

# Package ‘CytoPipeline’

April 15, 2024

**Title** Automation and visualization of flow cytometry data analysis pipelines

**Version** 1.2.0

**Description** This package provides support for automation and visualization of flow cytometry data analysis pipelines. In the current state, the package focuses on the preprocessing and quality control part. The framework is based on two main S4 classes, i.e. CytoPipeline and CytoProcessingStep. The pipeline steps are linked to corresponding R functions - that are either provided in the CytoPipeline package itself, or exported from a third party package, or coded by the user her/himself. The processing steps need to be specified centrally and explicitly using either a json input file or through step by step creation of a CytoPipeline object with dedicated methods. After having run the pipeline, obtained results at all steps can be retrieved and visualized thanks to file caching (the running facility uses a BiocFileCache implementation). The package provides also specific visualization tools like pipeline workflow summary display, and 1D/2D comparison plots of obtained flowFrames at various steps of the pipeline.

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aggregateAndSample	<i>Aggregate and sample multiple flow frames of a flow set together</i>
--------------------	---

---

**Description**

Aggregate multiple flow frames in order to analyze them simultaneously. A new FF, which contains about  $cTotal$  cells, with  $\text{ceiling}(cTotal/nFiles)$  cells from each file. Two new columns are added: a column indicating the original file by index, and a noisy version of this, for better plotting opportunities. This function is based on `PeacoQC::AggregateFlowframes()` where file names inputs have been replaced by a `flowSet` input.

**Usage**

```
aggregateAndSample(
  fs,
  nTotalEvents,
  seed = NULL,
  channels = NULL,
  writeOutput = FALSE,
  outputFile = "aggregate.fcs",
  keepOrder = FALSE
)
```

**Arguments**

<code>fs</code>	a <code>flowCore::flowset</code>
<code>nTotalEvents</code>	Total number of cells to select from the input flow frames
<code>seed</code>	seed to be set before sampling for reproducibility. Default NULL does not set any seed.
<code>channels</code>	Channels/markers to keep in the aggregate. Default NULL takes all channels of the first file.

writeOutput	Whether to write the resulting flowframe to a file. Default FALSE
outputFile	Full path to output file. Default "aggregate.fcs"
keepOrder	If TRUE, the random subsample will be ordered in the same way as they were originally ordered in the file. Default = FALSE.

**Value**

returns a new flowCore::flowFrame

**Examples**

```
data(OMIP021Samples)

nCells <- 1000
agg <- aggregateAndSample(
  fs = OMIP021Samples,
  nTotalEvents = nCells)
```

---

appendCellID	<i>append 'Original_ID' column to a flowframe</i>
--------------	---

---

**Description**

: on a flowCore::flowFrame, append a 'Original\_ID' column. This column can be used in plots comparing the events pre and post gating. If the 'Original\_ID' column already exists, the function does nothing

**Usage**

```
appendCellID(ff, eventIDs = seq_len(flowCore::nrow(ff)))
```

**Arguments**

ff	a flowCore::flowFrame
eventIDs	an integer vector containing the values to be added in expression matrix, as Original ID's.

**Value**

new flowCore::flowFrame containing the added 'Original\_ID' column

**Examples**

```
data(OMIP021Samples)

retFF <- appendCellID(OMIP021Samples[[1]])
```

---

applyScaleTransforms *apply scale transforms*

---

### Description

wrapper around `flowCore::transform()` that discards any additional parameter passed in (...) Additionally, some checks regarding channels correspondance is done: if `transList` contains transformations for channels that are not present in `x`, then these transformations are first removed.

### Usage

```
applyScaleTransforms(x, transList, verbose = FALSE, ...)
```

### Arguments

<code>x</code>	a <code>flowCore::flowSet</code> or a <code>flowCore::flowFrame</code>
<code>transList</code>	a <code>flowCore::transformList</code>
<code>verbose</code>	if TRUE, send a message per <code>flowFrame</code> transformed
<code>...</code>	other arguments (not used)

### Value

the transformed `flowFrame`

### Examples

```
data(OMIP021Samples)

transListPath <- file.path(system.file("extdata",
                                       package = "CytoPipeline"),
                           "OMIP021_TransList.rds")

transList <- readRDSObject(transListPath)

ff_c <- compensateFromMatrix(OMIP021Samples[[1]],
                             matrixSource = "fcs")

ff_t <- applyScaleTransforms(ff_c, transList = transList)
```

---

areFluoCols                    *find flow frame columns that represent fluorochrome channel*

---

### Description

: find flow frame columns that represent fluorochrome channel

### Usage

```
areFluoCols(
  x,
  toRemovePatterns = c("FSC", "SSC", "Time", "Original_ID", "File", "SampleID")
)
```

### Arguments

x                                a flowCore::flowFrame or a flowCore::flowSet  
 toRemovePatterns                a vector of string patterns that are to be considered as non fluorochrome

### Value

a vector of booleans of which the dimension is equal to the number of columns in ff

### Examples

```
data(OMIP021Samples)
areFluoCols(OMIP021Samples)
```

---

areSignalCols                    *find flow frame columns that represent true signal*

---

### Description

: find flow frame columns that represent true signal

### Usage

```
areSignalCols(
  x,
  toRemovePatterns = c("Time", "Original_ID", "File", "SampleID")
)
```

**Arguments**

`x` a `flowCore::flowFrame` or a `flowCore::flowSet`  
`toRemovePatterns` a vector of string patterns that are to be considered as non signal

**Value**

a vector of booleans of which the dimension is equal to the number of columns in `ff`

**Examples**

```
data(OMIP021Samples)
areSignalCols(OMIP021Samples)
```

---

`compensateFromMatrix` *compensation of fcs file(s) from matrix*

---

**Description**

executes the classical compensation function on a `flowSet` or `flowFrame`, given a compensation matrix. The matrix can be either retrieved in the `fcs` files themselves or provided as a `csv` file.

**Usage**

```
compensateFromMatrix(
  x,
  matrixSource = c("fcs", "import", "pData"),
  matrixPath = NULL,
  pDataVar = NULL,
  pDataPathMapping = NULL,
  updateChannelNames = TRUE,
  ...
)
```

**Arguments**

`x` a `flowCore::flowFrame` or `flowCore::flowSet`  
`matrixSource` if "fcs", the compensation matrix will be fetched from the `fcs` files (different compensation matrices can then be applied by `fcs` file) if "import", uses `matrixPath` to read the matrix (should be a `csv` file) if "pData", uses `pDataVar` and `pDataPathMapping` to link a specific phenotype data variable to map different matrix paths  
`matrixPath` if `matrixSource == "import"`, will be used as the input `csv` file path  
`pDataVar` variable name (column of pheno data) used to map the compensation matrix file

`pDataPathMapping`  
 a named list:
 

- item names are possible values of `pDataVar`
- item values are `character()` providing the `matrixPath` for the corresponding `pDataVar` value

`updateChannelNames`  
 if TRUE, updates the fluo channel names by prefixing them with "comp-"  
 ... additional arguments (not used)

**Value**

the compensated `flowSet` or `flowFrame`

**Examples**

```
rawDataDir <-
  system.file("extdata", package = "CytoPipeline")
sampleFiles <-
  file.path(rawDataDir, list.files(rawDataDir, pattern = "Donor"))

truncateMaxRange <- FALSE
minLimit <- NULL

# create flowCore::flowSet with all samples of a dataset
fsRaw <- readSampleFiles(
  sampleFiles = sampleFiles,
  whichSamples = "all",
  truncate_max_range = truncateMaxRange,
  min.limit = minLimit)

suppressWarnings(ff_m <- removeMarginsPeacoQC(x = fsRaw[[2]]))

ff_c <-
  compensateFromMatrix(ff_m,
    matrixSource = "fcs")
```

---

**computeScatterChannelsLinearScale**

*compute linear transformation of scatter channels found in `ff`, based on 5% and 95% of `referenceChannel`, set as target. If there is a transformation defined in `transList` for `referenceChannel`, it is applied first, before computing quantiles. Then the computed linear transformations (or each scatter channel) are added into the `transfo_list`. -A channels are computed, and same linear transformation is then applied to corresponding -W and -H channels (if they exist in `ff`).*

---

**Description**

based on a `referenceChannel`



**Usage**

```
computeScatterChannelsLinearScale(
  ff,
  transList = NULL,
  referenceChannel,
  silent = TRUE
)
```

**Arguments**

<code>ff</code>	a <code>flowCore::flowFrame</code>
<code>transList</code>	an initial <code>flowCore::transformList</code>
<code>referenceChannel</code>	the reference channel to take target quantile values from. Can be defined as marker or channel name.
<code>silent</code>	if <code>FALSE</code> , will output some information on the computed linear transformations

**Value**

the `transList` with added linear scale transformations

**Examples**

```
data(OMIP021Samples)

ff <- OMIP021Samples[[1]]
refMarker <- "APCCy7 - CD4"
refChannel <- "780/60Red-A"
transList <- flowCore::estimateLogicle(ff,
                                     channels = refChannel)

retTransList <-
  computeScatterChannelsLinearScale(ff,
                                   transList = transList,
                                   referenceChannel = refMarker,
                                   silent = TRUE
  )
```

---

CytoPipeline

*CytoPipeline package*

---

**Description**

CytoPipeline is a package that provides support for automation and visualization of flow cytometry data analysis pipelines. In the current state, the package focuses on the preprocessing and quality control part.

The framework is based on two main S4 classes, i.e. `CytoPipeline` and `CytoProcessingStep`. The `CytoProcessingStep` defines the link between pipeline step names and corresponding R functions that are either provided in the `CytoPipeline` package itself, or exported from a third party

package, or coded by the user her/himself. The processing steps need to be specified centrally and explicitly using either a json input file or through step by step creation of a CytoPipeline object with dedicated methods.

After having run the pipeline, obtained results at all steps can be retrieved and visualized thanks to file caching (the running facility uses a BiocFileCache implementation). The package provides also specific visualization tools like pipeline workflow summary display, and 1D/2D comparison plots of obtained flowFrames at various steps of the pipeline.

For a step by step example using CytoPipeline, please have a look at the vignette!

