Package ‘ggcyto’

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Type Package
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Description With the dedicated fortify method implemented for flowSet, ncdfflowSet and GatingSet classes, both raw and gated flow cytometry data can be plotted directly with ggplot. ggcyto wrapper and some customized layers also make it easy to add gates and population statistics to the plot.
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'fortify_fs.R' 'geom_gate.R' 'geom_hvline.R'
'geom_multi_range.R' 'geom_overlay.R' 'geom_stats.R'
'getFlowFrame.R' 'ggcyto.R' 'ggcyto_GatingLayout.R'
'ggcyto_GatingSet.R' 'ggcyto_flowSet.R' 'labs.R' 'ggcyto_par.R'
'ggplot_data_frame.R' 'merge_quad.gates.R' 'replace_data.R'
scales_flowCore_fasinh.R' scales_flowJo_bieexp.R'
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It fortifies the data, fills some default settings and returns a regular ggplot object.

Description

The orginal data format is preserved during the ggcyo constructor because they still need to be used during the plot building process. This function is usually called automatically in the print/plot method of ggcyto. Sometime it is useful to coerce it to ggplot explicitily by user so that it can be used as a regular ggplot object.

Usage

as.ggplot(x, pre_binning = FALSE)

Arguments

x: ggcyto object with the data that has not yet been fortified to data.frame.

pre_binning: whether to pass the binned data to ggplot to avoid the overhead to scaling the original raw data for geom_hex layer

Value

ggplot object

Examples

data(GvHD)
fs <- GvHD[1:3]
# construct the `ggcyto` object (inherits from `ggplot` class)
p <- ggcyto(fs, aes(x = `FSC-H`)) + geom_histogram()
class(p) # a ggcyto object
p$data # data has not been fortified
p1 <- as.ggplot(p) # convert it to a ggplot object explicitily
class(p1)
p1$data # data is fortified
autoplot.flowSet

Plot cytometry data in one or two dimension with the ggcyo package.

Description

Overloaded autoplot methods for the cytometry data structure: flowFrame or flowSet, Gatinghierarchy, GatingSet. It plots the cytometry data with geom_histogram, geom_density or geom_hex. When autoplot is called on a GatingSet/Gatinghierarchy, the second argument should be a gate or population node. And the dimensions(channels/markers) are deduced from the gate dimensions.

Usage

```r
## S3 method for class 'flowSet'
autoplot(object, x, y = NULL, bins = 30, ...)

## S3 method for class 'ncdfFlowList'
autoplot(object, ...)

## S3 method for class 'cytoset'
autoplot(object, ...)

## S3 method for class 'cytoframe'
autoplot(object, ...)

## S3 method for class 'flowFrame'
autoplot(object, x, ...)

## S3 method for class 'GatingSetList'
autoplot(object, ...)

## S3 method for class 'GatingSet'
autoplot(
  object,
  gate,
  x = NULL,
  y = "SSC-A",
  bins = 30,
  axis_inverse_trans = TRUE,
  ...
)

## S3 method for class 'GatingHierarchy'
autoplot(
  object,
  gate,
  y = "SSC-A",
  bool = FALSE,
...
autoplot.flowSet

```r
arrange.main = sampleNames(object),
arrange = TRUE,
merge = TRUE,
projections = list(),
strip.text = c("parent", "gate"),
path = "auto",
... )
```

**Arguments**

- `object` The data source. A core cytometry data structure. A flowFrame, flowSet, GatingSet or GatingHierarchy object
- `x` define the x dimension of the plot (not used when object is a GatingSet). When object is a flowFrame, it can be missing, which plots 1d density plot on all the channels.
- `y` define the y dimension of the plot. Default is NULL, which means 1d density-plot.
- `bins` passed to geom_hex
- `...` other arguments passed to ggplot
- `gate` the gate to be plotted
- `axis_inverse_trans` logical flag indicating whether to add `axis_x_inverse_trans` and `axis_x_inverse_trans` layers.
- `bool` whether to plot boolean gates
- `arrange.main` the main title of the arranged plots
- `arrange` whether to use arrangeGrob to put multiple plots in the same page
- `merge` whether to merge multiple gates into the same panel when they share the same parent and projections
- `projections` a list of customized projections
- `strip.text` either "parent" (the parent population name) or "gate" (the gate name). The latter usually is used when merge is FALSE
- `path` the gating path format (passed to `gs_get_pop_paths`)

**Value**

- a ggcyto object

**Examples**

```r
library(flowCore)
data(GvHD)
fs <- GvHD[subset(pData(GvHD), Patient %in% 5:7 & Visit %in% c(5:6))[["name"]]

