

# flowQ

April 19, 2009

---

aggregatorList-class

*Class "aggregatorList"*

---

## Description

A list of qaAggregators

## Details

This class directly extends class "list" and is intended to exclusively hold objects of class [qaAggregator](#), where each list item represents the outcome of a QA subprocess for a single [flowFrame](#). It mainly exists to allow for method dispatch and should never be populated manually; instead, use the constructor `qaAggregatorList` which checks for valid objects.

## Objects from the Class

Objects should be created using the constructor:

`aggregatorList(...)`, where `{...}` are objects inheriting from class [qaAggregator](#) or a list of such objects.

## Slots

**.Data:** Object of class "list", the list data

## Extends

Class "list", from data part. Class "[vector](#)", by class "list", distance 2.

## Methods

**initialize** signature(.Object = "aggregatorList"): constructor

**show** signature(object = "aggregatorList"): print object details

## Author(s)

Florian Hahne

**See Also**

[qaGraph](#), [writeQAReport](#), [qaProcess](#), [qaAggregator](#)

**Examples**

```
showClass("aggregatorList")
```

---

```
binaryAggregator-class  
  Class "binaryAggregator"
```

---

**Description**

Abstraction of a binary type of aggregator with possible states "passed" and "not passed"

**Objects from the Class**

Objects can be created by calls of the form `new("binaryAggregator", ...)`, or using the constructor `binaryAggregator(passed)`, where `passed` is a logical scalar.

**Slots**

**passed:** Object of class "logical" indicating whether the process has passed the QA requirements

**Extends**

Class "[qaAggregator](#)", directly.

**Methods**

**show** signature(object = "binaryAggregator"): print object details

**writeLines** signature(text = "binaryAggregator", con = "file", sep = "missing"): write to HTML file connection

**Author(s)**

Florian Hahne

**See Also**

[qaProcess.marginevents](#), [qaReport](#), [qaProcess](#), [qaProcess.timeline](#), [discreteAggregator](#), [factorAggregator](#), [numericAggregator](#), [stringAggregator](#), [rangeAggregator](#),

**Examples**

```
showClass("binaryAggregator")
```

---

```
discreteAggregator-class  
  Class "discreteAggregator"
```

---

### Description

Abstraction of a discrete type of aggregator with possible states "passed", "not passed" and "warning"

### Objects from the Class

Objects can be created by calls of the form `new("discreteAggregator", ...)` or using the constructor `discreteAggregator(x)`, where `x` is an integer value in `[0, 1, 2]` or a factor with levels 0, 1 and 2.

### Slots

**x:** Object of class "factor" One in 0 (not passes), 1 (passed) or 2 (warning)

**passed:** Object of class "logical" indicating whether the process has passed the QA requirements (not evaluated)

### Extends

Class "[qaAggregator](#)", directly.

### Methods

**show** signature(object = "discreteAggregator"): print object details

**writeLines** signature(text = "discreteAggregator", con = "file", sep = "missing"): write to HTML file connection

### Author(s)

Florian Hahne

### See Also

[qaProcess.marginevents](#), [qaReport](#), [qaProcess](#), [qaProcess.timeline](#), [binaryAggregator](#), [factorAggregator](#), [numericAggregator](#), [stringAggregator](#), [rangeAggregator](#),

### Examples

```
showClass("discreteAggregator")
```

---

evaluateProcess      *Evaluate QA processes*

---

### Description

Re-evaluate an object of class `qaProcess`, e.g. for the case that a threshold value has changed.

### Usage

```
evaluateProcess(process, thresh, ...)
```

### Arguments

<code>process</code>	An object of class <code>qaProcess</code> .
<code>thresh</code>	The new threshold on which the process is to be evaluated.
<code>...</code>	Further arguments that are passed on to the individual functions for each QA process type.

### Details

It is sometimes useful to update the state of aggregators in a `qaProcess`, for instances after changing the threshold value, without having to recompute all images, which can be very time consuming.

### Value

An updated object of class `qaProcess`

### Note

This function needs to be extended for new types of `qaProcess`.

### Author(s)

Florian Hahne

### See Also

`qaProcess`, `writeQAReport`

### Examples

```
## Not run:
data(GvHD)
dest <- tempdir()
qp1 <- qaProcess.timeline(GvHD[1:3], channel="FL1-H", outdir=dest,
cutoff=1)
evaluateProcess(qp1, thresh=4)
## End(Not run)
```

---

```
factorAggregator-class
      Class "factorAggregator"
```

---

### Description

Abstraction of a factor type of aggregator with possible states coded by the factor levels

### Objects from the Class

Objects can be created by calls of the form `new("factorAggregator", ...)` or using the constructor `factorAggregator(x, passed)`, where `x` is a factor, or an object which can be coerced to a factor, and `passed` is a logical scalar.