## Usage

```
## S4 method for signature 'CytoPipeline'
show(object)

## S4 method for signature 'missing'
CytoPipeline(
  object,
  experimentName = "default_experiment",
  sampleFiles = character(),
  pData = NULL
)

## S4 method for signature 'list'
CytoPipeline(
  object,
  experimentName = "default_experiment",
  sampleFiles = character(),
  pData = NULL
)

## S4 method for signature 'character'
CytoPipeline(
  object,
  experimentName = "default_experiment",
  sampleFiles = character(),
  pData = NULL
)

## S3 method for class 'CytoPipeline'
as.list(x, ...)

experimentName(x)

experimentName(x) <- value

sampleFiles(x)

sampleFiles(x) <- value
```

```
pData(x)
```

```
pData(x) <- value
```

### Arguments

object	a character() containing a JSON input
experimentName	the experiment name
sampleFiles	the sample files
pData	the pheno Data (data.frame or NULL)
x	a CytoPipeline object
...	additional arguments (not used here)
value	the new value to be assigned

### Value

- for `as.list.CytoPipeline`: the obtained list

### See Also

[CytoPipelineClass](#), [CytoProcessingStep](#)

---

CytoPipeline-class      *CytoPipeline class*

---

### Description

Class representing a flow cytometry pipeline, and composed of two processing queues, i.e. lists of `CytoProcessingStep` objects :

- a list of `CytoProcessingStep`(s) for pre-calculation of scale transformations per channel
- a list of `CytoProcessingStep`(s) for the pre-processing of flow frames

### Value

nothing

### Slots

`scaleTransformProcessingQueue` A list of `CytoProcessingStep` objects containing the steps for obtaining the scale transformations per channel

`flowFramesPreProcessingQueue` A list of `CytoProcessingStep` objects containing the steps for pre-processing of the samples flow frames

`experimentName` A character containing the experiment (run) name

sampleFiles A character vector storing all fcs files to be run into the pipeline

pData An optional data.frame containing additional information for each sample file. The pData raw names must correspond to basename(sampleFiles) otherwise validation of the CytoPipeline object will fail!

## Examples

```
### *** EXAMPLE 1: building CytoPipeline step by step *** ###

rawDataDir <-
  system.file("extdata", package = "CytoPipeline")
experimentName <- "OMIP021_PeacoQC"
sampleFiles <- file.path(rawDataDir, list.files(rawDataDir,
                                                pattern = "Donor"))

outputDir <- base::tempdir()

# main parameters : sample files and output files
pipL <- CytoPipeline(experimentName = experimentName,
                    sampleFiles = sampleFiles)

### SCALE TRANSFORMATION STEPS ###

pipL <-
  addProcessingStep(pipL,
                    whichQueue = "scale transform",
                    CytoProcessingStep(
                      name = "flowframe_read",
                      FUN = "readSampleFiles",
                      ARGS = list(
                        whichSamples = "all",
                        truncate_max_range = FALSE,
                        min.limit = NULL
                      )
                    )
  )

pipL <-
  addProcessingStep(pipL,
                    whichQueue = "scale transform",
                    CytoProcessingStep(
                      name = "remove_margins",
                      FUN = "removeMarginsPeacoQC",
                      ARGS = list()
                    )
  )

pipL <-
  addProcessingStep(pipL,
                    whichQueue = "scale transform",
                    CytoProcessingStep(
                      name = "compensate",
```

```

        FUN = "compensateFromMatrix",
        ARGS = list(matrixSource = "fcs")
    )
)

pipL <-
  addProcessingStep(pipL,
    whichQueue = "scale transform",
    CytoProcessingStep(
      name = "flowframe_aggregate",
      FUN = "aggregateAndSample",
      ARGS = list(
        nTotalEvents = 10000,
        seed = 0
      )
    )
  )

pipL <-
  addProcessingStep(pipL,
    whichQueue = "scale transform",
    CytoProcessingStep(
      name = "scale_transform_estimate",
      FUN = "estimateScaleTransforms",
      ARGS = list(
        fluoMethod = "estimateLogicle",
        scatterMethod = "linear",
        scatterRefMarker = "BV785 - CD3"
      )
    )
  )

### PRE-PROCESSING STEPS ###

pipL <-
  addProcessingStep(pipL,
    whichQueue = "pre-processing",
    CytoProcessingStep(
      name = "flowframe_read",
      FUN = "readSampleFiles",
      ARGS = list(
        truncate_max_range = FALSE,
        min.limit = NULL
      )
    )
  )

pipL <-
  addProcessingStep(pipL,
    whichQueue = "pre-processing",
    CytoProcessingStep(
      name = "remove_margins",
      FUN = "removeMarginsPeacoQC",

```

```

        ARGES = list()
    )
)

pipL <-
  addProcessingStep(pipL,
    whichQueue = "pre-processing",
    CytoProcessingStep(
      name = "compensate",
      FUN = "compensateFromMatrix",
      ARGES = list(matrixSource = "fcs")
    )
  )

pipL <-
  addProcessingStep(
    pipL,
    whichQueue = "pre-processing",
    CytoProcessingStep(
      name = "remove_debris",
      FUN = "removeDebrisManualGate",
      ARGES = list(
        FSCChannel = "FSC-A",
        SSCChannel = "SSC-A",
        gateData = c(73615, 110174, 213000, 201000, 126000,
                    47679, 260500, 260500, 113000, 35000))
    )
  )

pipL <-
  addProcessingStep(pipL,
    whichQueue = "pre-processing",
    CytoProcessingStep(
      name = "remove_dead_cells",
      FUN = "removeDeadCellsManualGate",
      ARGES = list(
        FSCChannel = "FSC-A",
        LDMarker = "L/D Aqua - Viability",
        gateData = c(0, 0, 250000, 250000,
                    0, 650, 650, 0)
      )
    )
  )

pipL <-
  addProcessingStep(
    pipL,
    whichQueue = "pre-processing",
    CytoProcessingStep(
      name = "perform_QC",
      FUN = "qualityControlPeacoQC",
      ARGES = list(
        preTransform = TRUE,
        min_cells = 150, # default

```

```

        max_bins = 500, # default
        step = 500, # default,
        MAD = 6, # default
        IT_limit = 0.55, # default
        force_IT = 150, # default
        peak_removal = 0.3333, # default
        min_nr_bins_peakdetection = 10 # default
    )
)
)

pipL <-
  addProcessingStep(pipL,
                    whichQueue = "pre-processing",
                    CytoProcessingStep(
                      name = "transform",
                      FUN = "applyScaleTransforms",
                      ARGS = list()
                    )
  )

### *** EXAMPLE 2: building CytoPipeline from JSON file *** ###

jsonDir <- system.file("extdata", package = "CytoPipeline")
jsonPath <- file.path(jsonDir, "pipelineParams.json")

pipL2 <- CytoPipeline(jsonPath,
                     experimentName = experimentName,
                     sampleFiles = sampleFiles)

```

---

CytoProcessingStep      *Cyto Processing step*

---

## Description

Class containing the function and arguments to be applied in a lazy-execution framework.

Objects of this class are created using the `CytoProcessingStep()` function. The processing step is executed with the `executeProcessingStep()` function.

## Usage

```
CytoProcessingStep(name = character(), FUN = character(), ARGS = list())
```

```
## S4 method for signature 'CytoProcessingStep'
show(object)
```

```
executeProcessingStep(x, ...)
```

```
getCPSName(x)

getCPSFUN(x)

getCPSARGS(x)

## S3 method for class 'CytoProcessingStep'
as.list(x, ...)

as.json.CytoProcessingStep(x, pretty = FALSE)

from.json.CytoProcessingStep(jsonString)
```

### Arguments

name	character denoting a name to the step, which can be different from the function name
FUN	function or character representing a function name.
ARGS	list of arguments to be passed along to FUN.
object	a CytoProcessingStep object.
x	a CytoProcessingStep object.
...	other arguments (not used)
pretty	formatting set-up (see jsonlite::toJSON doc)
jsonString	a character() containing a JSON string.

### Details

This object contains all relevant information of a data analysis processing step, i.e. the function and all of its arguments to be applied to the data.

### Value

The CytoProcessingStep function returns an object of type CytoProcessingStep.

### Examples

```
## Create a simple processing step object
ps1 <- CytoProcessingStep("summing step", sum)

getCPSName(ps1)

getCPSFUN(ps1)

getCPSARGS(ps1)

executeProcessingStep(ps1, 1:10)

as.list(ps1)
```



```
js_str <- as.json.CytoProcessingStep(ps1)
ps2 <- from.json.CytoProcessingStep(js_str)
identical(ps1, ps2)
```

---

estimateScaleTransforms

*estimates scale transformations*

---

### Description

this function estimates the scale transformations to be applied on a flowFrame to obtain 'good behaving' distributions, i.e. the best possible separation between + population and - population. It distinguishes between scatter channels, where either linear, or no transform is applied, and fluo channels, where either logicle transform

- using flowCore::estimateLogicle - is estimated, or no transform is applied.

The idea of linear transform of scatter channels is as follows: a reference channel (not a scatter one) is selected and a linear transform ( $Y = AX + B$ ) is applied to all scatter channel, as to align their 5 and 95 percentiles to those of the reference channel For the estimateLogicle function, see flowCore documentation.

### Usage

```
estimateScaleTransforms(
  ff,
  fluoMethod = c("estimateLogicle", "none"),
  scatterMethod = c("none", "linearQuantile"),
  scatterRefMarker = NULL,
  specificScatterChannels = NULL
)
```

### Arguments

ff	a flowCore::flowFrame
fluoMethod	method to be applied to all fluo channels
scatterMethod	method to be applied to all scatter channels
scatterRefMarker	the reference channel that is used to align the
specificScatterChannels	vector of scatter channels for which we still want to apply the fluo method (and not the scatter Method)

**Value**

a `flowCore::flowFrame` with removed low quality events from the input

**Examples**

```
data(OMIP021Samples)

compMatrix <- flowCore::spillover(OMIP021Samples[[1]])$SPILL
ff_c <- runCompensation(OMIP021Samples[[1]], spillover = compMatrix)

transList <-
  estimateScaleTransforms(
    ff = ff_c,
    fluoMethod = "estimateLogicle",
    scatterMethod = "linear",
    scatterRefMarker = "BV785 - CD3")
```

---

execute

*executing CytoPipeline object*

---

**Description**

this function triggers the execution of the processing queues of a `CytoPipeline` object. First, the scale transform processing queue is run, taking the set of sample names as an implicit first input. At the end of the queue, a scale transform List is assumed to be created. Second, the `flowFrame` pre-processing queue, repeatedly for each sample file. The scale transform list generated in the previous step is taken as implicit input, together with the initial sample file. At the end of the queue run, a pre-processed `flowFrame` is assumed to be generated. No change is made on the input `CytoPipeline` object, all results are stored in the cache.