#1d- density plot
autoplot(fs, x = "SSC-H")
```
#1d- density plot on all channels
autoplot(fs[[1]])

#2d plot: default geom_hex plot
autoplot(fs, x = 'FSC-H', y = 'SSC-H')

#autplot for GatingSet
dataDir <- system.file("extdata", package = "flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual", full = TRUE))
autoplot(gs, "CD3+)
#display axis values in transformed scale
autoplot(gs, "CD3+", axis_inverse_trans = FALSE)

#autplot for GatingHierarchy
gh <- gs[[1]]
autoplot(gh) # by default the strip.text shows the parent population

#To display the gate name
#autoplot(gh, strip.text = "gate")

axis_x_inverse_trans

Display ggcyto axis labels using their raw values (as stored in the data structure)

Description

It is essentially a dummy continuous scale and will be instantiated by '+.ggcyto_GatingSet' with 'breaks' and 'labels' customized.

Usage

axis_x_inverse_trans(...)

axis_y_inverse_trans(...)

Arguments

... common continuous scale parameters passed to 'continuous_scale' (not used currently)

Value

a raw_scale object that inherits scale class.
compute_stats

Examples

dataDir <- system.file("extdata",package="flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual",full = TRUE))
p <- ggcyto(gs, aes(x = CD4, y = CD8), subset = "CD3") + geom_hex(bins = 64)
p <- p + geom_gate("CD4") + geom_stats() #plot CD4 gate and it is stats
p
p + axis_x_inverse_trans() #inverse transform the x axis into raw scale

compute_stats

compute the statistics of the cell population defined by gates

Description

It calls the underlining stats routine and merge it with the label position calculated by stat_position as well as the pData of flowSet.

Usage

compute_stats(fs = NULL, gates, type = "percent", value = NULL, ...)

Arguments

fs  
flowSet. can be NULL when precaculated 'value' is provided

gates  
a list of filters

type  
a vector of strings to specify the stats types. can be any or multiple values of "percent", "count", "gate_name", or "MFI" (MFI is currently not supported yet).

value  
the pre-calculated stats value. when supplied, the stats computing is skipped.

...  
other arguments passed to stat_position function

Details

This function is usually not called directly by user but used by ggcyto when geom_stat layer is added.

Value

a data.table that contains percent and centroid locations as well as pData that used as data for geom_btext layer.

Examples

data(GvHD)
fs <- GvHD[1:4]
rect.g <- rectangleGate(list("FSC-H" = c(300,500), "SSC-H" = c(50,200)), filterId = "P1")
rect.gates <- sapply(sampleNames(fs), function(sn)rect.g)
compute_stats(fs, rect.gates)
compute_stats(fs, rect.gates, type = c("gate_name", "percent"))
faust_gating_plot  plot faust gating schemes

Description
plot faust gating schemes

Usage
faust_gating_plot(gh, start_node, end_node, ...)

Arguments
start_node  faust start node
end_node    the terminal leaf node generated by faust

Examples
## Not run:
gs=load_gs("~/Downloads/ics")
end_node = "/S/LV/L/CD4+/CD3+/CD8-/TNF+/CD107a-/IL4-/IFNg+/IL2+/CD154-/IL17a-"
start_node = "/S/LV/L"
gh=gs[[1]]
p = faust_gating_plot(gh, start_node, end_node, bins=128)
plot(ggcyto_arrange(p, nrow=1))
## End(Not run)

flowCore_asinht_trans  Inverse hyperbolic sine transformation(flowCore version).

Description
Used to construct inverse hyperbolic sine transform object.

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

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

Value

asinht transformation object

Examples

trans.obj <- flowCore_asinht_trans(equal.space = TRUE)
data <- 1:1e3
brks.func <- trans.obj["breaks"]
brks <- brks.func(data)
brks # asinh space displayed at raw data scale

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

fortify.cytoframe  Convert a flowFrame/flowSet/GatingSet to a ggplot-compatible data.table

Description

It extracts events matrices and appends the pData to it so that ggplot can use the pData for facetting.

Usage

## S3 method for class 'cytoframe'
fortify(model, ...)

## S3 method for class 'flowFrame'
fortify(model, data, ...)

## S3 method for class 'flowSet'
fortify(model, data, ...)

## S3 method for class 'cytoset'
fortify(model, ...)

## S3 method for class 'ncdfFlowList'
fortify(model, ...)

## S3 method for class 'GatingSetList'
fortify(model, ...)

## S3 method for class 'GatingSet'
fortify(model, ...)
fortify.ellipsoidGate

Arguments

model ellipsoidGate, flowFrame, flowSet or GatingSet
... not used.
data not used.

Value
data.table
data.table
data.table

Examples
dataDir <- system.file("extdata",package="flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual",full = TRUE))
attr(gs, "subset") <- "CD4" #must attach subset information to GatingSet object before fortifying it
fortify(gs)

fs <- gs_pop_get_data(gs, "CD8")
f Fortify(fs)#fs is a flowSet/ncdfFlowSet

fr <- fs[[1]]
fortify(fr)#fr is a flowFrame

fortify.ellipsoidGate  Convert a ellipsoidGate to a data.table useful for ggplot

Description
It interpolates the ellipsoidGate to polygonGate before fortifying it.

Usage
## S3 method for class 'ellipsoidGate'
f Fortify(model, data = NULL, ...)

Arguments
model ellipsoidGate
data data range used for polygon interpolation.
... not used.

Value
data.table
Examples

```r
## 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)
fortify(eg)
```

---

**fortify.filterList**

*Convert a filterList to a data.table useful for ggplot*

### Description

It tries to merge with pData that is associated with filterList as attribute 'pd'

### Usage

```r
## S3 method for class 'filterList'
fortify(model, data = NULL, nPoints = NULL, ...)
```

### Arguments

- `model`: filterList
- `data`: not used
- `nPoints`: not used
- `...`: not used.

### Value

data.table

### Examples

```r
dataDir <- system.file("extdata", package="flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual", full = TRUE))
gates <- gs_pop_get_gate(gs, "CD4")
gates <- as(gates, "filterList") #must convert list to filterList in order for the method to dispatch properly
fortify(gates)
```
fortify.multiRangeGate

Convert a multiRangeGate to a data.table useful for ggplot

Description

It converts the boundaries slot into a data.table

Usage

## S3 method for class 'multiRangeGate'
fortify(model, data = NULL, ...)

Arguments

- model: multiRangeGate
- data: Not used
- ...: not used.
- nPoints: not used

Value

data.table

Examples

mrq = multiRangeGate(ranges = list(min=c(100, 350), max=c(250, 400)))
fortify(mrq)

fortify.polygonGate

Convert a polygonGate to a data.table useful for ggplot

Description

It converts the boundaries slot into a data.table

Usage

## S3 method for class 'polygonGate'
fortify(model, data = NULL, nPoints = NULL, ...)

Examples

mrq = polygonGate(boundaries = list(min=c(100, 350), max=c(250, 400)))
fortify(mrq)
**fortify.rectangleGate**

**Arguments**

- **model**: polygonGate
- **data**: data range used to reset off-bound gate coordinates to prevent interpolating on the extremely large space unnecessarily.
- **nPoints**: not used
- **...**: not used.

**Value**

data.table

**Examples**