### Slots

**x:** Object of class "factor" coding the outcome state

**passed:** Object of class "logical" indicating whether the process has passed the QA requirements

### Extends

Class "[qaAggregator](#)", directly.

### Methods

**show** signature(object = "factorAggregator"): print object details

**writeLines** signature(text = "factorAggregator", con = "file", sep = "missing"): write to HTML file connection

### Author(s)

Florian Hahne

### See Also

[qaProcess.marginevents](#), [qaReport](#), [qaProcess](#), [qaProcess.timeline](#), [discreteAggregator](#), [binaryAggregator](#), [numericAggregator](#), [stringAggregator](#), [rangeAggregator](#),

### Examples

```
showClass("factorAggregator")
```

---

flowQ-package

*Quality control for flow cytometry*

---

### **Description**

Functions and methods for quality control and QA of flow cytometry data. This package heavily depends on the flowCore package.

### **Details**

Package: flowQ  
Type: Package  
Version: 0.2.1  
Date: 2006-11-16  
License: Artistic

Quality control is an important aspect when dealing with large amounts of complex high-throughput data. This package comprises functionality for efficient QA of flow cytometry data.

### Author(s)

Maintainer: Florian Hahne <f.hahne@dkfz.de> Authors: R. Gentleman, F. Hahne, J. Kettman, N. Le Meur, M. Tang

### References

references go here

### See Also

[flowCore](#)

### Examples

```
## examples go here
```

---

```
numericAggregator-class  
  Class "numericAggregator"
```

---

### Description

Abstraction of a numeric type of aggregator for which possible states are coded by a numeric value

### Objects from the Class

Objects can be created by calls of the form `new("numericAggregator", ...)` or using the constructor `numericAggregator(x, passed)`, where `x` is a numeric scalar, and `passed` is a logical scalar.

### Slots

**x:** Object of class "numeric" coding the outcome state

**passed:** Object of class "logical" indicating whether the process has passed the QA requirements

### Extends

Class "[qaAggregator](#)", directly.

**Methods**

**show** signature(object = "numericAggregator"): print object details

**writeLines** signature(text = "numericAggregator", con = "file", sep = "missing"): write to HTML file connection

**Author(s)**

Florian Hahne

**See Also**

[qaProcess.marginevents](#), [qaReport](#), [qaProcess](#), [qaProcess.timeline](#), [discreteAggregator](#), [factorAggregator](#), [binaryAggregator](#), [stringAggregator](#), [rangeAggregator](#),

**Examples**

```
showClass("numericAggregator")
```

---

outlier-class      *Virtual Class "outlier"*

---

**Description**

A class to represent outlier tests

**Objects from the Class**

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

**Slots**

**test:** Object of class "character" ~~

**parameters:** Object of class "ANY" ~~

**Methods**

No methods defined with class "outlier" in the signature.

**Note**

~~further notes~~

**Author(s)**

~~who you are~~

**References**

~put references to the literature/web site here ~

**Examples**

```
## showClass("outlier")
```



---

```
outlierResult-class
      Class "outlierResult"
```

---

### Description

A class to hold the results of an outlier test

### Objects from the Class

Objects can be created by calls of the form `new("outlierResult", ...)`. `~~ describe objects here ~~`

### Slots

**frameId:** Object of class "character" `~~`

**filterDetails:** Object of class "list" `~~`

**test:** Object of class "character" `~~`

**parameters:** Object of class "ANY" `~~`

### Extends

Class "[outlier](#)", directly.

### Methods

No methods defined with class "outlierResult" in the signature.

### Note

`~~further notes~~`

### Author(s)

`~~who you are~~`

### References

`~put references to the literature/web site here ~`

### Examples

```
#showClass("outlierResult")
```

---

outliers-methods *~~ Methods for Function outliers in Package '.GlobalEnv' ~~*

---

### Description

~~ Methods for function outliers in Package '.GlobalEnv' ~~

### Methods

**x = "flowSet"** *~~describe this method here*

---

qaAggregator-class *Abstraction of the possible outcomes of a QA process*

---

### Description

Virtual parent class for different types of QA aggregators

### Details

In the context of this package, `qaAggregators` are objects that hold the outcome of a QA process. Each subclass implements its own `writeLine` method, which creates the appropriate HTML code for a graphical representation of the object.