**Usage**

```
execute(
  x,
  path = ".",
  rmCache = FALSE,
  useBiocParallel = FALSE,
  BPPARAM = BiocParallel::bpparam(),
  BPOPTIONS = BiocParallel::bpoptions/packages = c("flowCore"),
  saveLastStepFF = TRUE,
  saveFFSuffix = "_preprocessed",
  saveFFFormat = c("fcs", "csv"),
  saveFFCsvUseChannelMarker = TRUE,
  saveScaleTransforms = FALSE
)
```

**Arguments**

<code>x</code>	CytoPipeline object
<code>path</code>	base path, a subdirectory with name equal to the experiment will be created to store the output data, in particular the experiment cache
<code>rmCache</code>	if TRUE, starts by removing the already existing cache directory corresponding to the experiment
<code>useBiocParallel</code>	if TRUE, use BiocParallel for computation of the sample file pre-processing in parallel (one file per worker at a time). Note the BiocParallel function used is <code>bplapply()</code>
<code>BPPARAM</code>	if <code>useBiocParallel</code> is TRUE, sets the BPPARAM back-end to be used for the computation. If not provided, will use the top back-end on the <code>BiocParallel::registered()</code> stack.
<code>BPOPTIONS</code>	if <code>useBiocParallel</code> is TRUE, sets the BPOPTIONS to be passed to <code>bplapply()</code> function. Note that if you use a <code>SnowParams</code> back-end, you need to specify all the packages that need to be loaded for the different <code>CytoProcessingStep</code> to work properly (visibility of functions). As a minimum, the <code>flowCore</code> package needs to be loaded. (hence the default <code>BPOPTIONS = bpoptions/packages = c("flowCore")</code> )
<code>saveLastStepFF</code>	if TRUE, save the final result of the pre-processing, for each file. By convention, these output files are stored in <code>path/x@experimentName/output/</code> , the file names used are the same as the initial <code>fcs</code> file basenames, concatenated with <code>saveFFSuffix</code> , and with file extension corresponding to <code>saveFFFormat</code> .
<code>saveFFSuffix</code>	FF file name suffix
<code>saveFFFormat</code>	either <code>fcs</code> or <code>csv</code>
<code>saveFFCsvUseChannelMarker</code>	if TRUE (default), converts the channels to the corresponding marker names (where the Marker is not NA). This setting is only applicable to export in <code>csv</code> format.
<code>saveScaleTransforms</code>	if TRUE (default FALSE), save on disk (in RDS format) the <code>flowCore::transformList</code> object obtained after running the <code>scaleTransform</code> processing queue. The file name is hardcoded to <code>path/experimentName/RDS/scaleTransformList.rds</code>

**Value**

nothing

**Examples**

```
### *** EXAMPLE 1: building CytoPipeline step by step *** ###

rawDataDir <-
  system.file("extdata", package = "CytoPipeline")
experimentName <- "OMIP021_PeacoQC"
sampleFiles <- file.path(rawDataDir, list.files(rawDataDir,
```

```
                                pattern = "Donor"))

outputDir <- base::tempdir()

# main parameters : sample files and output files
pipelineParams <- list()
pipelineParams$experimentName <- experimentName
pipelineParams$sampleFiles <- sampleFiles
pipL <- CytoPipeline(pipelineParams)

### SCALE TRANSFORMATION STEPS ###

pipL <-
  addProcessingStep(pipL,
    whichQueue = "scale transform",
    CytoProcessingStep(
      name = "flowframe_read",
      FUN = "readSampleFiles",
      ARGS = list(
        whichSamples = "all",
        truncate_max_range = FALSE,
        min.limit = NULL
      )
    )
  )

pipL <-
  addProcessingStep(pipL,
    whichQueue = "scale transform",
    CytoProcessingStep(
      name = "remove_margins",
      FUN = "removeMarginsPeacoQC",
      ARGS = list()
    )
  )

pipL <-
  addProcessingStep(pipL,
    whichQueue = "scale transform",
    CytoProcessingStep(
      name = "compensate",
      FUN = "compensateFromMatrix",
      ARGS = list(matrixSource = "fcs")
    )
  )

pipL <-
  addProcessingStep(pipL,
    whichQueue = "scale transform",
    CytoProcessingStep(
      name = "flowframe_aggregate",
      FUN = "aggregateAndSample",
      ARGS = list(
```

```
        nTotalEvents = 10000,  
        seed = 0  
    )  
)  
  
pipL <-  
  addProcessingStep(pipL,  
    whichQueue = "scale transform",  
    CytoProcessingStep(  
      name = "scale_transform_estimate",  
      FUN = "estimateScaleTransforms",  
      ARGS = list(  
        fluoMethod = "estimateLogicle",  
        scatterMethod = "linear",  
        scatterRefMarker = "BV785 - CD3"  
      )  
    )  
  )  
  
### PRE-PROCESSING STEPS ###  
  
pipL <-  
  addProcessingStep(pipL,  
    whichQueue = "pre-processing",  
    CytoProcessingStep(  
      name = "flowframe_read",  
      FUN = "readSampleFiles",  
      ARGS = list(  
        truncate_max_range = FALSE,  
        min.limit = NULL  
      )  
    )  
  )  
  
pipL <-  
  addProcessingStep(pipL,  
    whichQueue = "pre-processing",  
    CytoProcessingStep(  
      name = "remove_margins",  
      FUN = "removeMarginsPeacoQC",  
      ARGS = list()  
    )  
  )  
  
pipL <-  
  addProcessingStep(pipL,  
    whichQueue = "pre-processing",  
    CytoProcessingStep(  
      name = "compensate",  
      FUN = "compensateFromMatrix",  
      ARGS = list(matrixSource = "fcs")  
    )  
  )
```

```

    )

    pipL <-
    addProcessingStep(
      pipL,
      whichQueue = "pre-processing",
      CytoProcessingStep(
        name = "remove_debris",
        FUN = "removeDebrisManualGate",
        ARGS = list(
          FSCChannel = "FSC-A",
          SSCChannel = "SSC-A",
          gateData = c(73615, 110174, 213000, 201000, 126000,
                      47679, 260500, 260500, 113000, 35000)
        )
      )
    )

    pipL <-
    addProcessingStep(pipL,
                      whichQueue = "pre-processing",
                      CytoProcessingStep(
                        name = "remove_dead_cells",
                        FUN = "removeDeadCellsManualGate",
                        ARGS = list(
                          FSCChannel = "FSC-A",
                          LDMarker = "L/D Aqua - Viability",
                          gateData = c(0, 0, 250000, 250000,
                                        0, 650, 650, 0)
                        )
                      )
    )

    pipL <-
    addProcessingStep(
      pipL,
      whichQueue = "pre-processing",
      CytoProcessingStep(
        name = "perform_QC",
        FUN = "qualityControlPeacoQC",
        ARGS = list(
          preTransform = TRUE,
          min_cells = 150, # default
          max_bins = 500, # default
          step = 500, # default,
          MAD = 6, # default
          IT_limit = 0.55, # default
          force_IT = 150, # default
          peak_removal = 0.3333, # default
          min_nr_bins_peakdetection = 10 # default
        )
      )
    )

```

```

pipl <-
  addProcessingStep(pipl,
                    whichQueue = "pre-processing",
                    CytoProcessingStep(
                      name = "transform",
                      FUN = "applyScaleTransforms",
                      ARGS = list()
                    )
  )

# execute pipeline, remove cache if existing with the same experiment name
suppressWarnings(execute(pipl, rmCache = TRUE, path = outputDir))

# re-execute as is without removing cache => all results found in cache!
suppressWarnings(execute(pipl, rmCache = FALSE, path = outputDir))

### *** EXAMPLE 2: building CytoPipeline from JSON file *** ###

jsonDir <- system.file("extdata", package = "CytoPipeline")
jsonPath <- file.path(jsonDir, "pipelineParams.json")

pipl2 <- CytoPipeline(jsonPath,
                     experimentName = experimentName,
                     sampleFiles = sampleFiles)

# note we temporarily set working directory into package root directory
# needed as json path mentions "./" path for sample files
suppressWarnings(execute(pipl2, rmCache = TRUE, path = outputDir))

### *** EXAMPLE 3: building CytoPipeline from cache (previously run) *** ###

experimentName <- "OMIP021_PeacoQC"
pipl3 <- buildCytoPipelineFromCache(
  experimentName = experimentName,
  path = outputDir)

suppressWarnings(execute(pipl3,
                        rmCache = FALSE,
                        path = outputDir))

```

---

exportCytoPipeline      *exporting CytoPipeline objects*

---

## Description

functions to export CytoPipeline objects in various formats

**Usage**

```
export2JSONFile(x, path)
```

**Arguments**

x	a CytoPipeline object
path	the full path to the name of the file to be created

**Value**

- for export2JSONFile: nothing

**Functions**

- export2JSONFile(): exports a CytoPipeline object to a JSON file (writing the file = side effect)

**Examples**

```
outputDir <- base::tempdir()

rawDataDir <-
  system.file("extdata", package = "CytoPipeline")
experimentName <- "OMIP021_PeacoQC"
sampleFiles <- file.path(rawDataDir, list.files(rawDataDir,
                                                pattern = "Donor"))

# build CytoPipeline object using json input
jsonPath <- file.path(system.file("extdata", package = "CytoPipeline"),
                      "pipelineParams.json")

pipL <- CytoPipeline(jsonPath,
                    experimentName = experimentName,
                    sampleFiles = sampleFiles)

# remove the last pre-processing step
nPreProcessing <- getNbProcessingSteps(pipL, whichQueue = "pre-processing")
pipL <- removeProcessingStep(pipL, whichQueue = "pre-processing",
                           index = nPreProcessing)

# export back to json file
export2JSONFile(pipL, path = file.path(outputDir, "newFile.json"))
```



---

findTimeChannel	<i>find time channel in flowSet/flowFrame</i>
-----------------	---

---

**Description**

tries to find a channel in a flowSet/flowFrame that could be the time channel. First tries to identify a channel name containing the 'time' string, then tries to identify a single monotonically increasing channel.

**Usage**

```
findTimeChannel(obj, excludeChannels = c())
```

**Arguments**

obj                    a flowCore::flowFrame or flowCore::flowSet  
excludeChannels        vector of column names to exclude in the search

**Value**

a character, name of the found channel that should be representing time. If not found, returns NULL.