```r
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", .gate= sqrcut)
fortify(pg)
```

**Description**

For 2d rectangleGate, it is converted to a polygonGate first and then dispatch to the fortify method for polygonGate. for 1d, uses geom_vline/hline format.

**Usage**

```r
## S3 method for class 'rectangleGate'
fortify(model, data = NULL, ...)
```

**Arguments**

- **model**: rectangleGate
- **data**: data range used for polygon interpolation.
- **...**: not used.

**Value**

data.table
Examples

```r
# 2d rectangleGate
rect.g <- rectangleGate(list("FSC-H" = c(300,500), "SSC-H" = c(50,200)))
fortify(rect.g)

# 1d gate
rg <- rectangleGate(list("FSC-H" = c(300,500)))
fortify(rg)
```

---

### fortify_fs

Fortify a model into flowSet object

Description

The method provides a universe interface to convert a generic R object into a flowSet useful for ggcyto

Usage

```r
fortify_fs(model, data, ...)
```

## S3 method for class 'flowSet'

```r
fortify_fs(model, data, ...)
```

## Default S3 method:

```r
fortify_fs(model, data, ...)
```

## S3 method for class 'flowFrame'

```r
fortify_fs(model, data, ...)
```

## S3 method for class 'cytoframe'

```r
fortify_fs(model, data, ...)
```

## S3 method for class 'GatingSetList'

```r
fortify_fs(model, data, ...)
```

## S3 method for class 'GatingSet'

```r
fortify_fs(model, data, ...)
```

Arguments

- **model**: flow object (flowFrame or GatingSet) to be converted to flowSet. When it is a GatingSet, it must contain the subset information stored as 'subset' attribute.
- **data**: original dataset, if needed
- **...**: other arguments passed to methods
**gate_null**

Value

a flowSet/ncdfFlowSet object

Examples

data(GvHD)
fr <- GvHD[[1]]
fortify_fs(fr)

dataDir <- system.file("extdata",package="flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual",full = TRUE))
attr(gs, "subset") <- "CD4"
fortify_fs(gs)

clear all the geom_gate() layer previously added

Description

clear all the geom_gate() layer previously added

Usage

gate_null()

Examples

dataDir <- system.file("extdata",package="flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual",full = TRUE))
#autoplot display pop stats by default
p <- autoplot(gs, "CD4")
#it is easy to remove the default gate
p <- p + gate_null()
#and add a new one
p <- p + geom_gate("CD8")
p

**geom_gate**

Add a gate layer to a ggcyto plot.

Description

When 'data' is a gate (or flowCore filter) or a list of gates or a filterList object. When it is used
directly with 'ggplot', pdata of the flow data must be supplied through 'pd' argument explicitly in
order for the gates to be dispatched to each panel. However It is not necessary when used with
'ggcyto' wrapper since the latter will attach pData automatically.
Usage

geom_gate(data, ...)

## S3 method for class 'filterList'
geom_gate(data, pd, nPoints = 100, ...)

## S3 method for class 'filter'
geom_gate(data, mapping = NULL, fill = NA, colour = "red", nPoints = 100, ...)

Arguments

data
  a filter (Currently only rectangleGate (1d or 2d), polygonGate, ellipsoidGate are supported.) or a list of these gates or filterList or character specifying a gated cell population in the GatingSet

... other arguments

pd
  pData (data.frame) that has rownames represents the sample names used as key to be merged with filterList

nPoints
  used for interpolating polygonGates to prevent them from losing shape when truncated by axis limits

mapping
  The aesthetic mapping

fill
  fill color for the gate. Not filled by default.

colour
  default is red

Details

When 'data' is a character, it construct an abstract geom layer for a character that represents nodes in a Gating tree and will be instantiated later as a specific geom_gate layer or layers based on the gates extracted from the given GatingSet object.

Value

a geom_gate layer

Examples

data(GvHD)
fs <- GvHD[subset(pData(GvHD), Patient %in% 5:7 & Visit %in% c(5:6))[["name"]]]
p <- ggcyto(fs, aes(x = `FSC-H`, y = `SSC-H`))
p <- p + geom_hex(bins = 128)
rect.g <- rectangleGate(list("FSC-H" = c(300,500), "SSC-H" = c(50,200)))
# constructor for a list of filters
rect.gates <- sapply(sampleNames(fs), function(sn)rect.g)
rect.gates <- sapply(sampleNames(fs), function(sn)rect.g)
p + geom_gate(rect.gates)
dataDir <- system.file("extdata", package = "flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual", full = TRUE))
p <- ggcyto(gs, aes(x = CD4, y = CD8), subset = "CD3+") + geom_hex(bins = 64)
# add gate layer by gate name
p + geom_gate("CD4")
geom_hvline

Vertical or horizontal line.

Description

This geom is based on the source code of `geom_hline` and `geom_vline`.

Usage

