Package 'flowFit'

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Type Package

Title Estimate proliferation in cell-tracking dye studies

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Description This package estimate the proliferation of a cell population in cell-tracking dye studies. The package uses an R implementation of the Levenberg-Marquardt algorithm (minpack.lm) to fit a set of peaks (corresponding to different generations of cells) over the proliferation-tracking dye distribution in a FACS experiment.

License Artistic-2.0

LazyLoad yes

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Collate flowFit-internal.R AllClasses.R AllGenerics.R show-methods.R summary-methods.R view-accessors.R coef-methods.R confint-methods.R plot-methods.R logTicks.R generationsDistance.R proliferationGrid.R parentFitting.R proliferationFitting.R proliferationIndex.R getGenerations.R

URL

BugReports Davide Rambaldi <davide.rambaldi@gmail.com>

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R topics documented:

`flowFit-package` *Estimate proliferation in cell-tracking dye studies*

Description

This package estimate the proliferation of a cell population in cell-tracking dye studies.

In cells proliferation tracking experiments, cells are stained with a tracking dye before culture. During cell division, the tracking dye is partitioned between daughter cells, so that each division brings about a halving of fluorescence intensity; the intensity of a cell, by comparison with the intensity of resting cells, provides an indication of how many divisions the cell has undergone since stimulation

This package uses an R implementation of the Levenberg-Marquardt algorithm (`nls.lm`) to fit a set of peaks (corresponding to different generations of cells) over the proliferation-tracking dye distribution in a FACS experiment.

The package define two data structure (S4 classes): `proliferationFittingData`, `parentFittingData` and their methods and accessors.

The package is integrated with other `www.bioconductor.org` libraries for analysis of flow cytometry data: `flowCore` and `flowViz`.

Details

Package:	flowFit
Type:	Package
Version:	0.2
Date:	2012-11-29
License:	Artistic-2.0

Author(s)

Maintainer: Davide Rambaldi <davide.rambaldi@gmail.com> Author: Davide Rambaldi

References

1. Timur V. Elzhov, Katharine M. Mullen and Ben Bolker (2012). **minpack.lm: R interface to the Levenberg-Marquardt nonlinear least-squares algorithm found in MINPACK.**
2. **Tracking antigen-driven responses by flow cytometry: Monitoring proliferation by dye dilution.** Paul K Wallace, Joseph D Tario, Jan L Fisher, Stephen S Wallace, Marc S Ernstoff, Katharine A Muirhead. Cytometry (2008) vol. 73A (11) pp. 1019-1034
3. **MEASURING MOLECULES OF EQUIVALENT FLUOROCHROME (MEF) USING SPHEROTM RAINBOW AND ULTRA RAINBOW CALIBRATION PARTICLES**, Spherotech, http://www.spherotech.com/tech_SpheroTech_Note_9.html
4. Benjamin J.C. Quah, Christopher R. Parish, **New and improved methods for measuring lymphocyte proliferation in vitro and in vivo using CFSE-like fluorescent dyes**, Journal of Immunological Methods, Volume 379, Issues 1-2, 31 May 2012, Pages 1-14, ISSN 0022-1759, 10.1016/j.jim.2012.02.012.

See Also

1. proliferationFitting generations fitting function.
2. parentFitting parent population fitting function.
3. proliferationIndex proliferation index calculator.
4. getGenerations get percentage of cells for generation.
5. logTicks draw a log scale on your FACS plots.
6. generationsDistance calculate the distance between 2 generations of cells on the FACS scale.