### Objects from the Class

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

### Slots

**passed:** Object of class "logical" indicating whether the process has passed the QA requirements

### Methods

No methods defined with class "qaAggregator" in the signature.

### Author(s)

Florian Hahne

### See Also

[qaProcess.marginevents](#), [qaReport](#), [qaProcess](#), [qaProcess.timeline](#), [binaryAggregator](#), [discreteAggregator](#), [factorAggregator](#), [numericAggregator](#), [stringAggregator](#), [rangeAggregator](#),

### Examples

```
showClass("qaAggregator")
```

---

qaGraph-class      *Class "qaGraph"*

---

### Description

Abstraction of the graphical output created in the cause of a QA process

### Objects from the Class

Objects should be created using the constructor:

`qaGraph(fileName, imageDir, width)`, where `fileName` is a path to an image file, `imageDir` is the destination path for the images and the optional argument `width` is the final width to which the bitmap images are converted. For the special case of an empty object one can use option `empty=TRUE`, in which case the constructor ignores all other arguments.

During object instantiation the image file will be converted, resized and copied if necessary.

### Slots

**fileNames:** Object of class "character" The paths to the image files, both the vectorized and unvectorized versions

**dimensions:** Object of class "matrix" The dimensions of the image files, both for the vectorized and unvectorized version

**types:** Object of class "character" The file extensions for both versions

**id:** Object of class "character" A unique identifier for the images

### Methods

**initialize** signature(.Object = "qaGraph"): constructor

**names** signature(x = "qaGraph"): returns the file name of the bitmap version of the image

**show** signature(object = "qaGraph"): print object details

### Author(s)

Florian Hahne

### See Also

[qaGraphList](#), [writeQAReport](#), [qaProcess](#)

### Examples

```
showClass("qaGraph")
```

---

qaGraphList-class *Class "qaGraphList"*

---

### Description

A list of [qaGraph](#) objects

### Details

This class directly extends class "list" and is intended to exclusively hold objects of class [qaGraph](#), where each list item represents the graphical output of a QA subprocess for a single [flowFrame](#). It mainly exists to allow for method dispatch and should never be populated manually; instead, use the constructor `qaGraphList` which makes sure, that all image files are converted into the appropriate types and sizes and copied to the expected file location.

### Objects from the Class

Objects should be created using the constructor:

`qaGraphList(imageFiles, imageDir, width)`, where `imageFiles` are paths to image files, `imageDir` is the destination path for the images and `width` is the final width to which the bitmap images are converted.

### Slots

**.Data:** Object of class "list", the list data

### Extends

Class "list", from data part. Class "[vector](#)", by class "list", distance 2.

### Methods

**initialize** signature(.Object = "qaGraphList"): constructor

**show** signature(object = "qaGraphList"): print object details

### Author(s)

Florian Hahne

### See Also

[qaGraph](#), [writeQAResult](#), [qaProcess](#)

### Examples

```
showClass("qaGraphList")
```

---

qaProcess-class      *Abstraction of the results of a QA process*

---

## Description

QA processes create graphical output which can be bundled in a single HTML document. This class stores all information that is needed by `writeQAReport` to produce such HTML reports.

## Objects from the Class

Objects should be created using the constructor functions. See `qaProcess.timeline` and `qaProcess.marginevents` for details. When writing new QA process functions, the constructors `qaProcessFrame` and `qaProcess` should be used. The latter expects the mandatory arguments `id`, `type` and `frameProcesses` and also accepts the optional arguments `name` and `summaryGraph`. See the vignette of this package for details.

## Slots

**id:** Object of class "character", the objects unique identifier

**name:** Object of class "character", the name of the process

**type:** Object of class "character", the type of process

**frameIDs:** Object of class "character", the identifiers of the `flowSets` to which the sub-processes are linked

**summaryGraph:** Object of class "qaGraph", a graphical summary of the process's outcome

**frameProcesses:** Object of class "list", more detailed information for each `flowFrame`

## Methods

**initialize** signature(.Object = "qaProcess"): constructor

## Author(s)

Florian Hahne

## See Also

`qaGraphList`, `writeQAReport`, `qaProcessFrame`

## Examples

```
showClass("qaProcess")
```

---

```
qaProcess.cellnumber
```

*Create QA process of type 'cellnumber'*

---

## Description

This function takes a [flowSet](#) as input and creates all necessary output for a 'cellnumber' type QA process. Objects created by this function can be laid out as HTML using [writeQAReport](#).

