## Package ‘ggcyto’

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**Type** Package  

**Title** Visualize Cytometry data with ggplot  

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**Description** With the dedicated fority 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 customed layers also make it easy to add gates and population statistics to the plot.

**VignetteBuilder** knitr  

**Depends** methods, ggplot2(>= 2.0.0), flowCore, ncdfflow(>= 2.17.1), flowWorkspace(>= 3.17.24)  

**Imports** plyr, scales, data.table, RColorBrewer, gridExtra  

**Suggests** testthat, flowWorkspaceData, knitr, rmarkdown, flowStats, openCyto, flowViz  

**License** Artistic-2.0  

**URL** [https://github.com/RGLab/ggcyto/issues](https://github.com/RGLab/ggcyto/issues)  

**biocViews** FlowCytometry, CellBasedAssays, Infrastructure, Visualization  


**RoxygenNote** 5.0.1  

**NeedsCompilation** no
R topics documented:

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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

```r
## S3 method for class 'ggcyto_flowSet'
e1 + e2

## S4 method for signature 'ggcyto_flowSet,ANY'
e1 + e2
```

Arguments

- `e1`: An object of class `ggcyto_flowSet`
- `e2`: A component to add to `e1`

Value

`ggcyto_flowSet` object

Examples

```r
data(GvHD)
fs <- GvHD[, subset(pData(GvHD), Patient %in% 5:7 & Visit %in% c(5:6))]["name"]
p <- ggcyto(fs, aes(x = \texttt{FSC-H}, y = \texttt{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()
```

Description

It adds the layer specified by `e2` to each individual `ggplot` object stored in `ggcyto_gate_layout`

Usage

```r
## S3 method for class 'ggcyto_GatingLayout'
e1 + e2

## S4 method for signature 'ggcyto_GatingLayout,ANY'
e1 + e2
```

Arguments

- `e1`: `ggcyto_gate_layout`
- `e2`: any `ggplot` layer

Value

- a modified `ggcyto_gate_layout` object
- a `GatingLayout` object
Examples

#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 ggcyo plots contained in GatingLayout object
p + theme(strip.text = element_text(size = 14))

+ ggcyo_GatingSet

overloaded '+' method for ggcyo.gs

Description

It takes care the speical format of some ggcyto layers. For example geom_gate or geom_stats layer with just gate(population) name specified, It only supports some special axis transformations. (See examples below)

Usage

## S3 method for class 'ggcyo_GatingSet'
e1 + e2

## S4 method for signature 'ggcyo_GatingSet,ANY'
e1 + e2

Arguments

e1 An object of class ggcyto

e2 A component to add to e1

Value

ggcyo_GatingSet object

Examples

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

It fortifies the data, fills some default settings and returns a regular ggplot object.

Description

The original data format is preserved during the ggcyto 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. Sometimes it is useful to coerce it to ggplot explicitly by user so that it can be used as a regular ggplot object.

Usage

as.ggplot(x)

Arguments

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

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$data # data has not been fortified
p1 <- as.ggplot(p) # convert it to a ggplot object explicitly
class(p1)
p1$data # data is fortified

autoplot.flowSet

Plot fluorescence intensity in one or two dimension.

Description

Overloaded autoplot for the cytometry data structure: flowFrame or flowSet, Gatinghierarchy, GatingSet. It plots the cytometry data with geom_histogram, geom_density or geom_hex.
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 '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, ...)

## S3 method for class 'GatingHierarchy'
autoplot(object, gate, y = "SSC-A", bool = FALSE,
         arrange.main = sampleNames(object), arrange = TRUE, merge = TRUE,
         projections = list(), strip.text = c("parent", "gate"), ...)
```

Arguments

- `object`: flowFrame, flowSet, GatingSet object
- `x`: define the x dimension of the plot. 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
- `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

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')

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

# autoplot 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 axis labels in raw scales

---

**Description**

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

**Usage**

```r
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.

**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, data_range = NULL, ...)

Arguments

fs      flowSet. can be NULL when precaculated 'value' is provided
gates   a list of filters
type    can be "percent", "count" or "MFI".
value   the pre-calculated stats value. when supplied, the stats computing is skipped.
data_range the data range for each channels
...     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)))
rect.gates <- sapply(sampleNames(fs), function(sn)rect.g)
compute_stats(fs, rect.gates)
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'
fortify(model, data = NULL, ...)

Arguments

- `model`: ellipsoidGate
- `data`: data range used for polygon interpolation.
- `...`: not used.

Value
data.table

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

Arguments

- `model`: filterList
- `data`: data range used for polygon interpolation
- `nPoints`: used for interpolating polygonGates to prevent it from losing shape when truncated by axis limits
- `...`: not used.
Value

data.table

Examples

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

---

**fortify.flowFrame**

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

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

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

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

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

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

Arguments

- `model` flowFrame, flowSet or GatingSet
- `data` not used.
- `...` not used.

