

Package ‘flowBeads’

January 19, 2026

Type Package

Version 1.48.0

Title flowBeads: Analysis of flow bead data

Author Nikolas Pontikos

Date 2013-03-01

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.

Maintainer Nikolas Pontikos <n.pontikos@gmail.com>

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

Imports flowCore, rrcov, knitr, xtable

Suggests flowViz

License Artistic-2.0

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' 'cytoalmef-data.R'
'flowBeads-package.R'

biocViews ImmunoOncology, Infrastructure, FlowCytometry,
CellBasedAssays

git_url <https://git.bioconductor.org/packages/flowBeads>

git_branch RELEASE_3_22

git_last_commit 233be48

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-01-19

Contents

flowBeads-package	2
absoluteNormalise	2
BeadFlowFrame-class	3

beads1	3
beads2	3
cytoalmef	4
dakomef	4
gateBeads	4
GatedBeadFlowFrame-class	5
generateReport	5
getClusteringStats	5
getDate	5
getMEFparams	6
getMEFtransform	6
getParams	6
getTransformFunction	6
hasMEF	6
length	7
mefTransform	7
plot	7
relativeNormalise	8
show	8
toMEF	8

Index 9

flowBeads-package	<i>flowBeads</i>
-------------------	------------------

Description

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

Author(s)

Nikolas Pontikos <n.pontikos@gmail.com>

absoluteNormalise	<i>absoluteNormalise</i>
-------------------	--------------------------

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	<i>BeadFlowFrame</i>
---------------------	----------------------

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

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

Slots

<code>fcs.filename</code> :	The file name of the FCS file from which to read.
<code>bead.filename</code> :	The file name of the bead config file.
<code>beads.mef</code> :	The <code>data.frame</code> containing the MEF of the bead populations on different channels.
<code>trans</code> :	The transform f to linearise the fluorescence.
<code>inv.trans</code> :	The inverse transform of f^{-1} .

beads1	<i>Dako beads on day 1</i>
--------	----------------------------

Description

Dako beads on day 1

beads2	<i>Dako beads on day 2</i>
--------	----------------------------

Description

Dako beads on day 2

cytocalmef	<i>Cytocal config file</i>
------------	----------------------------

Description

Cytocal config file

dakomef	<i>Dako config file</i>
---------	-------------------------

Description

Dako config file

gateBeads	<i>gateBeads</i>
-----------	------------------

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	
	<i>GatedBeadFlowFrame</i>

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	<i>generateReport</i>
----------------	-----------------------

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	<i>getClusteringStats</i>
--------------------	---------------------------

Description

Returns clustering stats as a 3-dimensional array.

getDate	<i>getDate</i>
---------	----------------

Description

getDate

Arguments

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

getMEFparams	<i>getMEFparams</i>
--------------	---------------------

Description

Returns all the MEF parameter names.

getMEFtransform	<i>getMEFtransform</i>
-----------------	------------------------

Description

Returns MEF transform function.

getParams	<i>getParams</i>
-----------	------------------

Description

Returns all the parameter names except the scatter channels.

getTransformFunction	<i>getTransformFunction</i>
----------------------	-----------------------------

Description

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

hasMEF	<i>hasMEF</i>
--------	---------------

Description

Checks whether we have the MEF for a channel name.

Arguments

bead.data	BeadFlowFrame
parameter	character

length	<i>length</i>
--------	---------------

Description

Returns the number of events in a `flowFrame` object.

Arguments

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

mefTransform	<i>Logicle transformation constructor</i>
--------------	---

Description

Input parameters are to be provided in decades

Usage

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

Arguments

<code>transformationId</code>	The name of the transformation.
<code>alpha</code>	The intercept of the MEF transform.
<code>beta</code>	The slope of the MEF transform.

plot	<i>Plot the results of the clustering. Plot only the requested channel which should have a corresponding entry in the MEF files</i>
------	---

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	<i>relativeNormalise</i>
-------------------	--------------------------

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 MFIs from day two

Value

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

show	<i>BeadFlowFrame</i>
------	----------------------

Description

- BeadFlowFrame
- GatedBeadFlowFrame

toMEF	<i>toMEF</i>
-------	--------------

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

- * **datasets**
 - beads1, [3](#)
 - beads2, [3](#)
 - cytoalmef, [4](#)
 - dakomef, [4](#)
- * **package**
 - flowBeads-package, [2](#)
- absoluteNormalise, [2](#)
- absoluteNormalise, GatedBeadFlowFrame, data.frame-method (absoluteNormalise), [2](#)
- BeadFlowFrame, [6](#)
- BeadFlowFrame (BeadFlowFrame-class), [3](#)
- BeadFlowFrame-class, [3](#)
- beads1, [3](#)
- beads2, [3](#)
- character, [6](#)
- cytoalmef, [4](#)
- dakomef, [4](#)
- data.frame, [2](#), [3](#)
- dBeadFlowFrame (BeadFlowFrame-class), [3](#)
- flowBeads (flowBeads-package), [2](#)
- flowBeads-package, [2](#)
- flowFrame, [3](#), [5](#), [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, [5](#)
- getDate, flowFrame-method (getDate), [5](#)
- 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, [6](#)
- hasMEF, BeadFlowFrame, character-method (hasMEF), [6](#)
- knitr, [5](#)
- length, [7](#)
- length, flowFrame-method (length), [7](#)
- mefTransform, [7](#)
- plot, [7](#)
- plot, BeadFlowFrame, character-method (plot), [7](#)
- plot, BeadFlowFrame, missing-method (plot), [7](#)
- plot, GatedBeadFlowFrame, character-method (plot), [7](#)
- read.csv, [3](#)
- read.FCS, [3](#)
- relativeNormalise, [8](#)
- relativeNormalise, GatedBeadFlowFrame, GatedBeadFlowFrame (relativeNormalise), [8](#)
- toMEF, [8](#)
- toMEF, GatedBeadFlowFrame, flowFrame-method (toMEF), [8](#)