## Usage

```
qaProcess.cellnumber(set, grouping=NULL, outdir, cFactor=0.5,
  name="cell number", sum.dimensions=c(7,7), ...)
```

## Arguments

<code>set</code>	A <a href="#">flowSet</a>
<code>grouping</code>	A character vector defining one of the variables in the <code>phenoData</code> of <code>set</code> used as a grouping variable. If this argument is used, comparisons will be made within groups rather than across all samples.
<code>outdir</code>	The directory to which the graphical output is to be saved. If multiple QA processes are to be combined, make sure to use the same directory every time.
<code>cFactor</code>	The threshold at which the QA process is considered to be failed. The factor of standard deviations away from the average number of cells per sample
<code>name</code>	The name of the process used for the headings in the HTML output
<code>sum.dimensions</code>	The pdf dimensions used for the summary.
<code>...</code>	Further arguments.

## Details

QA processes of type 'cellnumber' detect aberrations in the number of cells analyzed per frame.

For more details on how to layout [qaProcess](#) objects to HTML, see [writeQAReport](#) and [qaReport](#).

## Value

An object of class [qaProcess](#).

## Author(s)

Florian Hahne

## See Also

[writeQAReport](#), [qaReport](#), [qaProcess](#), [qaProcess.marginevents](#), [qaProcess.timeflow](#), [qaProcess.timeline](#)

**Examples**

```
## Not run:
data(GvHD)
dest <- tempdir()
qp <- qaProcess.cellnumber(GvHD, outdir=dest, cFactor=1)
qp
## End (Not run)
```

---

```
qaProcess.marginevents
      Create QA process of type 'marginevents'
```

---

**Description**

This function takes a [flowSet](#) as input and creates all necessary output for a 'marginevents' type QA process. Objects created by this function can be laid out as HTML using [writeQAReport](#).

**Usage**

```
qaProcess.marginevents(set, channels = NULL, grouping=NULL, outdir,
  cFactor = 1, ...)
```

**Arguments**

set	A <a href="#">flowSet</a>
channels	A character vector of channel names for which margin events are to be recorded
grouping	A character vector defining one of the variables in the phenoData of set used as a grouping variable. If this argument is uses, comparisons will be made within groups rather than across all samples.
outdir	The directory to which the graphical output is to be saved. If multiple QA processes are to be combined, make sure to use the same directory every time.
cFactor	The threshold at which the QA process is considered to have failed. This is the fold change of margin event percentages compared to the median percentage of events for the respective channel.
...	Further arguments.

**Details**

QA processes of type 'marginevents' record the number of events that fall on the margins of the measurement range for each channel. Unproportionally high numbers of such events can indicate problems with the instrument settings.

For more details on how to layout [qaProcess](#) objects to HTML, see [writeQAReport](#) and [qaReport](#).

**Value**

An object of class [qaProcess](#).

**Note**

This function is still experimental

**Author(s)**

Florian Hahne

**See Also**

[writeQAReport](#), [qaReport](#), [qaProcess](#), [qaProcess.timeline](#), [qaProcess.timeflow](#), [qaProcess.cellnumber](#)

**Examples**

```
## Not run:
data(GvHD)
dest <- tempdir()
qp <- qaProcess.marginevents(GvHD, channels=c("FL1-H", "FL2-H"),
  outdir=dest)
qp
## End(Not run)
```

---

qaProcess.timeflow *Create QA process of type 'timeflow'*

---

**Description**

This function takes a [flowSet](#) as input and creates all necessary output for a 'timeflow' type QA process. Objects created by this function can be laid out as HTML using [writeQAReport](#).

**Usage**

```
qaProcess.timeflow(set, outdir, cutoff=2, name="time flow",
  sum.dimensions=c(7,7), det.dimensions=c(7,7), ...)
```

**Arguments**

set	A <a href="#">flowSet</a>
outdir	The directory to which the graphical output is to be saved. If multiple QA processes are to be combined, make sure to use the same directory every time.
cutoff	The threshold at which the QA process is considered to be failed. An absolute value in the timeline deviation score as computed by the <a href="#">timeLinePlot</a> function
name	The name of the process used for the headings in the HTML output
sum.dimensions, det.dimensions	The pdf dimensions used for the summary and the detailed plots.
...	Further arguments.



## Details

QA processes of type 'timeflow' detect disturbances in the flow of cells over time.

For more details on how to layout `qaProcess` objects to HTML, see [writeQAReport](#) and [qaReport](#).

## Value

An object of class `qaProcess`.