**Examples**

```
data(OMIP021Samples)

ret <- findTimeChannel(OMIP021Samples[[1]])
ret # "Time"
```

---

getAcquiredCompensationMatrix	<i>extract compensation matrix from a flowCore::flowFrame</i>
-------------------------------	---

---

**Description**

helper function retrieving the compensation matrix stored in fcs file (if any). It scans the following keywords: \$SPILL, \$spillover and \$SPILLOVER

**Usage**

```
getAcquiredCompensationMatrix(ff)
```

**Arguments**

ff                    a flowCore::flowFrame

**Value**

the found compensation matrix

**Examples**

```
rawDataDir <-
  system.file("extdata", package = "CytoPipeline")
sampleFiles <-
  file.path(rawDataDir, list.files(rawDataDir, pattern = "Donor"))

truncateMaxRange <- FALSE
minLimit <- NULL

# create flowCore::flowSet with all samples of a dataset
fsRaw <- readSampleFiles(
  sampleFiles = sampleFiles,
  whichSamples = "all",
  truncate_max_range = truncateMaxRange,
  min.limit = minLimit)
compensationMatrix <- getAcquiredCompensationMatrix(fsRaw[[2]])
```

---

getChannelNamesFromMarkers

*get channel names from markers*

---

**Description**

finds name of channels corresponding to user provided markers

**Usage**

```
getChannelNamesFromMarkers(ff, markers)
```

**Arguments**

ff                    a flowCore::flowFrame

markers              a vector of markers, either provided as :

- an array of booleans (referring to flowFrame columns)
- an array of integers (indices in flowFrame columns)
- an array of characters (exact markers or channel patterns)

**Value**

a character vector, containing the names of the corresponding channels

**Examples**

```
data(OMIP021Samples)

# with existing markers
ret <- getChannelNamesFromMarkers(
  OMIP021Samples[[1]],
  c(
    "FSC-A",
    "L/D Aqua - Viability",
    "FITC - gdTCR",
    "PECy5 - CD28"
  ))

ret # c("FSC-A", "525/50Violet-A", "530/30Blue-A", "670/30Yellow-A")

# with boolean vector
indices <- c(1, 6, 14, 18)
boolInput <- rep(FALSE, 21)
boolInput[indices] <- TRUE
ret2 <- getChannelNamesFromMarkers(
  OMIP021Samples[[1]],
  boolInput)

ret2 # c("FSC-A", "525/50Violet-A", "530/30Blue-A", "670/30Yellow-A")

# with indices vector
ret3 <- getChannelNamesFromMarkers(
  OMIP021Samples[[1]],
  indices
)
ret3 # c("FSC-A", "525/50Violet-A", "530/30Blue-A", "670/30Yellow-A")
```

---

getFCSFileName	<i>get fcs file name</i>
----------------	--------------------------

---

**Description**

get basename of \$FILENAME keyword if exists

**Usage**

```
getFCSFileName(ff)
```

**Arguments**

ff                    a flowCore::flowFrame

**Value**

the basename of \$FILENAME keyword

**Examples**

```
data(OMIP021Samples)

fName <- getFCSFileName(OMIP021Samples[[1]])
```

---

<code>getTransfoParams</code>	<i>get transformation parameters for a specific channel</i>
-------------------------------	---

---

**Description**

investigates a `flowCore::transformList` object to get the type and parameters of the transformation applying to a specific channel

**Usage**

```
getTransfoParams(transList, channel)
```

**Arguments**

<code>transList</code>	a <code>flowCore::transformList</code>
<code>channel</code>	channel name

**Value**

If the transformation exists for the specified channel, and is either recognized as a logicle transfo or a linear transfo, a list with two slots:

- `$type` a character containing the transfo type ('logicle' or 'linear')
- `$params_list` a list of named numeric, according to transfo type

Otherwise, NULL is returned.

**Examples**

```
data(OMIP021Samples)

# set-up a hybrid transformation list :
# - two channels are logicle-ly transformed with automatic param estimates
# - one channel has explicit logicle transfo with default parameters
# - one channel has linear transformation
# - other channels have no transformation
translist <- flowCore::estimateLogicle(
  OMIP021Samples[[1]],
  c("450/50Violet-A", "525/50Violet-A")
```

```

)
translist <- c(
  translist,
  flowCore::transformList(
    "FSC-A",
    flowCore::linearTransform(
      a = 0.1,
      b = 0
    )
  ),
  flowCore::transformList(
    "540/30Violet-A",
    flowCore::logicleTransform()
  )
)

ret1 <- getTransfoParams(translist, channel = "FSC-A")
ret1$type # "linear"
ret1$paramsList # a = 0.1, b = 0.

ret2 <- getTransfoParams(translist, channel = "525/50Violet-A")
ret2$type # "logicle"
ret2$paramsList # a = 0., w = 0.2834, m = 4.5, t = 262143

ret3 <- getTransfoParams(translist, channel = "540/30Violet-A")
ret3$type # "logicle"
ret3$paramsList # a = 0., w = 0.5, m = 4.5, t = 262144

```

---

ggplotEvents

*plot events in 1D or 2D, using ggplot2*


---

## Description

plot events of specific channels of either : flowCore::flowFrame, or flowCore::flowSet in 2D or 1D, mimicking FlowJo type of graph.  
if 1D : geom\_density will be used  
if 2D : geom\_hex will be used

## Usage

```

ggplotEvents(
  obj,
  xChannel,
  yChannel = NULL,
  nDisplayCells = Inf,
  seed = NULL,
  bins = 216,
  fill = "lightblue",

```

```

alpha = 0.2,
xScale = c("linear", "logicle"),
yScale = c("linear", "logicle"),
xLogicleParams = NULL,
yLogicleParams = NULL,
xLinearRange = NULL,
yLinearRange = NULL,
transList = NULL,
runTransforms = FALSE
)

```

### Arguments

<code>obj</code>	a <code>flowCore::flowFrame</code> or <code>flowCore::flowSet</code>
<code>xChannel</code>	channel (name or index) or marker name to be displayed on x axis
<code>yChannel</code>	channel (name or index) or marker name to be displayed on y axis
<code>nDisplayCells</code>	maximum number of events that will be plotted. If the number of events exceed this number, a sub-sampling will be performed
<code>seed</code>	seed used for sub-sampling (if any)
<code>bins</code>	used in <code>geom_hex</code>
<code>fill</code>	used in <code>geom_density</code>
<code>alpha</code>	used in <code>geom_density</code>
<code>xScale</code>	scale to be used for the x axis (note "linear" corresponds to no transformation)
<code>yScale</code>	scale to be used for the y axis (note "linear" corresponds to no transformation)
<code>xLogicleParams</code>	if ( <code>xScale == "logicle"</code> ), the parameters of the logicle transformation to be used, as a list( <code>w = ...</code> , <code>m = ...</code> , <code>a = ...</code> , <code>t = ...</code> ). If <code>NULL</code> , these parameters will be estimated by <code>flowCore::estimateLogicle()</code>
<code>yLogicleParams</code>	if ( <code>yScale == "logicle"</code> ), the parameters of the logicle transformation to be used, as a list( <code>w = ...</code> , <code>m = ...</code> , <code>a = ...</code> , <code>t = ...</code> ). If <code>NULL</code> , these parameters will be estimated by <code>flowCore::estimateLogicle()</code>
<code>xLinearRange</code>	if ( <code>xScale == "linear"</code> ), the x axis range to be used
<code>yLinearRange</code>	if ( <code>yScale == "linear"</code> ), the y axis range to be used
<code>transList</code>	optional list of scale transformations to be applied to each channel. If it is non null, <code>'x/yScale'</code> , <code>'x/yLogicleParams'</code> and <code>'x/yLinear_range'</code> will be discarded.
<code>runTransforms</code>	(TRUE/FALSE) Will the application of non linear scale result in data being effectively transformed ? <ul style="list-style-type: none"> <li>• If TRUE, than the data will undergo transformations prior to visualization.</li> <li>• If FALSE, the axis will be scaled but the data themselves will not be transformed.</li> </ul>

### Value

a list of ggplot objects

**Examples**

```

data(OMIP021Samples)

### 1D Examples ###

# simple linear scale example
ggplotEvents(OMIP021Samples[[1]],
             xChannel = "FSC-A",
             xScale = "linear")

# with explicit linear range
ggplotEvents(OMIP021Samples[[1]],
             xChannel = "FSC-A",
             xScale = "linear",
             xLinearRange = c(0, 250000))

# with linear scale, several flow frames
ggplotEvents(OMIP021Samples, xChannel = "FSC-A", xScale = "linear")

# simple logicle scale example
ggplotEvents(OMIP021Samples[[1]],
             xChannel = "450/50Violet-A",
             xScale = "logicle")

# logicle scale, explicit parameters
ggplotEvents(OMIP021Samples[[1]],
             xChannel = "450/50Violet-A",
             xScale = "logicle", xLogicleParams = list(
               a = 1,
               w = 2,
               m = 7,
               t = 270000))

# with sub-sampling
ggplotEvents(OMIP021Samples[[2]],
             xChannel = "450/50Violet-A",
             xScale = "logicle", nDisplayCells = 5000)

# tuning some plot parameters
ggplotEvents(OMIP021Samples[[2]],
             xChannel = "450/50Violet-A",
             xScale = "logicle", alpha = 0.5, fill = "red")

# examples that use a transformation list, estimated after compensation
compensationMatrix <- flowCore::spillover(OMIP021Samples[[1]])$SPILL

ffc <- runCompensation(OMIP021Samples[[1]],
                     spillover = compensationMatrix,
                     updateChannelNames = FALSE)

transList <- flowCore::estimateLogicle(
  ffc,