Examples

```
if(require(flowFitExampleData)){
  data(QuahAndParish)
  parent.fitting.cfse <- parentFitting(QuahAndParish[[1]], "<FITC-A>")
 fitting.cfse <- proliferationFitting(QuahAndParish[[2]], "<FITC-A>", parent.fitting.cfse@parentPeakPosition,

  summary(fitting.cfse)
  confint(fitting.cfse)
  coef(fitting.cfse)
  Data(fitting.cfse)

  plot(parent.fitting.cfse)
  plot(fitting.cfse)

 # for this sample we use a Fixed Model: we keep fixed in the model the Parent Peak Position
  parent.fitting.cpd <- parentFitting(QuahAndParish[[1]], "<APC-A>")
 fitting.cpd <- proliferationFitting(QuahAndParish[[3]], "<APC-A>", parent.fitting.cpd@parentPeakPosition, par

  parent.fitting.ctv <- parentFitting(QuahAndParish[[1]], "<Alexa Fluor 405-A>")
 fitting.ctv <- proliferationFitting(QuahAndParish[[4]], "<Alexa Fluor 405-A>", parent.fitting.ctv@parentPeakPo

  # lets compare the generations across the 3 samples:
  par(mfrow=c(3,4))
```

```
 plot(parent.fitting.cfse, main="CFSE Non Stimulated")
 plot(fitting.cfse, which=3, main="CFSE")
 plot(fitting.cfse, which=4, main="CFSE")
 plot(fitting.cfse, which=5, main="CFSE")
 plot(parent.fitting.cpd, main="CPD Non Stimulated")
 plot(fitting.cpd, which=3, main="CPD")
 plot(fitting.cpd, which=4, main="CPD")
 plot(fitting.cpd, which=5, main="CPD")
 plot(parent.fitting.ctv, main="CTV Non Stimulated")
 plot(fitting.ctv, which=3, main="CTV")
 plot(fitting.ctv, which=4, main="CTV")
 plot(fitting.ctv, which=5, main="CTV")

 # ESTIMATE GOODNESS of FITTING with KS TEST
 perc.cfse <- fitting.cfse@generations
 perc.cpd <- fitting.cpd@generations
 perc.ctv <- fitting.ctv@generations
 perc.cfse <- c(perc.cfse, rep(0,6))

 # EXPLORATIVE PLOT
 par(mfrow=c(1,1), ask=FALSE)
plot(perc.cfse, type="b", axes=FALSE, ylim=c(0,50), xlab="generations", ylab="Percentage of cells", main="")
 lines(perc.cpd, type="b", col="red")
 lines(perc.ctv, type="b", col="blue")
legend("topleft", c("CFSE","CPD","CTV"), pch=1, col=c("black","red","blue"), bg = gray90,text.col = "green4")
 axis(2, at=seq(0,50,10), labels=paste(seq(0,50,10),"%"))
 axis(1, at=1:16,labels=1:16)

 # Pearsons Chi-squared Test for Count Data
 M <- rbind(perc.cfse, perc.cpd, perc.ctv)
 colnames(M) <- 1:16
 (Xsq <- chisq.test(M, B=100000, simulate.p.value=TRUE))
 text(8,40,paste("Chi-squared Test p=", round(Xsq$p.value, digits=4), sep=""))

 # PKH26
 # load data
 data(PKH26data)
 parent.fitting <-  parentFitting(PKH26data[[1]], "FL2-Height LOG")
my.fit <- proliferationFitting(PKH26data[[2]], "FL2-Height LOG", parent.fitting@parentPeakPosition, parent.fit
 my.fit
 summary(my.fit)
 confint(my.fit)
 coef(my.fit)
 Data(my.fit)
 # plot results
 plot(my.fit)

 # modeling with locked Peak Size
my.fitb <- proliferationFitting(PKH26data[[2]], "FL2-Height LOG", parent.fitting@parentPeakPosition, parent.fi
 plot(my.fitb)
 # modeling with locked Peak Size and Position
my.fitc <- proliferationFitting(PKH26data[[2]], "FL2-Height LOG", parent.fitting@parentPeakPosition, parent.fi
 plot(my.fitc)
```

```
  # modeling with locked Peak Size, Position and Distance
 my.fitd <- proliferationFitting(PKH26data[[2]], "FL2-Height LOG", parent.fitting@parentPeakPosition, parent.fi
  plot(my.fitd)
}
```

`generationsDistance` *Calculate the distance between 2 generations of cells on the FACS scale*

Description

This function calculate the distance between 2 generations of cells on the FACS scale.

Usage

```
generationsDistance(dataRange, logDecades)
```

Arguments

`dataRange`	Digital Data range on the FACS instrument
`logDecades`	Number of log decades on the FACS instrument (dynamic range)

Details

We can use this formula to convert FFI (FACS fluorescence Intensity) to RFI (Relative Fluorescence Intensity): $RFI = 10^{\frac{FFI \cdot l}{c}}$

The inverse formula is used to convert from RFI to FACS fluorescence: $FFI = \frac{c * \log(RFI)}{(l * \log(10))}$

Where:

RFI is the Relative Fluorescence Intensity

FFI is the fluorescence on the FACS scale

l is the number of log decades in the FACS instrument

c is the number of data points (channels) in the instrument.

Using this formulas it is possible to estimate the spacing between generations on the FACS scale. The spacing value is automatically computed, based on the number of decades and the assumption that each generation has one-half of the intensity of the previous generation.

Value

Return the spacing between generations on the FACS scale.