```r
geom_hvline(
  mapping = NULL,
  data = NULL,
  position = "identity",
  show.legend = FALSE,
  ...
)
```

Arguments

- **mapping**: The aesthetic mapping, usually constructed with `aes` or `aes_string`. Only needs to be set at the layer level if you are overriding the plot defaults.
- **data**: A layer specific dataset - only needed if you want to override the plot defaults.
- **position**: The position adjustment to use for overlapping points on this layer.
- **show.legend**: should a legend be drawn? (defaults to FALSE)
- **...**: other arguments passed on to `layer`. This can include aesthetics whose values you want to set, not map. See `layer` for more details.

Details

The goal is to determine the line to be either vertical or horizontal based on the 1-d data provided in this layer.

Value

A `geom_hvline` layer

Aesthetics

@section Aesthetics: `geom_vline()` understands the following aesthetics (required aesthetics are in bold):

- `xintercept`
- `alpha`
- `colour`
- `group`
• **linetype**
• **linewidth**

Learn more about setting these aesthetics in vignette("ggplot2-specs").

**Examples**

```r
p <- ggplot(mtcars, aes(x = wt, y = mpg)) + geom_point()
# vline
p + geom_hvline(data = data.frame(wt= 3))
# hline
p + geom_hvline(data = data.frame(mpg= 20))
```

---

**geom_multi_range**

*Draw multi-ranges as multiple rectangles on 1D or 2D plot*

**Description**

This geom is based on the source code of `geom_rect`.

**Usage**

```r
geom_multi_range(
  mapping = NULL,
  data = NULL,
  stat = "identity",
  position = "identity",
  ...,  
  linejoin = "mitre",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE
)
```

**Arguments**

- **mapping** The aesthetic mapping, usually constructed with `aes` or `aes_string`. Only needs to be set at the layer level if you are overriding the plot defaults.
- **data** A layer specific dataset - only needed if you want to override the plot defaults.
- **position** The position adjustment to use for overlapping points on this layer
- **...** other arguments passed on to `layer`. This can include aesthetics whose values you want to set, not map. See `layer` for more details.
- **show.legend** should a legend be drawn? (defaults to FALSE)
Details

The goal is to determine the line to be either vertical or horizontal based on the data provided in this layer. Also convert input 1D intervals to geom_rect acceptable shapes

Value

a geom_rect layer

Aesthetics

@section Aesthetics: geom_vline() understands the following aesthetics (required aesthetics are in bold):

- xintercept
- alpha
- colour
- group
- linetype
- linewidth

Learn more about setting these aesthetics in vignette("ggplot2-specs").

Description

It is useful for "backgating" plots.

Usage

geom_overlay(data, ...)

Arguments

data a filter (Currently only rectangleGate (1d or 2d), polygonGate, ellipsoidGate are supported.) or a list of these gates or filterList or character specifying a gated cell population in the GatingSet

... other arguments mapping, The mapping aesthetic mapping data a polygonGate fill polygonGate is not filled by default colour default is red pd pData (data.frame) that has rownames represents the sample names used as key to be merged with filterList

Value

a geom_overlay layer
**Examples**

library(ggcyto)
dataDir <- system.file("extdata",package="flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual",full = TRUE))
p <- autoplot(gs, "CD3+")

# add a flowSet as the overlay
fs <- gs_pop_get_data(gs, "DPT")
p + geom_overlay(data = fs, size = 0.3, alpha = 0.7)

# add overlay layer by gate name
p + geom_overlay(data = "DNT", size = 0.3, alpha = 0.7)

#add overlay for 1d densityplot
p <- ggcyto(gs, aes(x = CD4), subset = "CD3+") + geom_density(aes(y = ..count..))
p + geom_overlay("DNT", aes(y = ..count..), fill = "red")

---

**geom_stats**

*Add a population statistics layer to a ggcyto plot.*

**Description**

This is a virtual layer and will be instantiated as geom_label layer within ggcyto.+ operator.

**Usage**

