`, describing the parameters used to filter the `flowFrame`.

`filterId` Object of class `"character"`, referencing the filter.

Extends

Class "parameterFilter", directly.

Class "concreteFilter", by class parameterFilter, distance 2.

Class "filter", by class parameterFilter, distance 3.

Objects from the Class

Objects can be created by calls of the form new("timeFilter",...) or using the constructor timeFilter. Using the constructor is the recommended way.

Methods

%in% signature(x = "flowFrame", table = "timeFilter"): The workhorse used to evaluate the filter on data. This is usually not called directly by the user.

show signature(object = "timeFilter"): Print information about the filter.

Note

See the documentation of timeLinePlot in the flowViz package for details on visualizing temporal problems in flow cytometry data.

Author(s)

Florian Hahne

See Also

flowFrame, filter for evaluation of timeFilters and split and Subsetfor splitting and subsetting of flow cytometry data sets based on that.

Examples

```
## Loading example data
data(GvHD)
dat <- GvHD[1:10]

## create the filter
tf <- timeFilter("SSC-H", bandwidth=1, filterId="myTimeFilter")
tf

## Visualize problems
## Not run:
library(flowViz)
timeLinePlot(dat, "SSC-H")

## End(Not run)

## Filtering using timeFilters
fres <- filter(dat, tf)
fres[[1]]
```

```
summary(fres[[1]])
summary(fres[[7]])

## The result of rectangle filtering is a logical subset
cleanDat <- Subset(dat, fres)

## Visualizing after cleaning up
## Not run:
timeLinePlot(cleanDat, "SSC-H")

## End(Not run)

## We can also split, in which case we get those events in and those
## not in the gate as separate populations
allDat <- split(dat[[7]], fres[[7]])

par(mfcol=c(1,3))
plot(exprs(dat[[7]])[, "SSC-H"], pch=".")
plot(exprs(cleanDat[[7]])[, "SSC-H"], pch=".")
plot(exprs(allDat[[2]])[, "SSC-H"], pch=".")
```

`transform` *Transform a flowFrame or flowSet*

Description

Similar to the base transform method, this will transform the values of a flowFrame or flowSet object according to the transformations specified in one of two ways: 1. a [transformList][flowCore::transformList-class] or list of [transform][flowCore::transform-class] objects 2. named arguments specifying transformations to be applied to channels (see details)

Usage

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

Arguments

`_data`	a flowFrame or flowSet object
`translist`	a transformList object
`...`	other arguments. e.g. 'FL1-H' = myFunc('FL1-H')

Details

To specify the transformations in the second way, the names of these arguments should correspond to the new channel names and the values should be functions applied to channels currently present in the flowFrame or flowSet. There are a few examples below.

Examples

```
data(GvHD)
# logarithmically transform FL1-H and FL2-H for the entire flowSet
# using a transformList
fs <- transform(GvHD,
                transformList(c("FL1-H", "FL2-H"), list(log, log)))

# transform a single flowFrame using named arguments. Note the first
# transformation will overwrite FL1-H while the second will create a new
# channel
fr <- transform(GvHD[[1]],
                `FL1-H`=log(`FL1-H`),
                `logFL2`=log(`FL2-H`))
```

`transform-class` *'transform': a class for transforming flow-cytometry data by applying scale factors.*

Description

Transform objects are simply functions that have been extended to allow for specialized dispatch. All of the "...Transform" constructors return functions of this type for use in one of the transformation modalities.

Slots

`.Data` Object of class `"function"`

`transformationId` A name for the transformation object

Methods

`summary` Return the parameters

Author(s)

N LeMeur

See Also

`linearTransform`, `lnTransform`, `logicleTransform`, `biexponentialTransform`, `arcsinhTransform`, `quadraticTransform`, `logTransform`

Examples

```
cosTransform <- function(transformId, a=1, b=1){
  t = new("transform", .Data = function(x) cos(a*x+b))
  t@transformationId = transformId
  t
}

cosT <- cosTransform(transformId="CosT",a=2,b=1)

summary(cosT)
```

---

transformation-class *Class "transformation"*

Description

A virtual class to abstract transformations.