## Author(s)

Florian Hahne

## See Also

[writeQAReport](#), [qaReport](#), [qaProcess](#), [qaProcess.marginevents](#), [qaProcess.timeline](#), [qaProcess.cellnumber](#)

## Examples

```
## Not run:
data(GvHD)
dest <- tempdir()
qp <- qaProcess.timeflow(GvHD, outdir=dest, cutoff=1)
qp
## End (Not run)
```

---

`qaProcess.timeline` *Create QA process of type 'timeline'*

---

## Description

This function takes a `flowSet` as input and creates all necessary output for a 'timeline' type QA process. Objects created by this function can be laid out as HTML using [writeQAReport](#).

## Usage

```
qaProcess.timeline(set, channels=NULL, outdir, cutoff=1,
  name="time line", sum.dimensions=NULL, det.dimensions=c(7,7),
  ...)
```

**Arguments**

set	A <a href="#">flowSet</a>
channels	A character vector of channel names for which the qaReport is to be produced
outdir	The directory to which the graphical output is to be saved. If multiple QA processes are to be combined, make sure to use the same directory every time.
cutoff	The threshold at which the QA process is considered to be failed. An absolute value in the timeline deviation score as computed by the <a href="#">timeLinePlot</a> function
name	The name of the process used for the headings in the HTML output
sum.dimensions, det.dimensions	The pdf dimensions used for the summary and the detailed plots.
...	Further arguments.

**Details**

QA processes of type 'timeline' detect unusual patterns in the acquisition of fluorescence and light scatter measurements over time.

For more details on how to layout [qaProcess](#) objects to HTML, see [writeQAReport](#) and [qaReport](#).

**Value**

An object of class [qaProcess](#).

**Author(s)**

Florian Hahne

**See Also**

[writeQAReport](#), [qaReport](#), [qaProcess](#), [qaProcess.marginevents](#), [qaProcess.timeflow](#), [qaProcess.cellnumber](#)

**Examples**

```
## Not run:
data(GvHD)
GvHD <- transform(GvHD, "FL1-H"=asinh(`FL1-H`), "FL2-H"=asinh(`FL2-H`))
dest <- tempdir()
qp <- qaProcess.timeline(GvHD, channel="FL1-H", outdir=dest, cutoff=1)
qp
## End(Not run)
```

---

`qaProcessFrame-class`*Class "qaProcessFrame"*

---

## Description

Abstraction of subitems within a qQA process

## Details

This class bundles graphs and aggregators for a single `flowFrame`. This allows to create processes with subcomponents, where each item in the `frameAggregators` and `frameGraphs` lists corresponds to one subprocess, which can be used, for instance, to create individual plots for each flow channel. For QA processes without subcomponents, these slots would simply not be populated.

## Objects from the Class

Objects should be created using the constructor:

`qaProcessFrame(frameID, summaryAggregator, summaryGraph, frameAggregators, frameGraphs, details)` where `frameID` is the ID of the `flowFrame` the process is linked to, `summaryAggregator` is an object inheriting from class `qaAggregator` which summarizes the outcome, `summaryGraph` is an object of class `qaGraph` which is the overview graph of the process for the whole frame, `details` is a list containing any additional information regarding the QA process, `frameAggregators` is an object of class `aggregatorList` and `frameGraphs` is an object of class `qaGraphList`. The latter two are the collections of aggregators and graphs for each subprocess. Only `frameID` and `summaryAggregator` are mandatory arguments.

## Slots

**id:** Object of class "character", a unique ID of the object

**frameID:** Object of class "character", ID of the `flowFrame` the process is linked to

**summaryAggregator:** Object of class "qaAggregator", an aggregator summarizing the output of the process

**summaryGraph:** Object of class "qaGraph", a graphical summary of the process

**frameAggregators:** Object of class "aggregatorList" a list of aggregators for the subprocesses

**frameGraphs:** Object of class "qaGraphList" a list of graphical summaries for the subprocesses

**details:** A list for any additional information

## Methods

**initialize** signature(.Object = "qaProcessFrame"): constructor

## Author(s)

Florian Hahne

**See Also**

`qaGraphList`, `writeQAReport`, `qaProcess`

**Examples**

```
showClass("qaProcessFrame")
```

---

`qaProcessSummary`    *Class "qaProcessSummary"*

---

**Description**

An internal class to represent QA summaries

**Objects from the Class**

The class is internal and not ment for interactive use.

**Slots**

**panels:** Object of class "list"

**ranges:** Object of class "matrix"

**summary:** Object of class "list"

**mapping:** Object of class "list"

**Methods**

**writeLines** signature(text = "qaGraphList", con = "file"): HTML output

**show** signature(object = "qaGraphList"): print object details

**Author(s)**

Florian Hahne

---

`qaReport`    *Create HTML report using one or several QA process function(s)*

---

**Description**

This function combines all graphical output of multiple QA process functions for one `flowSet` in a single hyperlinked HTML document.