```r
geom_stats(
  gate = NULL,
  ...,
  value = NULL,
  type = "percent",
  negated = FALSE,
  adjust = 0.5,
  location = "gate",
  label.padding = unit(0.05, "lines"),
  label.size = 0,
  digits = 3
)
```

**Arguments**

- **gate**
  a 'filterList' or character (represent as a population node in GatingSet) if not supplied, ggcyto then tries to parse the gate from the first geom_gate layer.

- **...**
  other arguments passed to geom_label layer

- **value**
  the pre-calculated stats value. when supplied, the stats computing is skipped.

- **type**
  a vector of strings to specify the stats types. can be any or multiple values of "percent", "count", "gate_name", or "MFI" (MFI is currently not supported yet).
getFlowFrame

negated whether the gate needs to be negated
adjust see details for stat_position
location see details for stat_position
label.padding, label.size arguments passed to geom_label layer
digits control the stats format

Details

So it is dedicated for ggcyto context and thus cannot be added to ggplot object directly.

Value

a geom_popStats layer

Examples

dataDir <- system.file("extdata", package="flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual", full = TRUE))
p <- ggcyto(gs, aes(x = CD4, y = CD8), subset = "CD3+") + geom_hex(bins = 64)

# add gate and stats layer
p + geom_gate("CD4") + geom_stats()

# display gate name
p + geom_gate(c("CD4", "CD8")) + geom_stats(type = "gate_name")

# display gate name and percent
p + geom_gate(c("CD4", "CD8")) + geom_stats(type = c("gate_name", "percent"))

getFlowFrame extract flowFrame data structure from the given R object

Description

Mainly to get the channel and marker information.

Usage

getFlowFrame(x)

Arguments

x flowSet, ncdfFlowList, GatingSet, GatingHierarchy, or GatingSetList

Value

a flowFrame. When x is a ncdfFlowSet or GatingSet that is associated with ncdfFlowSet, the raw event data is not read and an empty flowFrame is returned.
Examples

data(GvHD)
fs <- GvHD[1:2]
getFlowFrame(fs)# fs is a flowSet

dataDir <- system.file("extdata",package="flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual",full = TRUE))
getFlowFrame(gs)# gs is a GatingSet

ggcyto-class

Plot cytometry data using the ggcyto API

Description

ggcyto() initializes a ggcyto object that inherits ggplot class. Similarly the + operator can be used to add layers to the existing ggcyto object.

Usage

ggcyto(data = NULL, ...)

## S3 method for class 'GatingSet'
ggcyto(data, mapping, subset = "_parent_", ...)

## S3 method for class 'GatingSetList'
ggcyto(data, ...)

## S3 method for class 'GatingHierarchy'
ggcyto(data, ...)

## S3 method for class 'flowSet'
ggcyto(data, mapping, filter = NULL, max_nrow_to_plot = 50000, ...)

Arguments

data The data source. A core cytometry data structure. (flowSet, flowFrame, ncdfFlowSet, GatingSet or GatingHierarchy)

... other arguments passed to specific methods

mapping default list of aesthetic mappings (these can be colour, size, shape, line type – see individual geom functions for more details)

subset character that specifies the node path or node name in the case of GatingSet. Default is "parent", which will be substituted with the actual node name based on the geom_gate layer to be added later.

filter a flowcore gate object or a function that takes a flowSet and channels as input and returns a data-dependent flowcore gate. The gate is used to filter the flow data before it is plotted.
max_nrow_to_plot
the maximum number of cells to be plotted. When the actual data exceeds it, The subsampling process will be triggered to speed up plotting. Default is 5e4. To turn off the subsampling, simply set it to a large enough number or Inf.

Details
To invoke ggcyto:

• ggcyto(fs, aes(x, y, <other aesthetics>))

Value

ggcyto object

Examples

data(GvHD)
fs <- GvHD[1:3]
#construct the `ggcyto` object (inherits from `ggplot` class)
p <- ggcyto(fs, aes(x = `FSC-H`))
p + geom_histogram()

# display density/area
p + geom_density()
p + geom_area(stat = "density")

# 2d scatter plot
p <- ggcyto(fs, aes(x = `FSC-H`, y = `SSC-H`))
p + geom_hex(bins = 128)
# do it programatically through aes_string and variables
col1 <- "FSC-H" #note that the dimension names with special characters needs to be quoted by backticks
col2 <- "SSC-H"
ggcyto(fs, aes_string(col1,col2)) + geom_hex()

## More flowSet examples
fs <- GvHD[subset(pData(GvHD), Patient %in% 5:7 & Visit %in% c(5:6))["name"]]
# 1d histogram/densityplot
p <- ggcyto(fs, aes(x = `FSC-H`))
#facet_wrap(~name) is used automatically
p1 <- p + geom_histogram()
p1

#overwriting the default faceeting
p1 + facet_grid(Patient~Visit)

#display density
p + geom_density()

#you can use ggridges package to display stacked density plot
require(ggridges)
#stack by fcs file (`name`)
p + geom_density_ridges(aes(y = name)) + facet_null() #facet_null is used to remove the default facet_wrap (by `name`) #or to stack by Visit and facet by patient
p + geom_density_ridges(aes(y = Visit)) + facet_grid(~Patient)

# 2d scatter/dot plot
p <- ggcyto(fs, aes(x = `FSC-H`, y = `SSC-H`))
p <- p + geom_hex(bins = 128)
p

### GatingSet
dataDir <- system.file("extdata", package = "flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual", full = TRUE))
# 2d plot
ggcyto(gs, aes(x = CD4, y = CD8), subset = "CD3+" ) + geom_hex(bins = 64)
# 1d plot
ggcyto(gs, aes(x = CD4), subset = "CD3+") + geom_density()

---

**ggcyto_add**

*overloaded `+` method for ggcyto*

### Description

It tries to copy pData from ggcyto object to the gate layers so that the gate layer does not need to have pd to be supplied explicitly by users. It also calculates population statistics when geom_stats layer is added. It supports addition ggcyto layers such as 'ggcyto_par' and 'labs_cyto'.

### Usage

e1 + e2

### Arguments

e1  
An object of class ggcyto or a class inheriting from ggcyto, such as ggcyto_flowSet, ggcyto_GatingSet, or ggcyto_GatingLayout. In the case of ggcyto_GatingLayout, the component of e2 will be added to each subsidiary plot.

e2  
A component to add to e1

### Value

ggcyto object

### Examples

```r
### flowSet
data(GvHD)
fs <- GvHD[subset(pData(GvHD), Patient %in% 5:7 & Visit %in% c(5:6))][["name"]]
p <- ggcyto(fs, aes(x = `FSC-H`, y = `SSC-H`)) + geom_hex(bins = 128)
# add rectangleGate layer (2d)
rect.g <- rectangleGate(list("FSC-H" = c(300,500), "SSC-H" = c(50,200)))
```
rect.gates <- sapply(sampleNames(fs), function(sn) rect.g)
p + geom_gate(rect.gates) + geom_stats()

## GatingSet
dataDir <- system.file("extdata",package="flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual", full = TRUE))
p <- ggcyto(gs, aes(x = CD4, y = CD8), subset = "CD3+") + geom_hex(bins = 64)
p <- p + geom_gate("CD4") + geom_stats() #plot CD4 gate and it is stats
p

## Gating_x_inverse_trans() #inverse transform the x axis into raw scale

## GatingLayout
#autplot for GatingSet
dataDir <- system.file("extdata",package="flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual", full = TRUE))
gh <- gs[[1]]
p <- autoplot(gh)
class(p)
# customize the font size of strip text for each ggcyto plots contained in GatingLayout object
p + theme(strip.text = element_text(size = 14))

---

**ggcyto_arrange**

Arrange a list of ggplot objects into gtable

---

**Description**

It is usually implicitly invoked by print and show method and can be called by user when the further manipulation is needed.

**Usage**

`ggcyto_arrange(x, ...)`

**Arguments**

- `x` : ggcyto_gate_layout, which is essentially a list of ggplot objects that were previously stored as ggcyto_gate_layout object by autoplot function.

- `...` : other arguments passed to arrangeGrob

**Value**

gtable

**Examples**