Objects from the Class

A virtual Class: No objects may be created from it.

Extends

Class "characterOrTransformation", directly.

Author(s)

N. Gopalakrishnan

---

transformFilter-class *A class for encapsulating a filter to be performed on transformed parameters*

Description

The transformFilter class is a mechanism for including one or more variable transformations into the filtering process. Using a special case of transform we can introduce transformations inline with the filtering process eliminating the need to process flowFrame objects before applying a filter.

Slots

transforms A list of transforms to perform on the target flowFrame

filter The filter to be applied to the transformed frame

filterId The name of the filter (chosen automatically)

Objects from the Class

Objects of this type are not generally created "by hand". They are a side effect of the use of the %on% method with a filter object on the left hand side and a transformList on the right hand side.

Extends

Class "filter", directly.

Author(s)

B. Ellis

See Also

"filter", "transform", transform

Examples

```
require(flowStats)
samp <- read.FCS(system.file("extdata", "0877408774.B08", package="flowCore"))

## Gate this object after log transforming the forward and side
## scatter variables
filter(samp, norm2Filter("FSC-H", "SSC-H", scale.factor=2)
       %on% transform("FSC-H"=log,"SSC-H"=log))
```

---

transformList-class *Class "transformList"*

Description

A list of transformMaps to be applied to a list of parameters.

Usage

```
transformList(from, tfun, to=from, transformationId =
"defaultTransformation")
```

Arguments

from, to	Characters giving the names of the measurement parameter on which to transform on and into which the result is supposed to be stored. If both are equal, the existing parameters will be overwritten.

`tfun` A list if functions or a character vector of the names of the functions used to transform the data. R's recycling rules apply, so a single function can be given to be used on all parameters.

`transformationId` The identifier for the object.

Slots

`transforms` Object of class `"list"`, where each list item is of class `transformMap`.

`transformationId` Object of class `"character"`, the identifier for the object.

Objects from the Class

Objects can be created by calls of the form `new("transformList", ...)`, by calling the `transform` method with key-value pair arguments of the form `key` equals character and `value` equals function, or by using the constructor `transformList`. See below for details

Methods

colnames `signature(x = "transformList")`: This returns the names of the parameters that are to be transformed.

c `signature(x = "transformList")`: Concatenate `transformLists` or regular lists and `transformLists`.

%on% `signature(e1 = "transformList", e2 = "flowFrame")`: Perform a transformation using the `transformList` on a `flowFrame` or `flowSet`.

Author(s)

B. Ellis, F. Hahne

See Also

`transform`, `transformMap`

Examples

```
tl <- transformList(c("FSC-H", "SSC-H"), list(log, asinh))
colnames(tl)
c(tl, transformList("FL1-H", "linearTransform"))
data(GvHD)
transform(GvHD[[1]], tl)
```

`transformMap-class` *A class for mapping transforms between parameters*

Description

This class provides a mapping between parameters and transformed parameters via a function.

Slots

`output` Name of the transformed parameter.

`input` Name of the parameter to transform.

`f` Function used to accomplish the transform.

Objects from the Class

Objects of this type are not usually created by the user, except perhaps in special circumstances. They are generally automatically created by the inline `transform` process during the creation of a `transformFilter`, or by a call to the `transformList` constructor.

Methods

show `signature(object = "transformList")`: Print details about the object.

Author(s)

B. Ellis, F. Hahne

See Also

`transform`, `transformList`

Examples

```
new("transformMap", input="FSC-H", output="FSC-H", f=log)
```

transformReference-class *Class "transformReference"*

Description

Class allowing for reference of transforms, for instance as parameters.