```

```
colnames(compensationMatrix))

transList <-
  c(transList,
    flowCore::transformList(
      "FSC-A",
      flowCore::linearTransform(a = 0.00001)))

# linear example, without running the transformations on data
ggplotEvents(OMIP021Samples[[1]],
  xChannel = "450/50Violet-A",
  xScale = "linear",
  transList = transList,
  runTransforms = FALSE)

# linear example, now running the transformations on data
ggplotEvents(OMIP021Samples[[1]],
  xChannel = "450/50Violet-A",
  xScale = "linear",
  transList = transList,
  runTransforms = TRUE)

# logicle example, without running the transformations on data
ggplotEvents(OMIP021Samples[[1]],
  xChannel = "FSC-A",
  xScale = "logicle",
  transList = transList,
  runTransforms = FALSE)

# logicle example, now running the transformations on data
ggplotEvents(OMIP021Samples[[1]],
  xChannel = "FSC-A",
  xScale = "logicle",
  transList = transList,
  runTransforms = TRUE)

### 2D examples ###

# simple linear example
ggplotEvents(OMIP021Samples[[1]],
  xChannel = "FSC-A",
  xScale = "linear",
  yChannel = "610/20Violet-A",
  yScale = "logicle")

# simple linear example, 2 flow frames
ggplotEvents(OMIP021Samples,
  xChannel = "FSC-A",
  xScale = "linear",
  yChannel = "SSC-A",
  yScale = "linear")
```



```
# logicle vs linear example
ggplotEvents(OMIP021Samples[[1]],
             xChannel = "450/50Violet-A",
             xScale = "logicle",
             yChannel = "SSC-A",
             yScale = "linear")

# 2X logicle example
ggplotEvents(OMIP021Samples[[1]],
             xChannel = "TETaGC",
             xScale = "logicle",
             yChannel = "CD27",
             yScale = "logicle")

# tuning nb of bins
ggplotEvents(OMIP021Samples[[1]],
             xChannel = "TETaGC",
             xScale = "logicle",
             yChannel = "CD27",
             yScale = "logicle",
             bins = 128)

# using transformation list, not run on data
ggplotEvents(OMIP021Samples[[1]],
             xChannel = "TETaGC",
             xScale = "logicle",
             yChannel = "CD27",
             yScale = "logicle",
             transList = transList,
             runTransforms = FALSE)

# using transformation list, run on data
ggplotEvents(OMIP021Samples[[1]],
             xChannel = "TETaGC",
             xScale = "logicle",
             yChannel = "CD27",
             yScale = "logicle",
             transList = transList,
             runTransforms = TRUE)
```

---

ggplotFilterEvents      *plot filtered events in 2D, using ggplot*

---

### Description

plot events of specific channels of either : flowCore::flowFrame, or flowCore::flowSet in 2D, showing the impact of applying a filter between :

- a 'pre' flowframe

**Usage**

```
ggplotFilterEvents(
  ffPre,
  ffPost,
  xChannel,
  yChannel,
  nDisplayCells = 10000,
  seed = NULL,
  size = 0.5,
  xScale = c("linear", "logicle"),
  yScale = c("linear", "logicle"),
  xLogicleParams = NULL,
  yLogicleParams = NULL,
  xLinearRange = NULL,
  yLinearRange = NULL,
  transList = NULL,
  runTransforms = FALSE,
  interactive = FALSE
)
```

**Arguments**

ffPre	a flowCore::flowFrame, before applying filter
ffPost	a flowCore::flowFrame, after applying filter
xChannel	channel (name or index) or marker name to be displayed on x axis
yChannel	channel (name or index) or marker name to be displayed on y axis
nDisplayCells	maximum number of events that will be plotted. If the number of events exceed this number, a subsampling will be performed
seed	seed used for sub-sampling (if any)
size	used by geom_point()
xScale	scale to be used for the x axis (note "linear" corresponds to no transformation)
yScale	scale to be used for the y axis (note "linear" corresponds to no transformation)
xLogicleParams	if (xScale == "logicle"), the parameters of the logicle transformation to be used, as a list(w = ..., m = ..., a = ..., t = ...) If NULL, these parameters will be estimated by flowCore::estimateLogicle()
yLogicleParams	if (yScale == "logicle"), the parameters of the logicle transformation to be used, as a list(w = ..., m = ..., a = ..., t = ...) If NULL, these parameters will be estimated by flowCore::estimateLogicle()
xLinearRange	if (xScale == "linear"), linear range to be used
yLinearRange	if (yScale == "linear"), linear range to be used
transList	optional list of scale transformations to be applied to each channel. If it is non null, 'x/yScale', 'x/yLogicleParams' and 'x/yLinear_range' will be discarded.
runTransforms	(TRUE/FALSE) Will the application of non linear scale result in data being effectively transformed ?

- If TRUE, than the data will undergo transformations prior to visualization.
  - If FALSE, the axis will be scaled but the data themselves are not transformed.
- interactive    if TRUE, transform the scaling formats such that the ggcyto::x\_scale\_logicle() and ggcyto::y\_scale\_logicle() do work with plotly::ggplotly()

**Value**

a ggplot object

**Examples**

```
data(OMIP021Samples)

ffPre <- OMIP021Samples[[1]]

# creating a manual polygon gate filter based on channels L/D and FSC-A

LDMarker <- "L/D Aqua - Viability"

LDChannel <- getChannelNamesFromMarkers(ffPre, markers = LDMarker)
liveGateMatrix <- matrix(
  data = c(
    50000, 50000, 100000, 200000, 200000,
    100, 1000, 2000, 2000, 1
  ),
  ncol = 2,
  dimnames = list(
    c(),
    c("FSC-A", LDChannel)
  )
)

liveGate <- flowCore::polygonGate(
  filterId = "Live",
  .gate = liveGateMatrix
)

selectedLive <- flowCore::filter(ffPre, liveGate)
ffL <- flowCore::Subset(ffPre, selectedLive)

# show the results

# subsample 5000 points
ggplotFilterEvents(
  ffPre = ffPre,
  ffPost = ffL,
  nDisplayCells = 5000,
  xChannel = "FSC-A", xScale = "linear",
  yChannel = LDMarker, yScale = "logicle") +
  ggplot2::ggtitle("Live gate filter - 5000 points")
```

```
# with all points
ggplotFilterEvents(
  ffPre = ffPre,
  ffPost = ffL,
  nDisplayCells = Inf,
  xChannel = "FSC-A", xScale = "linear",
  yChannel = LDMarker, yScale = "logicle") +
ggplot2::ggtitle("Live gate filter - all points")
```

---

ggplotFlowRate	<i>plot flow rate as a function of time, using ggplot2</i>
----------------	--

---

### Description

plot flow rate as a function of time, using ggplot2

### Usage

```
ggplotFlowRate(obj, title = "Flow Rate", timeUnit = 100)
```

### Arguments

obj	a flowCore::flowFrame or flowCore::flowSet
title	a title for the graph
timeUnit	which time interval is used to calculate "instant" flow rate (default = 100 ms)

### Value

a ggplot graph

### Examples

```
data(OMIP021Samples)

# single flowFrame plot
ggplotFlowRate(OMIP021Samples[[1]])

# two flowFrames plot
ggplotFlowRate(OMIP021Samples)

# single plot with title
ggplotFlowRate(OMIP021Samples[[1]], title = "Test Flow Rate plot")

# explicit time unit
ggplotFlowRate(OMIP021Samples[[1]], timeUnit = 50)
```

---

`handlingProcessingSteps`*handling processing steps in CytoPipeline objects*

---

**Description**

functions to manipulate processing steps in processing queues of CytoPipeline objects

**Usage**

```
addProcessingStep(  
  x,  
  whichQueue = c("scale transform", "pre-processing"),  
  newPS  
)  
  
removeProcessingStep(  
  x,  
  whichQueue = c("scale transform", "pre-processing"),  
  index  
)  
  
getNbProcessingSteps(x, whichQueue = c("scale transform", "pre-processing"))  
  
getProcessingStep(  
  x,  
  whichQueue = c("scale transform", "pre-processing"),  
  index  
)  
  
getProcessingStepNames(x, whichQueue = c("scale transform", "pre-processing"))  
  
cleanProcessingSteps(  
  x,  
  whichQueue = c("both", "scale transform", "pre-processing")  
)  
  
showProcessingSteps(x, whichQueue = c("scale transform", "pre-processing"))
```

**Arguments**

<code>x</code>	a CytoPipeline object
<code>whichQueue</code>	selects the processing queue for which we manage the processing steps
<code>newPS</code>	the new processing step to be added (CytoProcessingStep object)
<code>index</code>	index of the processing step to remove

**Value**

- for `addProcessingStep`: the updated `CytoPipeline` object
- for `removeProcessingStep`: the updated `CytoPipeline` object
- for `getNbProcessingSteps`: the number of processing steps present in the target queue
- for `getProcessingStep`: the obtained `CytoProcessingStep` object
- for `getProcessingStepNames`: the vector of step names
- for `cleanProcessingSteps`: the updated `CytoPipeline` object
- for `showProcessingSteps`: nothing (only console display side effect is required)

**Functions**

- `addProcessingStep()`: adds a processing step in one of the processing queues (at the end), returns the modified `CytoPipeline` object
- `removeProcessingStep()`: removes a processing step from one of the processing queues, returns the modified `CytoPipeline` object
- `getNbProcessingSteps()`: gets the number of processing steps in a processing queue
- `getProcessingStep()`: gets a processing step at a specific index of a processing queue
- `getProcessingStepNames()`: gets a character vector of all processing step names of a specific processing queue
- `cleanProcessingSteps()`: deletes all processing steps in one or both processing queues, returns the modified `CytoPipeline` object
- `showProcessingSteps()`: shows all processing steps in a processing queue

**Examples**

```
rawDataDir <-
  system.file("extdata", package = "CytoPipeline")
experimentName <- "OMIP021_PeacoQC"
sampleFiles <- file.path(rawDataDir, list.files(rawDataDir,
                                               pattern = "Donor"))

transListPath <-
  file.path(system.file("extdata", package = "CytoPipeline"),
            "OMIP021_TransList.rds")

# main parameters : sample files and experiment name
pipelineParams <- list()
pipelineParams$experimentName <- experimentName
pipelineParams$sampleFiles <- sampleFiles

# create CytoPipeline object (no step defined yet)
pipL <- CytoPipeline(pipelineParams)

# add a processing step in scale tranformation queue
```

```

pipL <- addProcessingStep(pipL,
  whichQueue = "scale transform",
  CytoProcessingStep(
    name = "scale_transform_read",
    FUN = "readRDS",
    ARGS = list(file = transListPath)
  ))

getNbProcessingSteps(pipL, "scale transform") # returns 1

# add another processing step in scale transformation queue
pipL <- addProcessingStep(pipL,
  whichQueue = "scale transform",
  CytoProcessingStep(
    name = "scale_transform_sum",
    FUN = "sum",
    ARGS = list()
  )
)

getNbProcessingSteps(pipL, "scale transform") # returns 2

getProcessingStepNames(pipL, whichQueue = "scale transform")

# removes second processing step in scale transformation queue
pipL <- removeProcessingStep(pipL,
  whichQueue = "scale transform",
  index = 2)

# get processing step object
pS <- getProcessingStep(pipL, whichQueue = "scale transform", index = 1)
getCPSName(pS) #"scale_transform_read"

# add a processing step in pre-processing queue
pipL <- addProcessingStep(pipL,
  whichQueue = "pre-processing",
  CytoProcessingStep(
    name = "pre-processing_sum",
    FUN = "sum",
    ARGS = list()
  ))

getNbProcessingSteps(pipL, "scale transform") # returns 1
getNbProcessingSteps(pipL, "pre-processing") # returns also 1

showProcessingSteps(pipL, whichQueue = "scale transform")
showProcessingSteps(pipL, whichQueue = "pre-processing")

# cleans both processing queues
pipL <- cleanProcessingSteps(pipL)
pipL