```r
## Not run:
# get ggcyto_GatingLayout object from first sample
res <- autoplot(gs[[1]], nodes, bins = 64)
class(res)
```
# arrange it as one-row gtable object
gt <- ggcyto_arrange(res, nrow = 1)

# do the same to the second sample
gt2 <- ggcyto_arrange(autoplot(gs[[2]], nodes, bins = 64), nrow = 1)
# combine the two and print it on the same page
gt3 <- gridExtra::gtable_rbind(gt, gt2)
plot(gt3)

## End(Not run)

---

**ggcyto_par_default**  
*Return The default ggcyto settings*

**Description**  
Return The default ggcyto settings

**Usage**  
```r
ggcyto_par_default()
```

**Value**  
a list of default settings for ggcyto

**Examples**  
```r
ggcyto_par_default()
```

---

**ggcyto_par_set**  
*Set some default parameters for ggcyto*

**Description**  
Use this function to modify ggcyto parameters. These are the regular (or to be instantiated as) scales, labs, facet objects. They can be added as a single layer to the plot for the convenience.

**Usage**  
```r
ggcyto_par_set(...)
```

**Arguments**  
```r
...
```
a list of element name, element pairings that modify the existing parameter settings
Value

a list of new settings for ggcyto

elements

The individual elements are:

limits can be "data" (default) or "instrument" or a list of numeric limits for x and y (e.g. list(x = c(0, 4000)))
facet the regular facet object
hex_fill default scale_fill_gradientn for geom_hex layer
lab labs_cyto object

Examples

library(ggcyto)
dataDir <- system.file("extdata", package="flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual", full = TRUE))

p <- ggcyto(gs, aes(x = CD4, y = CD8), subset = "CD3+")
# 2d plot
p <- p + geom_hex(bins = 64)
p

# use instrument range by overwritting the default limits settings
p + ggcyto_par_set(limits = "instrument")

# manually set limits
myPars <- ggcyto_par_set(limits = list(x = c(0, 3.2e3), y = c(-10, 3.5e3)))
p + myPars# or xlim(0,3.2e3) + ylim(-10, 3.5e3)

is.ggcyto "Reports whether x is a ggcyto object"

Description

Reports whether x is a ggcyto object

Usage

is.ggcyto(x)

Arguments

x An object to test

Value

TRUE/FALSE
Examples
data(GvHD)
fs <- GvHD[1:2]
p <- ggcyto(fs, aes(x = `FSC-H`))
is.ggcyto(p)

is.ggcyto_flowSet Reports whether x is a ggcyto_flowSet object

Description
Reports whether x is a ggcyto_flowSet object

Usage
is.ggcyto_flowSet(x)

Arguments
x An object to test

Value
TRUE or FALSE

Examples
data(GvHD)
fs <- GvHD[1:2]
p <- ggcyto(fs, aes(x = `FSC-H`))
is.ggcyto_flowSet(p)

is.ggcyto_par Reports whether x is a ggcyto_par object

Description
Reports whether x is a ggcyto_par object

Usage
is.ggcyto_par(x)

Arguments
x An object to test
labs_cyto

Value

TRUE or FALSE

Examples

myPar <- ggcyto_par_set(limits = "instrument")
is.ggcyto_par(myPar)

labs_cyto

Change axis labels and legend titles

Description

The actual labels text will be instantiated when it is added to ggcyto plot.

Usage

labs_cyto(labels = "both")

Arguments

labels
default labels for x, y axis. Can be "channel", "marker", or "both" (default)

Value

a list

Examples

dataDir <- system.file("extdata",package="flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual",full = TRUE))

# default is "both"
p <- ggcyto(gs, aes(x = CD4, y = CD8), subset = "CD3+") + geom_hex(bins = 64)
p

#use marker name as x,y labs
p + labs_cyto("marker")

#use channel name as x,y labs
p + labs_cyto("channel")
marginalFilter

Generate a marginal gate.

Description

It simply constructs an boundaryFilter that removes the marginal events. It can be passed directly to ggcyto constructor. See the examples for details.

Usage

marginalFilter(fs, dims, ...)

Arguments

fs flowSet (not used.)
dims the channels involved
...
arguments passed to boundaryFilter

Value

an boundaryFilter

Examples

data(GvHD)
fs <- GvHD[1]
chnls <- c("FSC-H", "SSC-H")
# before removing marginal events
summary(fs[, chnls])

# create marginal filter
g <- marginalFilter(fs, chnls)
g

# after remove marginal events
fs.clean <- Subset(fs, g)
summary(fs.clean[, chnls])

# pass the function directly to ggcyto
dataDir <- system.file("extdata", package="flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual", full = TRUE))
# with marginal events
ggcyto(gs, aes(x = CD4, y = CD8), subset = "CD3+") + geom_hex(bins = 64)

# using marginalFilter to remove these events
ggcyto(gs, aes(x = CD4, y = CD8), subset = "CD3+", filter = marginalFilter) + geom_hex(bins = 64)
merge.quad.gates

---

**merge.quad.gates**

extend the original flowWorkspace::mergeGates function to restore quadGate when applicable.

---

**Description**

For internal usage.

**Usage**

