Package 'flowBeads'

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Type Package

Version 1.4.0

Title flowBeads: Analysis of flow bead data

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Description This package extends flowCore to provide functionality specific to bead data. One of the goals of this package is to automate analysis of bead data for the purpose of normalisation.

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Depends R (>= 2.15.0), methods, Biobase, rrcov, flowCore

Imports flowCore, rrcov, knitr, xtable

Suggests flowViz

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InstallableEverywhere yes

Collate 'AllGenerics.R' 'AllClasses.R' 'get-methods.R' 'show-methods.R' 'plot-methods.R' 'beads.R' 'beads1-data.R' 'beads2-data.R' 'dakomef-data.R' 'cytocalmef-data.R' 'flowBeads-package.R'

biocViews Infrastructure, FlowCytometry, CellBasedAssays

R topics documented:

flowBeads-package 2
absoluteNormalise 2
BeadFlowFrame-class 3
beads1 3
beads2 3
cytocalmef 4
dakomef 4
gateBeads 4

GatedBeadFlowFrame-class 5
generateReport 5
getClusteringStats 5
getDate 6
getMEFparams 6
getMEFtransform 6
getParams 6
getTransformFunction 6
hasMEF 7
length 7
mefTransform 7
plot 8
relativeNormalise 8
show 8
toMEF 9

Index **10**

`flowBeads-package` *flowBeads*

Description

Bioconductor package for working with calibration beads in flow cytometry. Based on flowCore package.

Author(s)

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`absoluteNormalise` *absoluteNormalise*

Description

Absolute normalise to align peaks of bead.data to MEF.

Arguments

`bead.data`	`GatedBeadFlowFrame`
`mef.data`	data.frame

Value

A list of affine functions from transformed MFI relative coordinates to transformed MEF absolute coordinates.

BeadFlowFrame-class *BeadFlowFrame*

Description

Extension of `flowFrame` specific for bead data.

The constructor take as arguments the FCS file and the file containing the MEF values of the beads on the different detector channels

Usage

```
BeadFlowFrame(fcs.filename, bead.filename)
```

Arguments

`fcs.filename`	The file name of the FCS to load. File is loaded with the `read.FCS` function.
`bead.filename`	The file name of the MEF configuration files indicating the type of beads in the FCS file. The bead.file is read with read.csv.

Slots

`fcs.filename`**:** The file name of the FCS file from which to read.

`bead.filename`**:** The file name of the bead config file.

`beads.mef`**:** The `data.frame` containing the MEF of the bead populations on different channels.

`trans`**:** The transform f to linearise the fluorescence.

`inv.trans`**:** The inverse transform of f^{-1}.

beads1 *Dako beads on day 1*

Description

Dako beads on day 1

beads2 *Dako beads on day 2*

Description

Dako beads on day 2

`cytocalmef` *Cytocal config file*

Description

Cytocal config file

`dakomef` *Dako config file*

Description

Dako config file

`gateBeads` *gateBeads*

Description

`gateBeads` gates on all channels, apply scatter gate first. Find parameters in MEF data.frame which are also present in BeadFlowFrame The number of expected bead populations is by default six and it is assumed that that there is the same number of beads in each population.

Arguments

`bead.data`	The BeadFlowFrame object to gate.
`K`	The number of bead populations expected.
`verbose`	Whether to print debug information.

Value

GatedBeadFlowFrame

Examples

```
data(beads1)
gateBeads(beads1)
```

`GatedBeadFlowFrame-class` *GatedBeadFlowFrame*

Description

GatedBeadFlowFrame

Arguments

`labels`	The resulting labels of the clustering assigning each event to a different bead population.
`clustering.stats`	Three dimensional array summarising the stats per channel and population.
`mef.tranform`	The list of MEF transforms

`generateReport` *generateReport*

Description

Generate an HTML report from a Markdown template using knitr.

Arguments

`bead.data`	`GatedBeadFlowFrame`
`output.file`	name of the file to which to output the HTML report.

See Also

knitr

`getClusteringStats` *getClusteringStats*

Description

Returns clustering stats as a 3-dimensional array.

getDate *getDate*

Description

getDate

Arguments

flow.frame	flowFrame object on which to get the date field

getMEFparams *getMEFparams*

Description

Returns all the MEF parameter names.

getMEFtransform *getMEFtransform*

Description

Returns MEF transform function.

getParams *getParams*

Description

Returns all the parameter names except the scatter channels.

getTransformFunction *getTransformFunction*

Description

Returns transform function. The default is the logicle transform for FCS 3 and the log10 transform for FCS 2.

hasMEF *hasMEF*

Description

Checks whether we have the MEF for a channel name.