Slots

`.Data` The list of references.

`searchEnv` The environment into which the reference points.

`transformationId` The name of the transformation.

Objects from the Class

Objects will be created internally whenever necessary and this should not be of any concern to the user.

Extends

Class "transform", directly. Class "transformation", by class "transform", distance 2. Class "characterOrTransformation", by class "transform", distance 3.

Author(s)

N. Gopalakrishnan

transform_gate *Simplified geometric transformation of gates*

Description

Perform geometric transformations of Gate-type `filter` objects

Usage

```
## Default S3 method:
transform_gate(
  obj,
  scale = NULL,
  deg = NULL,
  rot_center = NULL,
  dx = NULL,
  dy = NULL,
  center = NULL,
  ...
)
```

Arguments

obj	A Gate-type filter object (quadGate, rectangleGate, ellipsoidGate, or polygonGate)
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.
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 specifiying 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 accompanyging scale transformation applied to its underlying data, see 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.

Value

A Gate-type filter object of the same type as gate, with the geometric transformations applied

Examples

```
## Not run:
# Scale the original gate non-uniformly, rotate it 15 degrees, and shift it
transformed_gate <- transform_gate(original_gate, 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)
transformed_gate <- transform_gate(original_gate, scale = c(2,3), mean = c(1500, 2000))

## End(Not run)
```

---

truncateTransform *Create the definition of a truncate transformation function to be applied on a data set*

Description

Create the definition of the truncate Transformation that will be applied on some parameter via the transform method. The definition of this function is currently x[x<a] <- a. Hence, all values less than a are replaced by a. The typical use would be to replace all values less than 1 by 1.

Usage

```
truncateTransform(transformationId="defaultTruncateTransform", a=1)
```

Arguments

transformationId	character string to identify the transformation
a	double that corresponds to the value at which to truncate

Value

Returns an object of class `transform`.

Author(s)

P. Haaland

See Also

`transform-class`, `transform`

Other Transform functions: `arcsinhTransform()`, `biexponentialTransform()`, `inverseLogicleTransform()`, `linearTransform()`, `lnTransform()`, `logTransform()`, `logicleTransform()`, `quadraticTransform()`, `scaleTransform()`, `splitScaleTransform()`

Examples

```
samp <- read.FCS(system.file("extdata",
   "0877408774.B08", package="flowCore"))
  truncateTrans <- truncateTransform(transformationId="Truncate-transformation", a=5)
  dataTransform <- transform(samp,transformList('FSC-H', truncateTrans))
```

---

unionFilter-class *Class unionFilter*

Description

This class represents the union of two filters, which is itself a filter that can be incorporated in to further set operations. `unionFilters` are constructed using the binary set operator `"|"` with operands consisting of a single `filter` or list of `filters`.

Slots

`filters` Object of class `"list"`, containing the component filters.

`filterId` Object of class `"character"` referencing the filter applied.

Extends

Class `"filter"`, directly.

Author(s)

B. Ellis

See Also

filter, setOperationFilter

Other setOperationFilter classes: complementFilter-class, intersectFilter-class, setOperationFilter-class, subsetFilter-class

---

`unitytransform-class` *Class "unitytransform"*

Description

Unity transform class transforms parameters names provided as characters into unity transform objects which can be evaluated to retrieve the corresponding columns from the data frame

Slots

`.Data` Object of class `"function"`.

`parameters` Object of class `"character"` – the flow parameters to be transformed.

`transformationId` Object of class `"character"` – a unique Id to reference the transformation.

Objects from the Class

Objects can be created by calls to the constructor `unitytransform(parameters,transformationId)`.

Extends

Class `"transform"`, directly.

Class `"transformation"`, by class "transform", distance 2.

Class `"characterOrTransformation"`, by class "transform", distance 3.