Author(s)

Davide Rambaldi

References

1. **Tracking antigen-driven responses by flow cytometry: Monitoring proliferation by dye dilution.** Paul K Wallace, Joseph D Tario, Jan L Fisher, Stephen S Wallace, Marc S Ernstoff, Katharine A Muirhead. Cytometry (2008) vol. 73A (11) pp. 1019-1034
2. FACS Formulas to convert between Relative Fluorescence and fluorescence on the FACS scale: **MEASURING MOLECULES OF EQUIVALENT FLUOROCHROME (MEF) USING SPHEROTM RAINBOW AND ULTRA RAINBOW CALIBRATION PARTICLES**, Spherotech, http://www.spherotech.com/tech_SpheroTech_Note_9.html

Examples

```
distance <- generationsDistance(1024, 4)
```

`getGenerations` *Get percentage of cells for generation in a flowFit model*

Description

getGenerations: get percentage of cells for generation in a flowFit model from an object of class `proliferationFittingData` generated by the `proliferationFitting` function.

Usage

```
getGenerations(object)
```

Arguments

`object`	An object of class `proliferationFittingData`

Details

This function return a `list`. In order to get the percentage of cells for generation as vector you can use th `slot` `generations` of the `proliferationFittingData` (see also examples).

Value

return a `list` object

Author(s)

Davide Rambaldi

See Also

`proliferationFitting` and `proliferationFittingData`

Examples

```
if(require(flowFitExampleData)){
  data(QuahAndParish)
  parent.fitting.cfse <- parentFitting(QuahAndParish[[1]], "<FITC-A>")
 fitting.cfse <- proliferationFitting(QuahAndParish[[2]], "<FITC-A>", parent.fitting.cfse@parentPeakPosition,
  generationList <- getGenerations(fitting.cfse)

  # to extract a vector of percentage of cells for generation you can use:
  fitting.cfse@generations
}
```

`logTicks` *Generate logTicks for FACS plotting*

Description

This function return a log scale to be used on your FACS plots

Usage

```
logTicks(dataRange, logDecades, doScale = TRUE)
```

Arguments

`dataRange`	Range of your data (number of data points in the FACS)
`logDecades`	Number of log decades in the FACS
`doScale`	Scale according to dataRange and logDecades: scale.factor = dataRange / logDecades

Value

Return a `list` with 3 elements:

`major`	Position of the Major ticks
`all`	Position of the All ticks
`label`	Labels for Major Ticks

Author(s)

Davide Rambaldi

Examples

```
if(require(flowFitExampleData)){
  # using flowViz

  # load data
  data(PKH26data)

  # plot data
  plot(PKH26data[[1]], "FL2-Height LOG", axes=FALSE, breaks=1024)

  # create ticks
  my.ticks <- logTicks(1024,4)

  # plot your ticks
  axis(1,my.ticks$all,label=FALSE)
  axis(1,at=my.ticks$major,labels=my.ticks$labels)
  axis(2)
}
```

`parentFitting` *Fitting a parent population*

Description

Estimate the proliferation of a cell population in cell-tracking dye studies. parentFitting: fit the parent population

Usage

```
parentFitting(flowframe, channel, estimatedPeakPosition = NA, estimatedPeakSize = NA, dataRange = NA,
```

Arguments

`flowframe`	An object of class `flowFrame` from `flowCore`
`channel`	FACS column/channel (`flowFrame` column)
`estimatedPeakPosition`	Estimated peak position. If not provided will be used the `exprs` mean
`estimatedPeakSize`	Estimated peak size. If not provided will be used the `exprs` standard deviation
`dataRange`	Number of digital data points on the machine. If not provided will be extracted from `flowFrame` using `keyword`
`logDecades`	FACS dynamic range (log decades). If not provided will be extracted from `flowFrame` using `keyword`
`binning`	Should I bin data? Some FACS have a large data range (Es: FACSCanto have 65536 data points, may be is convenient in this case to group data in bins to avoid acquiring too many cells). If you have you data log tranformed in range 0-5 it is mandatory to bin data

breaks	How many breaks if I bin data?
dataSmooth	Should I smooth data with a Kolmogorov-Zurbenko low-pass linear filter?
smoothWindow	Window used to smooth data with the Kolmogorov-Zurbenko low-pass linear filter.
fixedModel	Should I use a model with fixed parameters? (Peak Position or Size).
fixedPars	A list of fixed parameters. If you give me a value, I use that value, otherwise I use estimates (check examples)
verbose	Verbose mode.

Details

The formula used to fit the parent population:

$$a^2 \exp \frac{(x-\mu)^2}{2\sigma^2}$$

The algorithm estimate the position (μ) and size (σ) of the *Parent Population*.