```r
## S3 method for class 'quad.gates'
merge(gh, pops, bool = TRUE)
```

**Arguments**

- `gh`: a GatingHierarchy
- `pops`: a vector of population names
- `bool`: whether to deal with boolean gate

**Value**

a nested list of data structure that captures the information of parent, grouped populations (with the same projections) and the reconstructed quadGate object and the respective quadrant pattern

**Examples**

```r
library(flowWorkspace)
dataDir <- system.file("extdata", package="flowWorkspaceData")
gs <- load_gs(file.path(dataDir, "gs_manual"))
# get the GatingHierarchy object
gh <- gs[[1]]
pops <- gs_pop_get_children(gh, "CD4")
grps <- ggcyto:::merge.quad.gates(gh, pops)
length(grps) # pops are grouped into two
grps[[1]] # each group is annotated with quadGate information

ggcyto:::merge.quad.gates(gh, gs_pop_get_children(gh, "CD3+")) # cd3 subsets are not coercible to quadgate thus return
```
print.ggcyto

**Description**

A wrapper for `print.ggplot`. It converts the `ggcyto` to conventional `ggplot` object before printing it. This is usually invoked automatically when a `ggcyto` object is returned to R console.

**Usage**

```r
## S3 method for class 'ggcyto'
print(x, ...)

## S3 method for class 'ggcyto'
plot(x, ...)

## S3 method for class 'ggcyto'
show(object)
```

**Arguments**

- `x` : `ggcyto` object to display
- `...` : other arguments not used by this method
- `object` : `ggcyto` object

**Value**

nothing

---

print.ggcyto_GatingLayout

**Description**

print method for `ggcyto_gate_layout` class

**Usage**

```r
## S3 method for class 'ggcyto_GatingLayout'
print(x, ...)