**Usage**

```
qaReport(set, qaFunctions, outdir = "./qaReport", argLists, grouping =
NULL, ...)
```

**Arguments**

set	A <a href="#">flowSet</a>
qaFunctions	A character vector of the names of QA process functions to be used
outdir	The directory to which the HTML report is to be saved.
argLists	lists of argument lists for each of the QA process functions specified via <code>qaFunctions</code>
grouping	A character scalar indicating a variable in the <code>flowSet</code> 's <code>phenoData</code> that is used as a grouping factor in the output.
...	Further arguments that are passed on to <code>writeQAReport</code> .

**Details**

This is a simple convenience function to produce HTML QA reports for a single `flowSet` given a list of QA process functions. For more fine-grained control use function `writeQAReport` directly.

An entry point to the output of this function can be found at `outdir/index.html`.

**Value**

The function is called for its side effects

**Author(s)**

Florian Hahne

**See Also**

[qaProcess.marginevents](#), [writeQAReport](#), [qaProcess](#), [qaProcess.timeline](#)

**Examples**

```
## Not run:
data(GvHD)
GvHD <- transform(GvHD, "FL1-H"=asinh(`FL1-H`), "FL2-H"=asinh(`FL2-H`))
dest <- tempdir()
qaReport(GvHD, c("qaProcess.timeline", "qaProcess.marginevents"), dest,
  list(list(channel="FL1-H", cutoff=1), list(channels=c("FL1-H",
    "FL2-H"), cFactor=4)))
browseURL(file.path(dest, "index.html"))
## End(Not run)
```

---

rangeAggregator-class

*Class "rangeAggregator"*

---

**Description**

Abstraction of a range type of aggregator where possible states are within certain ranges (e.g. percentages)

### Objects from the Class

Objects can be created by calls of the form `new("rangeAggregator", ...)` or using the constructor `rangeAggregator(x, min, max, passed)`, where `x`, `min` and `max` are numeric scalars, with `x` in the range of `[min, max]`, and `passed` is a logical scalar.

### Slots

**min:** Object of class "numeric", the range minimum

**max:** Object of class "numeric", the range maximum

**x:** Object of class "numeric", the value within the range

**passed:** Object of class "logical" indicating whether the process has passed the QA requirements

### Extends

Class "[numericAggregator](#)", directly. Class "[qaAggregator](#)", by class "numericAggregator", distance 2.

### Methods

**show** signature(object = "rangeAggregator"): print object details

**writeLines** signature(text = "rangeAggregator", con = "file", sep = "missing"): write to HTML file connection

### Author(s)

Florian Hahne

### See Also

[qaProcess.marginevents](#), [qaReport](#), [qaProcess](#), [qaProcess.timeline](#), [discreteAggregator](#), [factorAggregator](#), [numericAggregator](#), [stringAggregator](#), [binaryAggregator](#),

### Examples

```
showClass("rangeAggregator")
```

---

```
stringAggregator-class
```

```
Class "stringAggregator"
```

---

### Description

Abstraction of a string type of aggregator for which possible states are indicated through a textual description

### Objects from the Class

Objects can be created by calls of the form `new("stringAggregator", ...)` or using the constructor `stringAggregator(x, passed)`, where `x` is a character scalar, and `passed` is a logical scalar.

**Slots**

**x:** Object of class "character" which is a textual description of the outcome

**passed:** Object of class "logical" indicating whether the process has passed the QA requirements

**Extends**

Class "[qaAggregator](#)", directly.

**Methods**

**show** signature(object = "stringAggregator"): print object details

**writeLines** signature(text = "stringAggregator", con = "file", sep = "missing"): write to HTML file connection

**Author(s)**

Florian Hahne

**See Also**

[qaProcess.marginevents](#), [qaReport](#), [qaProcess](#), [qaProcess.timeline](#), [discreteAggregator](#), [factorAggregator](#), [numericAggregator](#), [binaryAggregator](#), [rangeAggregator](#),

**Examples**

```
showClass("stringAggregator")
```

---

validProcess

*Validate a QAProcess object*

---

**Description**

Check for integrity and existence of files specified in a [qaProcess](#) object.

**Usage**

```
validProcess(object)
```

**Arguments**

object      A [qaProcess](#) object

**Value**

The function is called for its side effects

**Author(s)**

Florian Hahne

**See Also**

[qaProcess.marginevents](#), [qaReport](#), [qaProcess](#), [qaProcess.timeline](#), [writeQAReport](#)

---

writeQAReport      *Create HTML report for (lists of) qaProcess objects*

---

**Description**

This function combines all graphical output of multiple QA processes for one or several [flowSets](#) in a single hyperlinked HTML document.