Author(s)

Gopalakrishnan N, F.Hahne

See Also

dg1polynomial, ratio

Other mathematical transform classes: EHtrans-class, asinht-class, asinhtGml2-class, dg1polynomial-class, exponential-class, hyperlog-class, hyperlogtGml2-class, invsplitscale-class, lintGml2-class, logarithm-class, logicletGml2-class, logtGml2-class, quadratic-class, ratio-class, ratiotGml2-class, sinht-class, splitscale-class, squareroot-class

Examples

```
dat <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))
un1<-unitytransform(c("FSC-H","SSC-H"),transformationId="un1")
transOut<-eval(un1)(exprs(dat))
```

updateTransformKeywords

modify description to reflect the transformation Involve inserting/updating 'transformation' and flowCore_$PnRmax keywords

Description

modify description to reflect the transformation Involve inserting/updating 'transformation' and flowCore_$PnRmax keywords

Usage

```
updateTransformKeywords(fr)
```

Arguments

fr	flowFrame

Value

updated description slot

validFilters

Check if all filters in a filters matches same paramters

Description

Check if all filters in a filters matches same paramters

Usage

```
validFilters(flist)
```

Arguments

flist	a filters object

Value

TRUE or FALSE

write.FCS *Write an FCS file*

Description

Write FCS file from a flowFrame

Usage

```
write.FCS(x, filename, what="numeric", delimiter = "|", endian="big")
```

Arguments

x	A flowFrame.
filename	A character scalar giving the output file name.
what	A character scalar defining the output data type. One in integer, numeric, double. Note that forcing the data type to integer may result in considerable loss of precision if the data has been transformed. We recommend using the default data type unless disc space is an issue.
delimiter	a single character to separate the FCS keyword/value pairs. Default is : "|"
endian	a character, either "little" or "big" (default), specifying the most significant or least significant byte is stored first in a 32 bit word.

Details

The function write.FCS creates FCS 3.0 standard file from an object of class flowFrame.

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.

Value

A character vector of the file name.

Author(s)

F. Hahne

See Also

link[flowCore]{write.flowSet}

Examples

```
## a sample file
inFile <- system.file("extdata", "0877408774.B08", package="flowCore")
foo <- read.FCS(inFile, transform=FALSE)
outFile <- file.path(tempdir(), "foo.fcs")

## now write out into a file
write.FCS(foo, outFile)
bar <- read.FCS(outFile, transform=FALSE)
all(exprs(foo) == exprs(bar))
```

---

write.flowSet *Write an FCS file*

Description

Write FCS file for each flowFrame in a flowSet

Usage

```
write.flowSet(x, outdir=identifier(x), filename, ...)
```

Arguments

x	A flowSet.
outdir	A character scalar giving the output directory. As the default, the output of identifier(x) is used.
filename	A character scalar or vector giving the output file names. By default, the function will use the identifiers of the individual flowFrames as the file name, potentially adding the .fcs suffix unless a file extension is already present. Alternatively, one can supply either a character scalar, in which case the prefix i_ is appended (i being an integer in seq_len(length(x))), or a character vector of the same length as the flowSet x.
...	Further arguments that are passed on to write.FCS.

Details

The function write.flowSet creates FCS 3.0 standard file for all flowFrames in an object of class flowSet. In addition, it will write the content of the phenoData slot in the ASCII file "annotation.txt". This file can subsequently be used to reconstruct the whole flowSet using the read.flowSet function, e.g.:

```
read.flowSet(path=outdir, phenoData="annotation.txt"
```

The function uses write.FCS for the actual writing of the FCS files.

Value

A character vector of the output directory.

Author(s)

F. Hahne

See Also

link[flowCore]{write.FCS}

Examples

```
## sample data
data(GvHD)
foo <- GvHD[1:5]
outDir <- file.path(tempdir(), "foo")

## now write out into  files
write.flowSet(foo, outDir)
dir(outDir)

## and read back in
bar <- read.flowSet(path=outDir, phenoData="annotation.txt")
```

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