Value

data.table
data.table

---
Examples

```r
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 foritfy(gs)

fs <- getData(gs, "CD8")
fortify(fs)# fs is a flowSet/ncdfFlowSet

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

---

**fortify.polygonGate**  
*Convert a polygonGate to a data.table useful for ggplot*

### Description

It converts the boundaries slot into a data.table. When 'nPoints' is supplied, the method tries to interpolate the polygon with more vertices.

### Usage

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

### Arguments

- **model**: polygonGate
- **data**: data range used to reset off-bound gate coordinates to prevent interpolating on the extremely large space unnecessarily.
- **nPoints**: total number of vertices of the polygon after interpolation. Default is NULL, which is no interpolation. The actual number may be more or less based on the lengths of edges due to the maximum and minimum limits on each edge. Interpolation is mainly for the purpose of plotting (so that it won’t lose its shape from subsetting through ‘limits’). But it is not necessary for other purposes like centroid calculation.
- **...**: 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) # no interpolation
fortify(pg, nPoints = 30) # with interpolation
```
fortify_rectangleGate  

Convert a rectangleGate to a data.table useful for ggplot

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

## 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

#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

fortify_fs(model, data, ...)

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

## Default S3 method:
fortify_fs(model, data, ...)
## geom_gate

### 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

```r
geom_gate(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

## Value

A flowSet/ncdfFlowSet object

### Examples

```r
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)
```
# geom_gate

## S3 method for class 'filterList'
geom_gate(data, ...)

## S3 method for class 'polygonGate'
geom_gate(data, ...)

## S3 method for class 'rectangleGate'
geom_gate(data, ...)

## S3 method for class 'ellipsoidGate'
geom_gate(data, ...)

## S3 method for class 'character'
geom_gate(data, ...)

## S3 method for class 'filters'
geom_gate(data, ...)

## S3 method for class 'filtersList'
geom_gate(data, ...)

## S3 method for class 'logicalFilterResult'
geom_gate(data, ...)

## S3 method for class 'logical'
geom_gate(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

### 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)
geom_hvline

```
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)
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**

```
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**

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

- `xintercept`
- `alpha`
- `colour`
- `group`
- `linetype`
- `size`
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_overlay**

Overlay other populations on existing plots.

**Description**

It is useful for "backgating" plots.

**Usage**

```r
geom_overlay(data, ...)
```

### Default S3 method:

```r
geom_overlay(data, ...)
```

### S3 method for class 'character'

```r
geom_overlay(data, ...)
```

### S3 method for class 'flowSet'

```r
geom_overlay(data, ...)
```

### S3 method for class 'flowFrame'

```r
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

```r
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 <- getData(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**

Population statistics layer

**Description**

It 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",
          data_range = NULL, adjust = 0.5, label.padding = unit(0.05, "lines"),
          label.size = 0)
```

**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.
  - `NULL` otherwise.

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

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

- **type**
  - can be "percent", "count" or "MFI".

- **data_range**
  - the data range for each channels

- **adjust**
  - adjust the position of the centroid. from 0 to 1.

- **label.padding**
  - `NULL` or arguments passed to geom_label layer

- **label.size**
  - `NULL` or arguments passed to geom_label layer

**Details**

So it is dedicated for ggcyto context and thus can’t not be added to ggplot object directly.

**Value**

a geom_popStats layer
getFlowFrame

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

getFlowFrame(extract flowFrame data structure from the given R object)

Description

Mainly to get the channel and marker information.

Usage

getFlowFrame(x)

## S3 method for class 'flowSet'
getFlowFrame(x)

## S3 method for class 'ncdfFlowList'
getFlowFrame(x)

## S3 method for class 'GatingSetList'
getFlowFrame(x)

## S3 method for class 'GatingSet'
getFlowFrame(x)

## S3 method for class 'GatingHierarchy'
getFlowFrame(x)

Arguments

x flowSet or GatingSet/GatingHierarchy

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.flowSet

Create a new ggcyto plot from a flowSet

Description
Create a new ggcyto plot from a flowSet

Usage

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

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

Arguments

- data: default flowSet for plot
- mapping: default list of aesthetic mappings (these can be colour, size, shape, line type – see individual geom functions for more details)
- filter: a flowcore gate object or a function that takes 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.
- ...: ignored

Value

a ggcyto_GatingSet object which is a subclass of ggcyto class.

Examples

data(GvHD)
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()

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

#display density
p + geom_density()

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

Description
Create a new ggcyto plot from a GatingSet

Usage

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

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

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

Arguments

data GatingSet to plot
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 GatingSet. Default is "_parent_.", which will be substitute with the actual node name based on the geom_gate layer to be added later.
... ignored

Value

a ggcyto_GatingSet object which is a subclass of ggcyto_flowSet class.