**Usage**

```
writeQAReport(set, processes, outdir = "./qaReport", grouping = NULL,
pagebreaks = TRUE)
```

**Arguments**

set	A <a href="#">flowSet</a> or a list of several <a href="#">flowSets</a>
processes	A list of A <a href="#">qaProcess</a> objects or, in the case of multiple <a href="#">flowSets</a> , a list of lists of <a href="#">qaProcess</a> objects.
outdir	The directory to which the HTML report is to be saved. Make sure that each <a href="#">qaProcess</a> object was created in the same directory.
grouping	A character scalar indicating a variable in the <a href="#">flowSet</a> 's <code>phenoData</code> that is used as a grouping factor in the output.
pagebreaks	A logical indicating whether the output should be on one long page, or split on several pages.

**Details**

Both the information about graphical output and the results for a QA process are stored in objects of class [qaProcess](#). The creation of such objects is abstracted in dedicated functions and the user should call these functions directly rather than creating [qaProcess](#) manually. [writeQAReport](#) takes lists of such objects and combines their information in a unified HTML document. A grouping factor can be specified to indicate subgroups of the data. In the case of multiple panels, a list of [flowSets](#) can be given to [writeQAReport](#), and the function expects a list of lists of processes, where each process list is specific to one panel.

An entry point to the output of this function can be found at `outdir/index.html`.

**Value**

The function is called for its side effects

**Author(s)**

Florian Hahne



**See Also**

[qaProcess.marginevents](#), [qaReport](#), [qaProcess](#), [qaProcess.timeline](#)

**Examples**

```
## Not run:
data(GvHD)
GvHD <- transform(GvHD, "FL1-H"=asinh(`FL1-H`), "FL2-H"=asinh(`FL2-H`))
dest <- tempdir()
qp1 <- qaProcess.timeline(GvHD, channel="FL1-H", outdir=dest, cutoff=1)
qp2 <- qaProcess.marginevents(GvHD, channels=c("FL1-H", "FL2-H"),
  outdir=dest, cFactor=4)
writeQAReport(GvHD, processes=list(qp1, qp2), outdir=dest,
  grouping="Patient")
browseURL(file.path(dest, "index.html"))
## End(Not run)
```

# Index

## \*Topic **IO**

qaReport, 20  
writeQAReport, 24

## \*Topic **classes**

aggregatorList-class, 1  
binaryAggregator-class, 2  
discreteAggregator-class, 3  
factorAggregator-class, 5  
numericAggregator-class, 7  
outlier-class, 8  
outlierResult-class, 9  
qaAggregator-class, 10  
qaGraph-class, 11  
qaGraphList-class, 12  
qaProcess-class, 13  
qaProcessFrame-class, 19  
qaProcessSummary, 20  
rangeAggregator-class, 21  
stringAggregator-class, 22

## \*Topic **dynamic**

evaluateProcess, 4  
qaProcess.cellnumber, 14  
qaProcess.marginevents, 15  
qaProcess.timeflow, 16  
qaProcess.timeline, 17  
qaReport, 20  
writeQAReport, 24

## \*Topic **methods**

outliers-methods, 10

## \*Topic **misc**

validProcess, 23

## \*Topic **package**

flowQ-package, 6

aggregatorList, 19  
aggregatorList  
(*aggregatorList-class*), 1  
aggregatorList-class, 1

binaryAggregator, 3, 5, 8, 10, 22, 23  
binaryAggregator  
(*binaryAggregator-class*), 2  
binaryAggregator-class, 2

discreteAggregator, 2, 5, 8, 10, 22, 23  
discreteAggregator  
(*discreteAggregator-class*),  
3

discreteAggregator-class, 3

evaluateProcess, 4

factorAggregator, 2, 3, 8, 10, 22, 23  
factorAggregator  
(*factorAggregator-class*), 5  
factorAggregator-class, 5  
flowCore, 7  
flowFrame, 1, 12, 13, 19  
flowQ (*flowQ-package*), 6  
flowQ-package, 6  
flowSet, 13–18, 20, 21, 24