```

---

`inspectCytoPipelineObjects`*inspect CytoPipeline results objects*

---

**Description**

functions to obtain results objects formats

internal function for the time being

**Usage**

```
getCytoPipelineExperimentNames(  
  path = ".",  
  pattern = NULL,  
  ignore.case = FALSE,  
  fixed = FALSE  
)
```

```
getCytoPipelineObjectFromCache(  
  x,  
  path = ".",  
  whichQueue = c("scale transform", "pre-processing"),  
  sampleFile = NULL,  
  objectName  
)
```

```
getCytoPipelineObjectInfos(  
  x,  
  path = ".",  
  whichQueue = c("scale transform", "pre-processing"),  
  sampleFile = NULL  
)
```

```
getCytoPipelineFlowFrame(  
  x,  
  path = ".",  
  whichQueue = c("scale transform", "pre-processing"),  
  sampleFile,  
  objectName  
)
```

```
getCytoPipelineScaleTransform(  
  x,  
  path = ".",  
  whichQueue = c("scale transform", "pre-processing"),  
  sampleFile = NULL,
```



```

    objectName
  )

plotCytoPipelineProcessingQueue(
  x,
  whichQueue = c("pre-processing", "scale transform"),
  purpose = c("run status", "description"),
  sampleFile = NULL,
  path = ".",
  title = TRUE,
  box.type = "ellipse",
  lwd = 1,
  box.prop = 0.5,
  box.cex = 0.7,
  cex.txt = 0.7,
  box.size = 0.1,
  dtext = 0.15,
  ...
)

```

### Arguments

path	root path to locate the search for file caches
pattern	optional pattern limiting the search for experiment names
ignore.case	(TRUE/FALSE) used in pattern matching (grepl)
fixed	(TRUE/FALSE) used in pattern matching (grepl)
x	a CytoPipeline object
whichQueue	which queue to look into
sampleFile	which sampleFile is looked for: <ul style="list-style-type: none"> <li>• if whichQueue == "scale transform", the sampleFile is ignored</li> <li>• if NULL and whichQueue == "pre-processing", the sampleFile is defaulted to the first one belonging to the experiment</li> </ul>
objectName	(character) which object name to look for
purpose	purpose of the workflow plot <ul style="list-style-type: none"> <li>• if "run status" (default), the disk cache will be inspected and the box colours will be set according to run status (green = run, orange = not run, red = definition not consistent with cache). Moreover, the object classes and names will be filled in if found in the cache.</li> <li>• if "description", the workflow will be obtained from the step definition in the x object, not from the disk cache. As a result, all boxes will be coloured in black, and no object class and name will be provided.</li> </ul>
title	if TRUE, adds a title to the plot
box.type	shape of label box (rect, ellipse, diamond, round, hexa, multi)
lwd	default line width of arrow and box (one numeric value)

<code>box.prop</code>	length/width ratio of label box (one numeric value)
<code>box.cex</code>	relative size of text in boxes (one numeric value)
<code>cex.txt</code>	relative size of arrow text (one numeric value)
<code>box.size</code>	size of label box (one numeric value)
<code>dtext</code>	controls the position of arrow text relative to arrowhead (one numeric value)
<code>...</code>	other arguments passed to <code>diagram::plotmat()</code>

### Value

- for `getCytoPipelineExperimentNames`: a vector of character containing found experiment names
- for `getCytoPipelineObjectFromCache`: the found object (or stops with an error message if the target object is not found)
- for `getCytoPipelineObjectInfos`: a dataframe with the collected information about the found objects (or stops with an error message if no target object was found)
- for `getCytoPipelineFlowFrame`: the found `flowFrame` (or stops with an error message if the target object is not found, or if the object is no `flowFrame`)
- for `getCytoPipelineScaleTransform`: the found `flowFrame` (or stops with an error message if the target object is not found, or if the object is no `transformList`)
- for `plotCytoPipelineProcessingQueue`: nothing

### Functions

- `getCytoPipelineExperimentNames()`: This function looks into a path for stored file caches and gets the corresponding experiment names
- `getCytoPipelineObjectFromCache()`: Given a `CytoPipeline` object, this function retrieves a specific object in the corresponding file cache
- `getCytoPipelineObjectInfos()`: Given a `CytoPipeline` object, this function retrieves the information related to a specific object name, i.e. object name and object class
- `getCytoPipelineFlowFrame()`: Given a `CytoPipeline` object, this function retrieves a specific `flowCore::flowFrame` object in the corresponding file cache object name and object class
- `getCytoPipelineScaleTransform()`: Given a `CytoPipeline` object, this function retrieves a specific `flowCore::transformList` object in the corresponding file cache
- `plotCytoPipelineProcessingQueue()`: This functions displays a plot of a processing queue of a `CytoPipeline` object, using `diagram::plotmat()`.
  - If a step is in run state for all sample files, the corresponding box appears in green
  - If a step is in non run state for at least one sample file, the corresponding box appears in orange
  - If at least one step is not consistent with cache, the whole set of boxes appears in red



```

        path = outputDir,
        sampleFile = sampleFiles(pipL2)[1])

# get any object (output of one step)
obj <-
  getCytoPipelineObjectFromCache(pipL2, whichQueue = "scale transform",
                                objectName = "compensate_obj",
                                path = outputDir)

class(obj) # flowCore::flowSet

```

---

interactingWithCytoPipelineCache

*interaction between CytoPipeline object and disk cache*

---

## Description

functions supporting the interaction between a CytoPipeline object and the file cache on disk

## Usage

```

deleteCytoPipelineCache(x, path = ".")

buildCytoPipelineFromCache(experimentName, path = ".")

checkCytoPipelineConsistencyWithCache(
  x,
  path = ".",
  whichQueue = c("both", "scale transform", "pre-processing"),
  sampleFile = NULL
)

```

## Arguments

x	a CytoPipeline object
path	the full path to the experiment storage on disk (without the /.cache)
experimentName	the experimentName used to select the file cache on disk
whichQueue	which processing queue to check the consistency of
sampleFile	if whichQueue == "pre-processing" or "both": which sample file(s) to check on the disk cache

## Value

for deleteCytoPipelineCache: TRUE if successfully removed  
 for buildCytoPipelineFromCache: the built CytoPipeline object  
 for checkCytoPipelineConsistencyWithCache: a list with the following values:

- `isConsistent` (TRUE/FALSE)
- `inconsistencyMsg`: character filled in by an inconsistency message in case the cache and `CytoPipeline` object are not consistent with each other
- `scaleTransformStepStatus`: a character vector, containing, for each scale transform step, a status from `c("run", "not run", "inconsistent")`
- `preProcessingStepStatus`: a character matrix, containing, for each pre-processing step (rows), for each sample file (columns), a status from `c("run", "not run", "inconsistent")`

## Functions

- `deleteCytoPipelineCache()`: delete the whole disk cache corresponding to the experiment of a `CytoPipeline` object
- `buildCytoPipelineFromCache()`: builds a new `CytoPipeline` object, based on the information stored in the file cache
- `checkCytoPipelineConsistencyWithCache()`: check the consistency between the processing steps described in a `CytoPipeline` object, and what is stored in the file cache

## Examples

```
# preliminary run:
# build CytoPipeline object using json input, run and store results in cache
rawDataDir <-
  system.file("extdata", package = "CytoPipeline")
experimentName <- "OMIP021_PeacoQC"
sampleFiles <- file.path(rawDataDir, list.files(rawDataDir,
                                               pattern = "Donor"))

jsonDir <- system.file("extdata", package = "CytoPipeline")
jsonPath <- file.path(jsonDir, "pipelineParams.json")
outputDir <- base::tempdir()
pipL <- CytoPipeline(jsonPath,
                    experimentName = experimentName,
                    sampleFiles = sampleFiles)

# note we temporarily set working directory into package root directory
# needed as json path mentions "./" path for sample files
suppressWarnings(execute(pipL, rmCache = TRUE, path = outputDir))

# rebuild CytoPipeline from stored results in cache, for a specific
# experiment

experimentName <- "OMIP021_PeacoQC"
pipL2 <- buildCytoPipelineFromCache(
  experimentName = experimentName,
  path = outputDir)

# checking consistency between CytoPipeline object and cache
res <- checkCytoPipelineConsistencyWithCache(pipL2)
```

```
#res

suppressWarnings(execute(pipl2, rmCache = FALSE, path = outputDir))
# (everything is already stored in cache)

# deleting cache related to a specific experiment
pipl3 <- CytoPipeline(experimentName = experimentName)
deleteCytoPipelineCache(pipl3, path = outputDir)
```

---

OMIP021Samples	<i>OMIP021Samples dataset</i>
----------------	-------------------------------

---

### Description

OMIP021Samples dataset

### Format

a flowCore::flowSet with two different flowFrames each one contains one flow cytometry sample corresponding to Donor1.fcs and Donor2.fcs in following source. A subsampling of 5,000 events has been performed on each file.