Value

return a parentFittingData object

Author(s)

Davide Rambaldi

References

1. Timur V. Elzhov, Katharine M. Mullen and Ben Bolker (2012). **minpack.lm: R interface to the Levenberg-Marquardt nonlinear least-squares algorithm found in MINPACK.**

See Also

proliferationFitting

Examples

```
if(require(flowFitExampleData)){
  # CFSE
  data(QuahAndParish)
  parent.fitting.cfse <- parentFitting(QuahAndParish[[1]], "<FITC-A>")

  parent.fitting.cfse
  summary(parent.fitting.cfse)
  confint(parent.fitting.cfse)
  coef(parent.fitting.cfse)
  plot(parent.fitting.cfse)
  Data(parent.fitting.cfse)
```

```
 # PKH26
 data(PKH26data)
 parent.fitting <-  parentFitting(PKH26data[[1]], "FL2-Height LOG")
 parent.fitting
 summary(parent.fitting)
 confint(parent.fitting)
 coef(parent.fitting)
 plot(parent.fitting)
 Data(parent.fitting)

 # fixedModel with estimates
parent.fitting <- parentFitting(PKH26data[[1]], "FL2-Height LOG", fixedModel=TRUE, fixedPars=list(M=NA,S=NA))

 # fixedModel with user values
parent.fitting <- parentFitting(PKH26data[[1]], "FL2-Height LOG", fixedModel=TRUE, fixedPars=list(M=810,S=16)

 # fixedModel with locked Peak Size (one fixed parameter)
parent.fitting <- parentFitting(PKH26data[[1]], "FL2-Height LOG", fixedModel=TRUE, fixedPars=list(S=17))
}
```

`parentFittingData-class` *Class "parentFittingData"*

Description

Provides S4 data structure and basic infrastructure and functions to store proliferation tracking data of the Parent Population.

Objects from the Class

Objects can be created by calls of the form `new("parentFittingData", flowframe, channel, ...)`. This class is for internal use.

Slots

`data`: Object of class `"flowFrame"` ~~

`channel`: Object of class `"character"` ~~

`estimatedPeakPosition`: Object of class `"numeric"` ~~

`estimatedPeakSize`: Object of class `"numeric"` ~~

`dataRange`: Object of class `"numeric"` ~~

`logDecades`: Object of class `"numeric"` ~~

`parentPeakPosition`: Object of class `"numeric"` ~~

`parentPeakSize`: Object of class `"numeric"` ~~

`fittingDeviance`: Object of class `"numeric"` ~~

`fixedModel`: Object of class "`logical`" ~~

`fixedPars`: Object of class "`list`" ~~

`binning`: Object of class "`logical`" ~~

`breaks`: Object of class "`numeric`" ~~

`dataSmooth`: Object of class "`logical`" ~~

`smoothWindow`: Object of class "`numeric`" ~~

`parStart`: Object of class "`list`" ~~

`dataMatrix`: Object of class "`matrix`" ~~

`dataPoints`: Object of class "`data.frame`" ~~

`modelPoints`: Object of class "`data.frame`" ~~

`residFun`: Object of class "`function`" ~~

`lmOutput`: Object of class "`nls.lm`" ~~

Methods

plot Basic plots for `parentFittingData` objects. *Usage:* `plot(parentFittingData, main="Original data and Parent`

show Display details about the `parentFittingData` object.

summary Return a descriptive summary about the `parentFittingData` object.

Data Return the `flowFrame` object.

coef Return coefficients of the model.

confint Return confidence intervals of the model.

Author(s)

Davide Rambaldi

See Also

`parentFitting`

Examples

```
showClass("parentFittingData")
if(require(flowFitExampleData)){
  data(PKH26data)
  parent.fitting <-  parentFitting(PKH26data[[1]], "FL2-Height LOG")
  parent.fitting
  summary(parent.fitting)
  confint(parent.fitting)
  coef(parent.fitting)
  plot(parent.fitting)
  Data(parent.fitting)
}
```

plot-methods *Very basic plotting of flowFit objects:* proliferationFittingData *and* parentFittingData

Description

A basic method to plot proliferationFittingData and parentFittingData objects. See below for details.

Details

Basic plots for flowFit objects.

Supported arguments for parentFittingData:

1. main: an overall title for the plot, see title.
2. xlab: a title for the x axis, see title.
3. ylab: a title for the y axis, see title.
4. legend: show/hide messages.
5. logScale: put a log scale on the x axis.

Supported arguments for proliferationFittingData:

1. which: which plots I should show? ["all" or 1:5]
2. main: an overall title prefix for the plots.
3. xlab: a title for the x axis, see title.
4. ylab: a title for the y axis, see title.
5. legend: show/hide messages.
6. logScale: put a log scale on the x axis.
7. drawGrid: put some dashed lines at the generationsDistance expected positions.