initialize, aggregatorList-method  
(*aggregatorList-class*), 1

initialize, qaGraph-method  
(*qaGraph-class*), 11

initialize, qaGraphList-method  
(*qaGraphList-class*), 12

initialize, qaProcess-method  
(*qaProcess-class*), 13

initialize, qaProcessFrame-method  
(*qaProcessFrame-class*), 19

list, 1, 12

names, qaGraph-method  
(*qaGraph-class*), 11

numericAggregator, 2, 3, 5, 10, 22, 23

numericAggregator  
(*numericAggregator-class*),  
7

numericAggregator-class, 7

outlier, 9

outlier-class, 8

outlierResult-class, 9

outliers (*outliers-methods*), 10

outliers, flowSet-method  
(*outliers-methods*), 10

- outliers-methods, [10](#)
- qaAggregator, [1–3](#), [5](#), [7](#), [19](#), [22](#), [23](#)
- qaAggregator
  - (*qaAggregator-class*), [10](#)
- qaAggregator-class, [10](#)
- qaGraph, [2](#), [12](#), [19](#)
- qaGraph (*qaGraph-class*), [11](#)
- qaGraph-class, [11](#)
- qaGraphList, [11](#), [13](#), [19](#), [20](#)
- qaGraphList (*qaGraphList-class*), [12](#)
- qaGraphList-class, [12](#)
- qaProcess, [2–5](#), [8](#), [10–12](#), [14–18](#), [20–25](#)
- qaProcess (*qaProcess-class*), [13](#)
- qaProcess-class, [13](#)
- qaProcess.cellnumber, [14](#), [16–18](#)
- qaProcess.marginevents, [2](#), [3](#), [5](#), [8](#), [10](#), [13](#), [14](#), [15](#), [17](#), [18](#), [21–25](#)
- qaProcess.timeflow, [14](#), [16](#), [16](#), [18](#)
- qaProcess.timeline, [2](#), [3](#), [5](#), [8](#), [10](#), [13](#), [14](#), [16](#), [17](#), [17](#), [21–25](#)
- qaProcessFrame, [13](#)
- qaProcessFrame
  - (*qaProcessFrame-class*), [19](#)
- qaProcessFrame-class, [19](#)
- qaProcessSummary, [20](#)
- qaProcessSummary-class
  - (*qaProcessSummary*), [20](#)
- qaReport, [2](#), [3](#), [5](#), [8](#), [10](#), [14–18](#), [20](#), [22–25](#)
- rangeAggregator, [2](#), [3](#), [5](#), [8](#), [10](#), [23](#)
- rangeAggregator
  - (*rangeAggregator-class*), [21](#)
- rangeAggregator-class, [21](#)
- show, aggregatorList-method
  - (*aggregatorList-class*), [1](#)
- show, binaryAggregator-method
  - (*binaryAggregator-class*), [2](#)
- show, discreteAggregator-method
  - (*discreteAggregator-class*), [3](#)
- show, factorAggregator-method
  - (*factorAggregator-class*), [5](#)
- show, numericAggregator-method
  - (*numericAggregator-class*), [7](#)
- show, qaGraph-method
  - (*qaGraph-class*), [11](#)
- show, qaGraphList-method
  - (*qaGraphList-class*), [12](#)
- show, qaProcess-method
  - (*qaProcess-class*), [13](#)
- show, qaProcessFrame-method
  - (*qaProcessFrame-class*), [19](#)
- show, qaProcessSummary-method
  - (*qaProcessSummary*), [20](#)
- show, rangeAggregator-method
  - (*rangeAggregator-class*), [21](#)
- show, stringAggregator-method
  - (*stringAggregator-class*), [22](#)
- stringAggregator, [2](#), [3](#), [5](#), [8](#), [10](#), [22](#)
- stringAggregator
  - (*stringAggregator-class*), [22](#)
- stringAggregator-class, [22](#)
- timeLinePlot, [16](#), [18](#)
- validProcess, [23](#)
- vector, [1](#), [12](#)
- writeLines, binaryAggregator, file, missing-method
  - (*binaryAggregator-class*), [2](#)
- writeLines, data.frame, file, missing-method
  - (*writeQAReport*), [24](#)
- writeLines, discreteAggregator, file, missing-method
  - (*discreteAggregator-class*), [3](#)
- writeLines, factorAggregator, file, missing-method
  - (*factorAggregator-class*), [5](#)
- writeLines, numericAggregator, file, missing-method
  - (*numericAggregator-class*), [7](#)
- writeLines, qaProcessSummary, file, missing-method
  - (*qaProcessSummary*), [20](#)
- writeLines, rangeAggregator, file, missing-method
  - (*rangeAggregator-class*), [21](#)
- writeLines, stringAggregator, file, missing-method
  - (*stringAggregator-class*), [22](#)
- writeQAReport, [2](#), [4](#), [11–18](#), [20](#), [21](#), [24](#), [24](#)