### Value

nothing

### Source

<https://flowrepository.org/experiments/305>

---

qualityControlFlowAI	<i>perform QC with flowAI</i>
----------------------	-------------------------------

---

### Description

this function is a wrapper around flowAI::flow\_auto\_qc() function. It also pre-selects the channels to be handled (=> all signal channels)

### Usage

```
qualityControlFlowAI(
  ff,
  preTransform = FALSE,
  transList = NULL,
  outputDiagnostic = FALSE,
  outputDir = NULL,
  ...
)
```

**Arguments**

<code>ff</code>	a <code>flowCore::flowFrame</code>
<code>preTransform</code>	if TRUE, apply the <code>transList</code> scale transform prior to running the gating algorithm
<code>transList</code>	applied in conjunction with <code>preTransform</code>
<code>outputDiagnostic</code>	if TRUE, stores diagnostic files generated by <code>flowAI</code> in <code>outputDir</code> directory
<code>outputDir</code>	used in conjunction with <code>outputDiagnostic</code>
<code>...</code>	additional parameters passed to <code>flowAI::flow_auto_qc()</code>

**Value**

a `flowCore::flowFrame` with removed low quality events from the input

**Examples**

```
rawDataDir <-
  system.file("extdata", package = "CytoPipeline")
sampleFiles <-
  file.path(rawDataDir, list.files(rawDataDir, pattern = "Donor"))

truncateMaxRange <- FALSE
minLimit <- NULL

# create flowCore::flowSet with all samples of a dataset
fsRaw <- readSampleFiles(
  sampleFiles = sampleFiles,
  whichSamples = "all",
  truncate_max_range = truncateMaxRange,
  min.limit = minLimit)

suppressWarnings(ff_QualityControl <-
  qualityControlFlowAI(fsRaw[[2]],
    remove_from = "all", # all default
    second_fractionFR = 0.1,
    deviationFR = "MAD",
    alphaFR = 0.01,
    decompFR = TRUE,
    outlier_binsFS = FALSE,
    pen_valueFS = 500,
    max_cptFS = 3,
    sideFM = "both",
    neg_valuesFM = 1))
```

---

qualityControlPeacoQC *perform QC with PeacoQC*

---

### Description

this function is a wrapper around PeacoQC::PeacoQC() function. It also pre-selects the channels to be handled (=> all signal channels)

### Usage

```
qualityControlPeacoQC(
  ff,
  preTransform = FALSE,
  transList = NULL,
  outputDiagnostic = FALSE,
  outputDir = NULL,
  ...
)
```

### Arguments

ff	a flowCore::flowFrame
preTransform	if TRUE, apply the transList scale transform prior to running the gating algorithm
transList	applied in conjunction with preTransform
outputDiagnostic	if TRUE, stores diagnostic files generated by PeacoQC in outputDir directory
outputDir	used in conjunction with outputDiagnostic
...	additional parameters passed to PeacoQC::PeacoQC()

### Value

a flowCore::flowFrame with removed low quality events from the input

### Examples

```
rawDataDir <-
  system.file("extdata", package = "CytoPipeline")
sampleFiles <-
  file.path(rawDataDir, list.files(rawDataDir, pattern = "Donor"))

truncateMaxRange <- FALSE
minLimit <- NULL

# create flowCore::flowSet with all samples of a dataset
fsRaw <- readSampleFiles(
  sampleFiles = sampleFiles,
```



```
      whichSamples = "all",
      truncate_max_range = truncateMaxRange,
      min.limit = minLimit)

suppressWarnings(ff_m <- removeMarginsPeacoQC(x = fsRaw[[2]]))

ff_c <-
  compensateFromMatrix(ff_m,
                      matrixSource = "fcs")

transList <-
  estimateScaleTransforms(
    ff = ff_c,
    fluoMethod = "estimateLogicle",
    scatterMethod = "linear",
    scatterRefMarker = "BV785 - CD3")

ff_QualityControl <- suppressWarnings(
  qualityControlPeacoQC(
    ff_c,
    preTransform = TRUE,
    transList = transList,
    min_cells = 150,
    max_bins = 500,
    MAD = 6,
    IT_limit = 0.55,
    force_IT = 150,
    peak_removal = (1/3),
    min_nr_bins_peakdetection = 10))
```

---

readRDSObject

*read RDS object*

---

## Description

wrapper around readRDS, which discards any additional parameters passed in (...)

## Usage

```
readRDSObject(RDSFile, ...)
```

## Arguments

RDSFile	a RDS file containing a R object object
...	other arguments (not used)

**Value**

the read R object

**Examples**

```
data(OMIP021Samples)

transListPath <- file.path(system.file("extdata",
                                     package = "CytoPipeline"),
                           "OMIP021_TransList.rds")

transList <- readRDSObject(transListPath)

ff_c <- compensateFromMatrix(OMIP021Samples[[1]],
                            matrixSource = "fcs")

ff_t <- applyScaleTransforms(ff_c, transList = transList)
```

---

readSampleFiles	<i>Read fcs sample files</i>
-----------------	------------------------------

---

**Description**

Wrapper around `flowCore::read.fcs()` or `flowCore::read.flowSet()`. Also adds a "Cell\_ID" additional column, used in `flowFrames` comparison

**Usage**

```
readSampleFiles(
  sampleFiles,
  whichSamples = "all",
  nSamples = NULL,
  seed = NULL,
  pData = NULL,
  channelMarkerFile = NULL,
  ...
)
```

**Arguments**

sampleFiles	a vector of character path to sample files
whichSamples	one of: <ul style="list-style-type: none"> <li>• 'all' if all sample files need to be read</li> <li>• 'random' if some samples need to be chosen randomly (in that case, using <code>nSamples</code> and <code>seed</code>)</li> <li>• a vector of indexes pointing to the <code>sampleFiles</code> vector</li> </ul>

nSamples	number of samples to randomly select (if whichSamples == "random"). If nSamples is higher than nb of available samples, the output will be all samples
seed	an optional seed parameters (provided to ease reproducibility).
pData	an optional data.frame containing additional information for each sample file. The pData row names must correspond to basename(sampleFiles).
channelMarkerFile	an optional path to a csv file which provides the mapping between channels and markers. If provided, this csv file should contain a Channel column, and a Marker column. Optionally a 'Used' column can be provided as well (TRUE/FALSE). Channels for which the 'Used' column is set to FALSE will not be incorporated in the created flowFrame.
...	additional parameters passed to flowCore file reading functions.

### Value

either a flowCore::flowSet or a flowCore::flowFrame if length(sampleFiles) == 1

### Examples

```
rawDataDir <-
  system.file("extdata", package = "CytoPipeline")
sampleFiles <-
  file.path(rawDataDir, list.files(rawDataDir, pattern = "Donor"))

truncateMaxRange <- FALSE
minLimit <- NULL

# create flowCore::flowSet with all samples of a dataset
res <- readSampleFiles(
  sampleFiles = sampleFiles,
  whichSamples = "all",
  truncate_max_range = truncateMaxRange,
  min.limit = minLimit)

#res

# create a flowCore::flowFrame with one single sample
res2 <- readSampleFiles(
  sampleFiles = sampleFiles,
  whichSamples = 2,
  truncate_max_range = truncateMaxRange,
  min.limit = minLimit)

#res2
```

---

```
removeChannels          remove channels from a flowFrame
```

---

**Description**

: in a flowCore::flowFrame, remove the channels of the given names.

**Usage**

```
removeChannels(ff, channels)
```

**Arguments**

```
ff          a flowCore::flowFrame
channels    the channel names to be removed
```

**Value**

a new flowCore::flowFrame with the removed channels

**Examples**

```
data(OMIP021Samples)

retFF <- removeChannels(OMIP021Samples[[1]],
                        channel = "FSC-A")
```

---

```
removeDeadCellsManualGate
          remove dead cells from a flowFrame using manual gating
```

---

**Description**

remove dead cells from a flowFrame, using manual gating in the FSC-A, '(a)Live/Dead' 2D representation. The function uses flowCore::polygonGate()

**Usage**

```
removeDeadCellsManualGate(
  ff,
  preTransform = FALSE,
  transList = NULL,
  FSCchannel,
  LDMarker,
  gateData,
  ...
)
```



---

 removeDebrisManualGate

*remove debris from a flowFrame using manual gating*


---

### Description

remove debris from a flowFrame, using manual gating in the FSC-A, SSC-A 2D representation. The function internally uses flowCore::polygonGate()

### Usage

```
removeDebrisManualGate(ff, FSCChannel, SSCChannel, gateData, ...)
```

### Arguments

ff	a flowCore::flowFrame
FSCChannel	a character containing the exact name of the forward scatter channel
SSCChannel	a character containing the exact name of the side scatter channel
gateData	a numerical vector containing the polygon gate coordinates first the FSCChannel channel coordinates of each points of the polygon gate, then the SSCChannel channel coordinates of each points.
...	additional parameters passed to flowCore::polygonGate()

### Value

a flowCore::flowFrame with removed debris events from the input

### Examples

```
rawDataDir <-
  system.file("extdata", package = "CytoPipeline")
sampleFiles <-
  file.path(rawDataDir, list.files(rawDataDir, pattern = "Donor"))

truncateMaxRange <- FALSE
minLimit <- NULL

# create flowCore::flowSet with all samples of a dataset
fsRaw <- readSampleFiles(
  sampleFiles = sampleFiles,
  whichSamples = "all",
  truncate_max_range = truncateMaxRange,
  min.limit = minLimit)

suppressWarnings(ff_m <- removeMarginsPeacoQC(x = fsRaw[[2]]))

ff_c <-
  compensateFromMatrix(ff_m,
```

```

matrixSource = "fcs")

remDebrisGateData <- c(73615, 110174, 213000, 201000, 126000,
                      47679, 260500, 260500, 113000, 35000)

ff_cells <-
  removeDebrisManualGate(ff_c,
                        FSCChannel = "FSC-A",
                        SSCChannel = "SSC-A",
                        gateData = remDebrisGateData)

```

---

```
removeDoubletsCytoPipeline
```

*remove doublets from a flowFrame, using CytoPipeline custom algorithm*

---

## Description

Wrapper around `CytoPipeline::singletGate()`. Can apply the `flowStats` function subsequently on several channel pairs, e.g. (FSC-A, FSC-H) and (SSC-A, SSC-H)

## Usage

```
removeDoubletsCytoPipeline(ff, areaChannels, heightChannels, nmads, ...)
```

## Arguments

<code>ff</code>	a <code>flowCore::flowFrame</code>
<code>areaChannels</code>	a character vector containing the name of the 'area type' channels one wants to use
<code>heightChannels</code>	a character vector containing the name of the 'height type' channels one wants to use
<code>nmads</code>	a numeric vector with the bandwidth above the ratio allowed, per channels pair (cells are kept if the ratio between -A channel[i] and -H channel[i] is smaller than the median ratio + <code>nmad[i]</code> times the median absolute deviation of the ratios). Default is 4, for all channel pairs.
<code>...</code>	additional parameters passed to <code>CytoPipeline::singletGate()</code>

## Value

a `flowCore::flowFrame` with removed doublets events from the input

**Examples**

```

rawDataDir <-
  system.file("extdata", package = "CytoPipeline")
sampleFiles <-
  file.path(rawDataDir, list.files(rawDataDir, pattern = "Donor"))

truncateMaxRange <- FALSE
minLimit <- NULL

# create flowCore::flowSet with all samples of a dataset
fsRaw <- readSampleFiles(
  sampleFiles = sampleFiles,
  whichSamples = "all",
  truncate_max_range = truncateMaxRange,
  min.limit = minLimit)

suppressWarnings(ff_m <- removeMarginsPeacoQC(x = fsRaw[[2]]))

ff_c <-
  compensateFromMatrix(ff_m,
                      matrixSource = "fcs")

ff_s <-
  removeDoubletsCytoPipeline(ff_c,
                             areaChannels = c("FSC-A", "SSC-A"),
                             heightChannels = c("FSC-H", "SSC-H"),
                             nmads = c(3, 5))

```

---

removeMarginsPeacoQC *remove margin events using PeacoQC*

---

**Description**

Wrapper around PeacoQC::RemoveMargins(). Also pre-selects the channels to be handled (=> all signal channels) If input is a flowSet, it applies removeMargins() to each flowFrame of the flowSet.

