

# Package ‘flowTime’

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**Title** Annotation and analysis of biological dynamical systems using flow cytometry

**Version** 1.34.0

**Description** This package facilitates analysis of both timecourse and steady state flow cytometry experiments. This package was originally developed for quantifying the function of gene regulatory networks in yeast (strain W303) expressing fluorescent reporter proteins using BD Accuri C6 and SORP cytometers. However, the functions are for the most part general and may be adapted for analysis of other organisms using other flow cytometers. Functions in this package facilitate the annotation of flow cytometry data with experimental metadata, as often required for publication and general ease-of-reuse. Functions for creating, saving and loading gate sets are also included. In the past, we have typically generated summary statistics for each flowset for each timepoint and then annotated and analyzed these summary statistics. This method loses a great deal of the power that comes from the large amounts of individual cell data generated in flow cytometry, by essentially collapsing this data into a bulk measurement after subsetting. In addition to these summary functions, this package also contains functions to facilitate annotation and analysis of steady-state or time-lapse data utilizing all of the data collected from the thousands of individual cells in each sample.

**Depends** R (>= 3.4), flowCore

**License** Artistic-2.0

**LazyData** true

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addbs	<i>Add background subtraction to a summary data frame</i>
-------	---

---

### Description

Makes a new column from column with the background value of a given baseline control from a chosen identifier column baseline\_column subtracted from the values of column.

### Usage

```
addbs(data, column, baseline_column, baseline = "noYFP")
```

**Arguments**

data	the summary data frame of a flowSet (from <code>summarizeFlow</code> or <code>flsummary</code> ) to be used in calculating the background subtracted column
column	the column containing the fluorescent (or other) measurement to be background subtracted
baseline_column	the column containing the identifier of the rows containing background values
baseline	character the identified or name of representing background fluorescent values

**Value**

A summary data frame with an additional column `column_bs` containing the background subtracted values

**Examples**

```
dat<-read.flowSet(path=system.file("extdata", "tc_example",
package = "flowTime"),alter.names = TRUE)
annotation <- read.csv(system.file("extdata", "tc_example.csv",
package = "flowTime"))
annotation[which(annotation$treatment == 0), 'strain'] <- 'background'
adat <- annotateFlowSet(dat, annotation)
dat_sum <- summarizeFlow(adat, gated = TRUE,
channel = 'FL1.A')
dat_sum <- addbs(data = dat_sum, column = FL1.Amean,
baseline_column = strain,
baseline = "background")
```

---

addnorm

*Normalize fluorescence*


---

**Description**

Produces a normalized fluorescence column 'normed'. Expects the 'FL1.A\_bs' column to exist or a column to be specified. Has three different methods, version 1 and version 2, described in the script

**Usage**

```
addnorm(
  frame,
  factor_in = c("strain", "treatment"),
  method = 1,
  column = "FL3.Amean_bs"
)
```

**Arguments**

frame	data frame of summary statistics to be normalized
factor_in	character vector containing the variables to split the data frame by
method	which normalization method to use, 1, 2 or 3.
column	character the column to apply the normalization to

## Details

Method 1, the default normalization method, takes the highest point in each dataset grouped by 'factor\_in' and normalizes all values in the group by this point. This method is default because it works regardless of whether the data is a time series. Method 2 finds the mean value of all time points with time values less than 0 for each group and normalizes each group by this respective value. Requires a time series with negative time values to work. Method 3 fits a linear model to the pre-zero time points for each groups, infers the y-intercept, and normalizes using this intercept. Method 3 also requires a time series with negative time values to work.

## Value

data frame containing the additional normalized variable

## Examples

```
dat <- read.flowSet(path=system.file("extdata", "tc_example",
package = "flowTime"), alter.names = TRUE)
annotation <- read.csv(system.file("extdata", "tc_example.csv",
package = "flowTime"))
adat <- annotateFlowSet(dat, annotation)
loadGates(gatesFile = 'C6Gates')
dat_sum <- summarizeFlow(adat, ploidy = "diploid", only = "singlets",
channel = "FL1.A")
dat_sum <- addnorm(dat_sum, c("strain", "treatment"), method = 1,
column = "FL1.Amean")
```