## S3 method for class 'ggcyto_GatingLayout'
show(object)
```
Arguments

\( x \quad \text{ggcyto\_gate\_layout, which is essentially a list of ggplot objects that were previously stored as ggcyto\_gate\_layout object by autoplot function.} \)

\( \ldots \quad \text{other arguments passed to arrangeGrob object} \)

Value

nothing

---

replace_data  
replace current cytometry data

Description

It essentially reconstructs the entire ggcyto plot object based on the new data and the original mapping and layers recorded in the plot object.

Usage

e1 %++% e2

Arguments

e1  
the ggcyto object

e2  
the new cytometry data. It can be ‘GatingSet’ or ‘flowSet’.

Value

the new ggcyto object

Examples

dataDir <- system.file("extdata",package="flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs\_bcell\_auto",full = TRUE))
gs1 <- gs[1]
gs2 <- gs[2]

#construct the ggcyto object for gs1
p <- ggcyto(gs1, aes(cd24, cd38)) + geom_hex(bins = 128)
p <- p + geom_gate("Transitional") #add gate
#customize the stats layer
p <- p + geom_stats(type = "count", size = 6, color = "white", fill = "black", adjust = 0.3) #add another population as the overlay dots
p <- p + geom_overlay("IgD-CD27-", col = "black", size = 1.2, alpha = 0.4)
p

#replace the data with gs2 and see the same visual effect
p %+% gs2

types

\begin{verbatim}
scales_flowjo_biexp

\textit{Add a flowJo biexponential scale to the x or y axes of a ggcyto plot.}
\end{verbatim}

Description

Add a flowJo biexponential scale to the x or y axes of a ggcyto plot.

Usage

scale_x_flowjo_biexp(
  ..., 
  maxValue = 262144, 
  widthBasis = -10, 
  pos = 4.5, 
  neg = 0, 
  equal.space = FALSE 
)

scale_y_flowjo_biexp(
  ..., 
  maxValue = 262144, 
  widthBasis = -10, 
  pos = 4.5, 
  neg = 0, 
  equal.space = FALSE 
)

Arguments

... common continuous scale parameters passed to 'continuous_scale' (not used currently)
maxValue, widthBasis, pos, neg
  see 'help(flowjo_biexp')
equal.space whether to display the breaks in equal.space format

Value

ScaleContinuous object
Examples

data(GvHD)
fr <- GvHD[[1]]
p <- ggcyto(fr, aes(x = \texttt{FL1-H})) + geom_density()
# display at raw scale
p
# display at transformed scale
p + scale_x_flowjo_fasinh(maxValue = 1e4, widthBasis = 0)

---

scales_flowjo_fasinh \hspace{1cm} \textit{Add a flowJo inverse hyperbolic sine scale to the x or y axes of a ggcyto plot.}

Description

Add a flowJo inverse hyperbolic sine scale to the x or y axes of a ggcyto plot.

Usage

scale_x_flowjo_fasinh(
  ..., m = 4, t = 1200
)

scale_y_flowjo_fasinh(
  ..., m = 4, t = 1200
)

Arguments

... \hspace{1cm} common continuous scale parameters passed to \texttt{continuous_scale} (not used currently)

m, t \hspace{1cm} see \texttt{help(flowjo_fasinh)}

Value

ScaleContinuous object

Examples

data(GvHD)
fr <- GvHD[[1]]
p <- ggcyto(fr, aes(x = \texttt{FL1-H})) + geom_density()
# display at raw scale
p
# display at transformed scale
p + scale_x_flowjo_fasinh(t = 1e4)
scale_x_flowCore_fasinh

Add a flowCore inverse hyperbolic sine scale to the x or y axes of a ggcyto plot.

Description

Add a flowCore inverse hyperbolic sine scale to the x or y axes of a ggcyto plot.

Usage

scale_x_flowCore_fasinh(..., a = 1, b = 1, c = 0)
scale_y_flowCore_fasinh(..., a = 1, b = 1, c = 0)

Arguments

... common continuous scale parameters passed to 'continuous_scale' (not used currently)

a, b, c see 'help(arcsinhTransform)'

Value

ScaleContinuous object

Examples

data(GvHD)
fr <- GvHD[[1]]
p <- ggcyto(fr, aes(x = `FL1-H`)) + geom_density()
#display at raw scale
p
#display at transformed scale
p + scale_x_flowCore_fasinh(a = 2)

scale_x_logicle

Add a logicle scale to the x or y axes of a ggcyto plot.

Description

Add a logicle scale to the x or y axes of a ggcyto plot.

Usage

scale_x_logicle(..., w = 0.5, t = 262144, m = 4.5, a = 0)
scale_y_logicle(..., w = 0.5, t = 262144, m = 4.5, a = 0)
Arguments

... common continuous scale parameters passed to 'continuous_scale' (not used currently)

w, t, m, a see 'help(logicleTransform')

Value

ScaleContinuous object

Examples

data(GvHD)
fr <- GvHD[[1]]
p <- ggcyto(fr, aes(x = `FL1-H`)) + geom_density()
#display at raw scale
p
#display at transformed scale
p + scale_x_logicle(t = 1e4)

_________________________________________________________________

stats_null clear all the geom_stats() layer previously added

_________________________________________________________________

Description

clear all the geom_stats() layer previously added

Usage

stats_null()

Examples

dataDir <- system.file("extdata",package="flowWorkspaceData")
gs <- load_gs(list.files(dataDir, pattern = "gs_manual",full = TRUE))
#autoplot display pop stats by default
p <- autoplot(gs, "CD4")
#it is easy to remove the default stats
p <- p + stats_null()
#and add a new one
p <- p + geom_stats(type = "count")
stat_position

Compute the positions of the population statistics based on the geometric gate centroid for a ggcyto plot.

Description

It is usually not called directly by user but mainly used by compute_stats function (which is called by ggcyto add method when geom_states layer is added).

Usage

stat_position(gate, ...)

## S3 method for class 'filter'
stat_position(
gate,
negated = FALSE,
adjust = 0.5,
location = "gate",
data_range = NULL,
limits = NULL,
...
)

Arguments

gate a flowCore filter
...
other arguments
negated logical indicating whether position needs to be moved to negative side of gate
adjust see details
location see details
data_range a two-row data.frame representing the actual data range. Each column is a a range for a specific channel. First row is min, Second row is max.
limits used to fix the gate range

Details

Specifying location for statistical annotation:
The adjust and location arguments allow for a few different ways to adjust the location of the statistical annotation for a gate on a ggcyto plot. The valid values for location are "gate" (default), "data", "plot", and "fixed".

Relative location:
If location is not "fixed", the starting position of the annotation will be determined with respect to a rectangular window whose bounds are determined in the following way:

- For location = "gate", the window will be set by the range of the data in the gate.
- For `location = "data"`, the window will be set by the range of values in all of the data on the plot (provided by `data_range`)
- For `location = "plot"`, the window will be set by the axis limits of the plot (adjusted by `ggcyto_par_set`)

This starting position can then be adjusted by passing values in a vector to the `adjust` parameter, where they will be interpreted as relative proportions of the window dimension, where 0.0 represents the lower bound of the dimension and 1.0 represents the upper bound. So, for a 2-D plot, `adjust=c(0,0)` places the annotation at the lower left corner of this window and `adjust=c(1,1)` places it at the upper right corner.

As another example, for a 2-D gate, if `location = "gate"` and `adjust=c(0.25, 0.75)`, the statistical annotation will be placed 1/4 of the way across the x-range of the gate and 3/4 of the way across the y-range of the gate.

The `adjust` argument will also accept values less than 0.0 or greater than 1.0. This can be an easy way to simply move the annotation outside of a gate so it does not obstruct the view of the data within. For example, `location == "gate"` and `adjust=c(-0.2, 1.2)` will move the annotation outside of the upper left corner of the gate range.

*Fixed location:*

If `location = "fixed"`, the numeric vector passed to `adjust` will be interpreted as values on the data scales of the plot to provide an explicit location for the annotation. For example, if the annotation should be at the location 3000, 5000 on the plot, that could be done with `location="fixed"` and `adjust = c(3000,5000)`.

*Default:*

The default behavior if no values are provided to `location` or `adjust` will be to place the annotation at the center of the range of the data in the gate.

**Value**

a data.table of gate centroid coordinates

**Examples**

```r
data(GvHD)
fs <- GvHD[1:4]
rect.g <- rectangleGate(list("FSC-H" = c(300,500), "SSC-H" = c(50,200)))
rect.gates <- sapply(sampleNames(fs), function(sn)rect.g)
stat_position(rect.gates)
```

---

### transform-gate

rescale methods for gates

**Description**

rescale the gate coordinates with the transformation provided
Usage

\texttt{transform(`_data`, ...)}

\texttt{rescale\_gate(gate, trans, param)}

Arguments

\_data the filter or filterList object. Currently support polygonGate, ellipsoidGate, rectangleGate and quadGate.

... trans the transformation function or transformList object param the parameter/dimension to be transformed. When trans is transformList object, param is not needed since it is derived from transformList.

gate gate object

trans the transformation function

param the parameter/dimension to be transformed.

Value

the transformed filter/filterList object
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