Examples

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_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**

```r
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)  

gt  
# 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::rbind.gtable(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()  
```
ggcyto_par_set

Value

a list of default settings for ggcyto

Examples

`ggcyto_par_default()`

---

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

`ggcyto_par_set(...)`

Arguments

`...` 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

```r
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 overwriting 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)))
```
is.ggcyto

\[ p + \text{mypars} \# \text{ or } \text{xlim}(0, 3.2e3) + \text{ylim}(-10, 3.5e3) \]

\[ \text{is.ggcyto} \]

\textbf{is.ggcyto} \hspace{1cm} \textit{Reports whether x is a ggcyto object}

\textbf{Description}

Reports whether x is a ggcyto object

\textbf{Usage}

\texttt{is.ggcyto(x)}

\textbf{Arguments}

\texttt{x} \hspace{1cm} \text{An object to test}

\textbf{Value}

\texttt{TRUE/FALSE}

\textbf{Examples}

\begin{verbatim}
data(GvHD)
fs <- GvHD[1:2]
p <- ggcyto(fs, aes(x = `FSC-H`))
is.ggcyto(p)
\end{verbatim}

\texttt{is.ggcyto\_flowSet} \hspace{1cm} \textit{Reports whether x is a ggcyto\_flowSet object}

\textbf{Description}

Reports whether x is a ggcyto\_flowSet object

\textbf{Usage}

\texttt{is.ggcyto\_flowSet(x)}

\textbf{Arguments}

\texttt{x} \hspace{1cm} \text{An object to test}

\textbf{Value}

\texttt{TRUE or FALSE}

\textbf{Examples}

\begin{verbatim}
data(GvHD)
fs <- GvHD[1:2]
p <- ggcyto(fs, aes(x = `FSC-H`))
is.ggcyto\_flowSet(p)
\end{verbatim}
\textbf{is.ggcYto_par} \quad \textit{Reports whether \( x \) is a ggcYto_par object}

\subsection*{Description}
Reports whether \( x \) is a ggcYto_par object

\subsection*{Usage}
\texttt{is.ggcYto_par(x)}

\subsection*{Arguments}
\begin{itemize}
\item \texttt{x} \quad \text{An object to test}
\end{itemize}

\subsection*{Value}
\begin{itemize}
\item TRUE or FALSE
\end{itemize}

\subsection*{Examples}
\begin{verbatim}
myPar <- ggcYto_par_set(limits = "instrument")
is.ggcYto_par(myPar)
\end{verbatim}

\textbf{labs_cyto} \quad \textit{Change axis labels and legend titles}

\subsection*{Description}
The actual labels text will be instantiated when it is added to ggcYto plot.

\subsection*{Usage}
\texttt{labs_cyto(labels = "both")}

\subsection*{Arguments}
\begin{itemize}
\item \texttt{labels} \quad \text{default labels for x, y axis. Can be "channel", "marker", or "both" (default)}
\end{itemize}

\subsection*{Value}
\begin{itemize}
\item a list
\end{itemize}
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")

---

code

marginalFilter Generate a marginal gate.

Description

It simply constructs a 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 <- syste.m.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)

---

**print.ggcyto**

*Draw ggcyto on current graphics device.*

**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, ...)

## S4 method for signature 'ggcyto'
print(x, ...)

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

## S4 method for signature '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

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

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

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

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

object ggcyto_GatingLayout

Value

nothing

scale_x_flowJo_biexp flowJo biexponential scale

Description

flowJo biexponential scale

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)
scale_x_flowJo_fasinh

Arguments

... common continuous scale parameters passed to `continuous_scale` (not used currently)
maxValue, widthBasis, pos, neg
see 'help(flowJoTrans')
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 = 'FL1-H')) + geom_density()
#display at raw scale
p
#display at transformed scale
p + scale_x_flowJo_biexp(maxValue = 1e4, widthBasis = 0)

scale_x_flowJo_fasinh `flowJo inverse hyperbolic sine scale`

Description

flowJo inverse hyperbolic sine scale

Usage

scale_x_flowJo_fasinh(..., m = 4, t = 1200)
scale_y_flowJo_fasinh(..., m = 4, t = 1200)

Arguments

... common continuous scale parameters passed to `continuous_scale` (not used currently)
m, t see 'help(flowJo.fasinh')

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_flowJo_fasinh(t = 1e4)
scale_x_logicle

flowJo inverse hyperbolic sine scale

Description

flowJo inverse hyperbolic sine scale

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)

stat_position

compute the positions of the population statistics based on the geometric gate centroid

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, ...)

## S3 method for class 'filterList'
stat_position(gate, ...)

## S3 method for class 'list'
stat_position(gate, ...)

### Arguments

- **gate**
  - a flowCore filter

- **...**
  - other arguments
    - `adjust`
      - adjust the position of the centroid
    - `abs`
      - logical
    - `data_range`
      - the actual data range

### Value

- a data.table
  - the 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)
```
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