---

annotateFlowSet

*Annotate a flowSet with experimental metadata*

---

## Description

Add annotations to a flowSets phenoData and plate numbers, strain names, and treatment also set T0

## Usage

```
annotateFlowSet(yourFlowSet, annotation_df, mergeBy = "name")
```

## Arguments

yourFlowSet	a flowSet with sampleNames of the format 'plate#_Well', we typically use the following code chunk to read data from individual plates as exported from BD Accuri C6 software.
annotation_df	A data frame with columns 'well', 'strain', 'treatment', containing all of the wells in the flowset labeled with the strain and treatment in that well.
mergeBy	the unique identifier column

## Value

An annotated flowSet

**Examples**

```
dat <- read.flowSet(path = system.file("extdata", "ss_example",
package = "flowTime"), alter.names = TRUE)
annotation <- read.csv(system.file("extdata", "ss_example.csv", package =
"flowTime"))
annotateFlowSet(dat, annotation, mergeBy = "name")
```

---

createAnnotation      *Create an annotation dataframe*

---

**Description**

Creates a data frame with rows containing the sample names of your flow set that can then be filled in with experimental metadata.

**Usage**

```
createAnnotation(yourFlowSet)
```

**Arguments**

yourFlowSet      the flowSet to create an annotation data frame for

**Value**

annotation\_df a data frame containing the sample names of your flow set

**Examples**

```
dat <- read.flowSet(path = system.file("extdata", "ss_example",
package = "flowTime"), alter.names = TRUE)
annotation <- createAnnotation(yourFlowSet = dat)
head(annotation)
```

---

dipdoubletGate      *A gate for the set of all diploid doublets*

---

**Description**

A gate for the set of all diploid doublets

**Usage**

```
data(dipdoubletGate)
```

**Format**

formal class polygonGate

---

dipsingletGate	<i>A gate for the set of all diploid singlet yeast cells</i>
----------------	--

---

**Description**

Typically set in FSC.A by FSC.H space Diploids are typically 5um x 6um ellipsoids while haploids are typically 4um x 4um spheroids. As a result, diploids are longer and you get a larger 'area/volume'.

**Usage**

```
data(dipsingletGate)
```

**Format**

```
formal class polygonGate
```

---

flsummary	<i>Get summary statistics for fluorescence or other data channels of a flowSet</i>
-----------	--

---

**Description**

Get summary statistics for fluorescence or other data channels of a flowSet

**Usage**

```
flsummary(flowset, channel)
```

**Arguments**

flowset	the flowSet to create summary statistics for
channel	option character vector of the data channel(s) to summarize. By default all channels will be summarized. Setting channels does not reduce computation time

**Value**

A data frame containing summary statistics (mean, median, SD) for the specified fluorescent channel and time moments of the flowSet.

**Examples**

```
plate1 <- read.flowSet(path = system.file("extdata",
"ss_example", package = "flowTime"), alter.names = TRUE)
flsummary(flowset = plate1, channel = "FL1.A")
```

---

getTime	<i>Get the time at which at flowFrame began collection</i>
---------	--

---

**Description**

Get the time at which at flowFrame began collection

**Usage**

```
getTime(flowframe)
```

**Arguments**

flowframe      The flowFrame for which you would like the initial time

**Value**

numeric time value in minutes

**Examples**

```
plate1<-read.flowSet(path = system.file("extdata", "ss_example", package =  
"flowTime"),alter.names = TRUE)  
getTime(plate1$A01.fcs)
```

---

hapdoubletGate	<i>A gate for the set of all haploid doublets</i>
----------------	---

---

**Description**

A gate for the set of all haploid doublets

**Usage**

```
data(hapdoubletGate)
```

**Format**

formal class polygonGate

---

hapsingletGate	<i>A gate for the set of all haploid singlets</i>
----------------	---

---

**Description**

A gate for the set of all haploid singlets

**Usage**

```
data(hapsingletGate)
```

**Format**

formal class polygonGate

---

loadGates	<i>Load a yeast gate file</i>
-----------	-------------------------------

---

**Description**

Loads a set of yeast gates into active memory to be used in analysis functions

**Usage**

```
loadGates(gatesFile = NULL, path = NULL, envir = environment())
```

**Arguments**

gatesFile	the gates file to be loaded into memory, or path to the gates file
path	The path to the gates file. If 'NULL' this will look through lazy loaded data for the gatesFile
envir	The environment in which to load the gates