Arguments

bead.data	BeadFlowFrame
parameter	character

length *length*

Description

Returns the number of events in a flowFrame object.

Arguments

flow.frame	flowFrame object on which to get number of beads

mefTransform *Logicle transformation constructor*

Description

Input parameters are to be provided in decades

Usage

```
mefTransform(transformationId = "mefTransform", alpha,
  beta)
```

Arguments

transformationId	The name of the transformation.
alpha	The intercept of the MEF transform.
beta	The slope of the MEF transform.

`plot` *Plot the results of the clustering. Plot only the requested channel which should have a corresponding entry in the MEF files*

Description

Plot the results of the clustering. Plot only the requested channel which should have a corresponding entry in the MEF files

Ungated bead data, simply draw all channels individually (no colours).

If no argument specified then plot all parameters

`relativeNormalise` *relativeNormalise*

Description

Relative normalise to align peaks of bead.data1 to those of bead.data2 Returns a list of affine functions from transformed MFI day one coordinates to transformed MFI day two coordinates. This permits comparison of channels across two days, provided the detector is stable, even in the absence of absolute MEF values.

Arguments

`bead.data1:`	`GatedBeadFlowFrame` object with MFIs from day one
`bead.data2:`	`GatedBeadFlowFrame` object with MFIIs from day two

Value

A list of affine functions from MFI day one coordinates to MFI day two coordinates.

`show` *BeadFlowFrame*

Description

BeadFlowFrame

GatedBeadFlowFrame

toMEF *toMEF*

Description

Given bead.data and a flow.data apply the MEF transform to matching channels in `flow.data`.

Arguments

`bead.data`	The GatedBeadFlowFrame object containing the MEF transform.
`flow.data`	The flowFrame object on which to apply the transform.

Index

∗Topic **datasets**
beads1, 3
beads2, 3
cytocalmef, 4
dakomef, 4
∗Topic **package**
flowBeads-package, 2

absoluteNormalise, 2
absoluteNormalise,GatedBeadFlowFrame,data.frame-method *(absoluteNormalise)*, 2

BeadFlowFrame, *7*
BeadFlowFrame *(BeadFlowFrame-class)*, 3
BeadFlowFrame-class, 3
beads1, 3
beads2, 3

character, *7*
cytocalmef, 4

dakomef, 4
data.frame, *2, 3*
dBeadFlowFrame *(BeadFlowFrame-class)*, 3

flowBeads *(flowBeads-package)*, 2
flowBeads-package, 2
flowFrame, *3*, *6, 7*

gateBeads, 4
gateBeads,BeadFlowFrame-method *(gateBeads)*, 4
GatedBeadFlowFrame, *2*, *4, 5*, *8*
GatedBeadFlowFrame *(GatedBeadFlowFrame-class)*, 5
GatedBeadFlowFrame-class, 5
generateReport, 5
generateReport,GatedBeadFlowFrame,character-method *(generateReport)*, 5
getClusteringStats, 5
getClusteringStats,GatedBeadFlowFrame-method *(getClusteringStats)*, 5
getDate, 6
getDate,flowFrame-method *(getDate)*, 6
getMEFparams, 6
getMEFparams,BeadFlowFrame-method *(getMEFparams)*, 6
getMEFtransform, 6
getMEFtransform,GatedBeadFlowFrame-method *(getMEFtransform)*, 6
getParams, 6
getParams,flowFrame-method *(getParams)*, 6
getTransformFunction, 6
getTransformFunction,BeadFlowFrame-method *(getTransformFunction)*, 6

hasMEF, 7
hasMEF,BeadFlowFrame,character-method *(hasMEF)*, 7

knitr, *5*

length, 7
length,flowFrame-method *(length)*, 7

mefTransform, 7

plot, 8
plot,BeadFlowFrame,character-method *(plot)*, 8
plot,BeadFlowFrame,missing-method *(plot)*, 8
plot,GatedBeadFlowFrame,character-method *(plot)*, 8

read.csv, *3*
read.FCS, *3*
relativeNormalise, 8
relativeNormalise,GatedBeadFlowFrame,GatedBeadFlowFrame-method *(relativeNormalise)*, 8

show, 8

toMEF, 9
toMEF,GatedBeadFlowFrame,flowFrame-method
(toMEF), 9