**Usage**

```
removeMarginsPeacoQC(x, channelSpecifications = NULL, ...)
```

**Arguments**

**x** a flowCore::flowSet or a flowCore::flowFrame  
**channelSpecifications**

A list of lists with parameter specifications for certain channels. This parameter should only be used if the values in the internal parameters description is too strict or wrong for a number or all channels. This should be one list per channel with first a minRange and then a maxRange value. This list should



have the channel name found back in `colnames(flowCore::exprs(ff))`, or the corresponding marker name (found in `flowCore::pData(flowCore::description(ff))`). If a channel is not listed in this parameter, its default internal values will be used. The default of this parameter is `NULL`. If the name of one list is set to `AllFluoChannels`, then the `minRange` and `maxRange` specified there will be taken as default for all fluorescent channels (not scatter)

... additional parameters passed to `PeacoQC::RemoveMargins()`

### Value

either a `flowCore::flowSet` or a `flowCore::flowFrame` depending on the input.

### Examples

```
rawDataDir <-
  system.file("extdata", package = "CytoPipeline")
sampleFiles <-
  file.path(rawDataDir, list.files(rawDataDir, pattern = "Donor"))

truncateMaxRange <- FALSE
minLimit <- NULL
fsRaw <- readSampleFiles(sampleFiles,
  truncate_max_range = truncateMaxRange,
  min.limit = minLimit)
suppressWarnings(ff_m <- removeMarginsPeacoQC(x = fsRaw[[2]]))
ggplotFilterEvents(ffPre = fsRaw[[2]],
  ffPost = ff_m,
  xChannel = "FSC-A",
  yChannel = "SSC-A")
```

---

resetCellIDs	<i>reset 'Original_ID' column in a flowframe</i>
--------------	--

---

### Description

: on a `flowCore::flowFrame`, reset 'Original\_ID' column. This column can be used in plots comparing the events pre and post gating. If the 'Original\_ID' column already exists, the function replaces the existing IDs by the user provided ones. If not, an `appendCellID()` is called.

### Usage

```
resetCellIDs(ff, eventIDs = seq_len(flowCore::nrow(ff)))
```

### Arguments

<code>ff</code>	a <code>flowCore::flowFrame</code>
<code>eventIDs</code>	an integer vector containing the values to be set in expression matrix, as Original ID's.

**Value**

new flowCore::flowFrame containing the amended (or added) 'Original\_ID' column

**Examples**

```
data(OMIP021Samples)

ff <- appendCellID(OMIP021Samples[[1]])

subsample_ff <- subsample(ff, 100, keepOriginalCellIDs = TRUE)

# re-create a sequence of IDs, ignoring the ones before subsampling
reset_ff <- resetCellIDs(subsample_ff)
```

---

runCompensation

*compensate with additional options*

---

**Description**

: this is a simple wrapper around the flowCore::compensate() utility, allowing to trigger an update of the fluo channel names with a prefix 'comp-' (as in FlowJo)

**Usage**

```
runCompensation(obj, spillover, updateChannelNames = TRUE)
```

**Arguments**

obj                    a flowCore::flowFrame or flowCore::flowSet  
 spillover            compensation object or spillover matrix or a list of compensation objects  
 updateChannelNames   if TRUE, add a 'comp-' prefix to all fluorochrome channels (hence does not impact the columns related to FSC, SSC, or other specific keyword like TIME, Original\_ID, File,...) Default TRUE.

**Value**

a new object with compensated data, and possibly updated column names

**Examples**

```
data(OMIP021Samples)

ff <- OMIP021Samples[[1]]
compMatrix <- flowCore::spillover(ff)$SPILL
ff <- runCompensation(ff,
                     spillover = compMatrix,
                     updateChannelNames = TRUE)
```

---

singletsGate

*Clean doublet events from flow cytometry data*


---

### Description

will adjust a polygon gate aimed at cleaning doublet events from the flowFrame. The main idea is to use the ratio between the two indicated channel as an indicator and select only the events for which this ratio is 'not too far' from the median ratio. More specifically, the computed ratio is  $ch1/(1+ch2)$ . However, instead of looking at a constant range of this ratio, as is done in `PeacoQC::removeDoublets()`, which leads to a semi-conic gate, we apply a parallelogram shaped gate, by keeping a constant range of channel 2 intensity, based on the target ratio range at the mid value of channel 1.

### Usage

```
singletsGate(
  ff,
  filterId = "Singlets",
  channel1 = "FSC-A",
  channel2 = "FSC-H",
  nmad = 4,
  verbose = FALSE
)
```

### Arguments

<code>ff</code>	A <code>flowCore::flowframe</code> that contains flow cytometry data.
<code>filterId</code>	the name for the filter that is returned
<code>channel1</code>	The first channel that will be used to determine the doublet events. Default is "FSC-A"
<code>channel2</code>	The second channels that will be used to determine the doublet events. Default is "FSC-H"
<code>nmad</code>	Bandwidth above the ratio allowed (cells are kept if their ratio is smaller than the median ratio + <code>nmad</code> times the median absolute deviation of the ratios). Default is 4.
<code>verbose</code>	If set to TRUE, the median ratio and width will be printed. Default is FALSE.

### Value

This function returns a `flowCore::polygonGate`.

### Examples

```
data(OMIP021Samples)

# simple example with one single singlets gate filter
```

```

# FSC-A and FSC-H channels are used by default

mySingletsGate <- singletsGate(OMIP021Samples[[1]], nmad = 3)

selectedSinglets <- flowCore::filter(
  OMIP021Samples[[1]],
  mySingletsGate)

ff_1 <- flowCore::Subset(OMIP021Samples[[1]], selectedSinglets)

linRange <- c(0, 250000)

ggplotFilterEvents(
  ffPre = OMIP021Samples[[1]],
  ffPost = ff_1,
  xChannel = "FSC-A", xLinearRange = linRange,
  yChannel = "FSC-H", yLinearRange = linRange)

# application of two singlets gates one after the other

singletsGate1 <- singletsGate(OMIP021Samples[[1]], nmad = 3)
singletsGate2 <- singletsGate(OMIP021Samples[[1]],
  channel1 = "SSC-A",
  channel2 = "SSC-H",
  filterId = "Singlets2")

singletCombinedGate <- singletsGate1 & singletsGate2

selectedSinglets <- flowCore::filter(
  OMIP021Samples[[1]],
  singletCombinedGate)

ff_1 <- flowCore::Subset(OMIP021Samples[[1]], selectedSinglets)

ggplotFilterEvents(
  ffPre = OMIP021Samples[[1]],
  ffPost = ff_1,
  xChannel = "FSC-A", xLinearRange = linRange,
  yChannel = "FSC-H", yLinearRange = linRange)

ggplotFilterEvents(
  ffPre = OMIP021Samples[[1]],
  ffPost = ff_1,
  xChannel = "SSC-A", xLinearRange = linRange,
  yChannel = "SSC-H", yLinearRange = linRange)

```

**Description**

: sub-samples a flowFrame with the specified number of samples, without replacement. adds also a column 'Original\_ID' if not already present in flowFrame.

**Usage**

```
subsample(ff, nEvents, seed = NULL, keepOriginalCellIDs = TRUE, ...)
```

**Arguments**

ff	a flowCore::flowFrame
nEvents	number of events to be obtained using sub-sampling
seed	can be set for reproducibility of event sub-sampling
keepOriginalCellIDs	if TRUE, adds (if not already present) a 'OriginalID' column containing the initial IDs of the cell (from 1 to nrow prior to subsampling). if FALSE, does the same, but takes as IDs (1 to nrow after subsampling)
...	additional parameters (currently not used)

**Value**

new flowCore::flowFrame with the obtained subset of samples

**Examples**

```
data(OMIP021Samples)

# take first sample of dataset, subsample 100 events and create new flowFrame
ff <- subsample(OMIP021Samples[[1]], nEvents = 100)
```

---

updateMarkerName	<i>update marker name of a given flowFrame channel</i>
------------------	--

---

**Description**

: in a flowCore::flowFrame, update the marker name (stored in 'desc' of parameters data) of a given channel. Also update the corresponding keyword in the flowFrame.

**Usage**

```
updateMarkerName(ff, channel, newMarkerName)
```

**Arguments**

ff                    a flowCore::flowFrame  
channel                the channel for which to update the marker name  
newMarkerName        the new marker name to be given to the selected channel

**Value**

a new flowCore::flowFrame with the updated marker name

**Examples**

```
data(OMIP021Samples)

retFF <- updateMarkerName(OMIP021Samples[[1]],
                          channel = "FSC-A",
                          newMarkerName = "Fwd Scatter-A")
```

---

writeFlowFrame            *write flowFrame to disk*

---

**Description**

wrapper around flowCore::write.FCS() or utils::write.csv that discards any additional parameter passed in (...)

**Usage**

```
writeFlowFrame(
  ff,
  dir = ".",
  useFCSFileName = TRUE,
  prefix = "",
  suffix = "",
  format = c("fcs", "csv"),
  csvUseChannelMarker = TRUE,
  ...
)
```

**Arguments**

ff                    a flowCore::flowFrame  
dir                    an existing directory to store the flowFrame,  
useFCSFileName        if TRUE filename used will be based on original fcs filename  
prefix                file name prefix  
suffix                file name suffix

format            either fcs or csv  
csvUseChannelMarker    if TRUE (default), converts the channels to the corresponding marker names (where the Marker is not NA). This setting is only applicable to export in csv format.  
...                other arguments (not used)

**Value**

nothing

**Examples**

```
rawDataDir <-  
  system.file("extdata", package = "CytoPipeline")  
sampleFiles <-  
  file.path(rawDataDir, list.files(rawDataDir, pattern = "Donor"))  
  
truncateMaxRange <- FALSE  
minLimit <- NULL  
  
# create flowCore::flowSet with all samples of a dataset  
res <- readSampleFiles(  
  sampleFiles = sampleFiles,  
  whichSamples = "all",  
  truncate_max_range = truncateMaxRange,  
  min.limit = minLimit)  
  
ff_c <- compensateFromMatrix(res[[2]], matrixSource = "fcs")  
outputDir <- base::tempdir()  
writeFlowFrame(ff_c,  
  dir = outputDir,  
  suffix = "_fcs_export",  
  format = "csv")
```

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