**Value**

gate objects created in the current environment

**Examples**

```
loadGates(system.file("extdata/SORPGates.RData", package = "flowTime"))
```

---

meanMedianSD	<i>Summary statistic columns for a flow frame</i>
--------------	---

---

**Description**

Summary statistic columns for a flow frame

**Usage**

```
meanMedianSD(frame)
```

**Arguments**

frame            a flowFrame

**Value**

a matrix with a single row for the flow frame and mean, median, and sd columns for each column of the expression measurements

**Examples**

```
plate1<-read.flowSet(path = system.file("extdata", "ss_example", package =  
"flowTime"), alter.names = TRUE)  
meanMedianSD(plate1@frames$A01.fcs)  
fsApply(plate1, meanMedianSD)
```

---

ploidy	<i>Guess the ploidy of a given flowframe</i>
--------	--

---

**Description**

Use the FSC.A/FSC.H ratio. Diploids are typically 5um x 6um ellipsoids while haploids are typically 4um x 4um spheroids. As a result, diploids are longer and you get a larger 'area/volume' FSC.A. 'Width' might also be useful on certain cytometers.

**Usage**

```
ploidy(flowframe)
```

**Arguments**

flowframe        the flowFrame you would like to identify the ploidy of

**Value**

"Diploid" or "Haploid" and the mean FSC.A/FSC.H quotient

**Examples**

```
dat <- read.flowSet(path = system.file("extdata", "ss_example",
package = "flowTime"), alter.names = TRUE)
ploidy(dat$A01.fcs)
```

---

**polyGate***Create a polygon gate*

---

**Description**

Create a polygon gate

**Usage**

```
polyGate(x, y, filterID = "newGate", channels = c("FSC.A", "FSC.H"))
```

**Arguments**

x                    a vector of x coordinates  
y                    a vector of y coordinates  
filterID            name of the gate  
channels            vector containing the channels matching the x and y coordinates above

**Value**

a polygon gate object

**Examples**

```
polyGate(x = c(1,1,10000,10000), y = c(1,10000, 10000, 1), )
```

---

**qaGating***Quality assurance check*

---

**Description**

Check whether a flowSet (or a single flowFrame) contains empty values, in which case normalization may fail (divide by zero). This is particularly useful for removing wash wells from a flowSet.

**Usage**

```
qaGating(x, threshold = 100)
```

**Arguments**

x                    flowSet or flowFrame to be checked  
threshold           flowFrames with fewer events than this threshold will be identified.

**Value**

A vector containing the flowFrames with fewer events than the threshold.

**Examples**

```
plate1<-read.flowSet(path = system.file("extdata", "ss_example", package =
"flowTime"), alter.names = TRUE)
qaGating(plate1)
```

---

read.plateSet	<i>Read FCS files from set of plates</i>
---------------	--

---

**Description**

Reads all folders within the specified path containing the specified pattern in the folder names. Each folder contains a set a plate of FCS files. These folders typically make up a whole experiment. Plates are numbered according to the standard lexicographical ordering of your operating system.

**Usage**

```
read.plateSet(path = getwd(), pattern = "", ...)
```

**Arguments**

path	The path to search for folders containing FCS files
pattern	The <a href="#">regex</a> pattern used to identify the folders of FCS files to be read
...	Additional arguments passed to read.flowSet. Note that 'alter.names' is forced to be TRUE in this implementation.

**Value**

A single flowSet containing all FCS files within the identified folders. The index of each folder in the list according to lexicographical ordering (1,2,...) is prepended to the sampleNames.

**Examples**

```
# Read in both of the example data sets as a single flowSet
plate1<-read.plateSet(path = system.file("extdata", package = "flowTime"),
pattern = "")
```

---

`saveGates`*Save a yeast gate set*

---

**Description**

Save a yeast gate set

**Usage**

```
saveGates(  
  yeastGate = NULL,  
  dipsingletGate = NULL,  
  dipdoubletGate = NULL,  
  hapsingletGate = NULL,  
  hapdoubletGate = NULL,  
  path = getwd(),  
  fileName = "defaultGates.RData"  
)
```

**Arguments**

`yeastGate` a gate object defining the population of yeast cells  
`dipsingletGate` a gate object defining the population of diploid singlet cells  
`dipdoubletGate` a gate object defining the population of diploid doublet cells  
`hapsingletGate` a gate object defining the population of haploid singlet cells  
`hapdoubletGate` a gate object defining the population of haploid doublet cells  
`path` path to the folder in which you would like to save the gates  
`fileName` name of the .Rdata file you would like to save these gates within

**Value**

a .RData file in the "extdata" folder of the package containing the specified gates

**Examples**

```
loadGates(system.file("extdata/SORPGates.RData", package = "flowTime"))  
#not run:  
#saveGates()
```

---

steadyState	<i>Analysis of steady state fluorescence flow cytometry</i>
-------------	---

---

**Description**

Generates a data frame which can be used to visualize and analyze steady state flow cytometry data. Steady state in this case means that

**Usage**

```
steadyState(flowset, gated = FALSE, ploidy = NA, only = NA)
```

**Arguments**

flowset	your flowSet to be analyzed
gated	boolean is the data already gated?
ploidy	character gate to subset your flowset based on the ploidy of you strains
only	character which population of events to analyze, 'yeast', 'singlets', or 'doublets'?

**Value**

a data frame containing all of the selected subset of events from the original flowSet

**Examples**

```
dat <- read.flowSet(path = system.file("extdata", "ss_example",
package = "flowTime"), alter.names = TRUE)
annotation <- read.csv(system.file("extdata", "ss_example.csv",
package = "flowTime"))
dat <- annotateFlowSet(dat, annotation, mergeBy = "name")
loadGates(gatesFile = 'SORPGates')
steadyState(dat, gated = FALSE, ploidy = "diploid", only = "singlets")
```

---

summarizeFlow	<i>Generate summary statistics for a flowSet</i>
---------------	--

---

**Description**

Gates a sample to all yeast, then singlet, then doublets. Also calculates singlet to doublet ratio. Returns a list of data frames, e.g. output\$singlets, output\$doublets, etc.

**Usage**

```
summarizeFlow(
  flowset,
  channel = NA,
  gated = FALSE,
  ploidy = FALSE,
  only = FALSE
)
```

**Arguments**

flowset	the flowSet to be summarized
channel	character vector which data channel(s) should be summarized? If excluded (or NA) all channels will be summarized (default)
gated	boolean is the data already appropriately gated?
ploidy	character does the flowSet contain haploid or diploid cells?
only	character summarize only "singlet", "doublet", or all "yeast" cells, FALSE will return all

**Value**

data frame containing the specified summary statistics of the specified cell populations for each frame

**Examples**

```
plate1 <- read.flowSet(path = system.file("extdata", "ss_example",
package = "flowTime"), alter.names = TRUE)
summarizeFlow(plate1, channel = "FL1.A", gated = TRUE,
ploidy = "diploid", only = "yeast")
```

---

tidyFlow

*Generate a tidy dataset from time-course flow cytometry data*


---

**Description**

Generates a tibble containing all parameters and phenoData from a flowSet which can be used to visualize and analyze timecourse flow cytometry data.

**Usage**

```
tidyFlow(flowset, gated = TRUE, ploidy = NA, only = NA)
```

**Arguments**

flowset	your flowSet to be analyzed
gated	boolean is the data already gated?
ploidy	character gate to subset your flowset based on the ploidy of you strains
only	character which population of events to analyze, 'yeast', 'singlets', or 'doublets'?

**Value**

a data frame containing all of the selected subset of events from the original flowSet for all parameters including experiment time, etime, the time after the initial reading at which each event was collected.

**Examples**

```
plate1<-read.flowSet(path=system.file("extdata", "tc_example",  
package = "flowTime"), alter.names = TRUE)  
annotation <- read.csv(system.file("extdata", "tc_example.csv",  
package = "flowTime"))  
plate1 <- annotateFlowSet(plate1, annotation)  
tidy_dat <- tidyFlow(plate1, gated = TRUE)  
head(tidy_dat)
```

---

yeastGate

*A gate for the set of all yeast cells*

---

**Description**

Typically set in FSC.A by SSC.A space to excluded any debris

**Usage**

```
data(yeastGate)
```

**Format**

formal class polygonGate

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