Methods

x = "proliferationFittingData", y = "missing" Multiple plots of generations fitting data (data generated by the function proliferationFitting)

x = "parentFittingData", y= "missing") Single plot of a parent population fitting (data generated by the function parentFitting)

Author(s)

Davide Rambaldi

See Also

proliferationFitting, parentFitting

`proliferationFitting` *Estimate proliferation in cell-tracking dye studies*

Description

The algorithm fit a set of N peaks on the `flowFrame` data using the `nls.lm` function. The number of peaks to be fitted is automatically estimated using `generationsDistance`.

The algorithm take the position (μ) and size (σ) of the *Parent Population* as estimates and fit a set of peaks on a `flowFrame` data.

The first peak correspond to the parent population:

$$a^2 \exp \frac{(x-\mu)^2}{2\sigma^2}$$

The next peak (corresponding to the next generation of cells) will be:

$$b^2 \exp \frac{(x-(\mu-D))^2}{2\sigma^2}$$

Where D is the estimated distance between 2 generations of cells.

The complete formula for the fitting of the 15 peaks is the following:

$$a^2 \exp \frac{(x-M)^2}{2s^2} + b^2 \exp \frac{(x-(M-D))^2}{2s^2} + ... + p^2 \exp \frac{(x-(M-14\cdot D))^2}{2s^2}$$

Where the parameters [a-q] represent an estimate of the number of cells for a given generation.

In the Levenberg-Marquadt algorithm implementation we use this formula to estimate the error between the model and the real data:

$$residFun = (Observed - Model)^2$$

The ration between the intergral of a single peak and the integral of all model formula is an estimate of the percentage of cells in a given generation.

Usage

```
proliferationFitting(
  flowframe,
  channel,
  estimatedParentPosition,
  estimatedParentSize,
  dataRange = NA,
  logDecades = NA,
  estimatedDistance = NA,
  binning = TRUE,
```

```
  breaks = 1024,
  dataSmooth = TRUE,
  smoothWindow = 2,
  fixedModel = FALSE,
  fixedPars = NA,
  verbose = FALSE
  )
```

Arguments

flowframe	An object of class flowFrame from flowCore
channel	FACS column/channel (flowFrame column)
estimatedParentPosition	Estimated parent peak position.
estimatedParentSize	Estimated parent peak size.
dataRange	Number of digital data points on the machine. If not provided will be extracted from flowFrame using keyword
logDecades	FACS dynamic range (log decades). If not provided will be extracted from flowFrame using keyword
estimatedDistance	Estimated distance between generations. If not provided will be estimated with generationsDistance
binning	Should I bin data? Some FACS have a large data range (Es: FACSCanto have 65536 data points, may be is convenient in this case to group data in bins to avoid acquiring too many cells). If you have you data log tranformed in range 0-5 it is mandatory to bin data
breaks	How many breaks if I bin data?
dataSmooth	Should I smooth data with a Kolmogorov-Zurbenko low-pass linear filter (kz)?
smoothWindow	Window used to smooth data with the Kolmogorov-Zurbenko low-pass linear filter (kz).
fixedModel	Should I use a model with fixed parameters? (Peak Position or Size).
fixedPars	A list of fixed parameters. If you give me a value, I use that value, otherwise I use estimates (check examples)
verbose	Verbose mode.

Details

See the vignette for more details on this function.

Value

return a proliferationFittingData object

Author(s)

Davide Rambaldi

References

1. Timur V. Elzhov, Katharine M. Mullen and Ben Bolker (2012). **minpack.lm: R interface to the Levenberg-Marquardt nonlinear least-squares algorithm found in MINPACK.**

Examples

```
if(require(flowFitExampleData)){
  # PKH26
  data(PKH26data)
  parent.fitting <-  parentFitting(PKH26data[[1]], "FL2-Height LOG")
 my.fit <- proliferationFitting(PKH26data[[2]], "FL2-Height LOG", parent.fitting@parentPeakPosition, parent.fit
  my.fit
  summary(my.fit)
  confint(my.fit)
  coef(my.fit)
  Data(my.fit)
  # plot results
  plot(my.fit)

  # modeling with locked Peak Size
 my.fit <- proliferationFitting(PKH26data[[2]], "FL2-Height LOG", parent.fitting@parentPeakPosition, parent.fit
  # modeling with locked Peak Size and Position
 my.fit <- proliferationFitting(PKH26data[[2]], "FL2-Height LOG", parent.fitting@parentPeakPosition, parent.fit
  # modeling with locked Peak Size, Position and Distance
 my.fit <- proliferationFitting(PKH26data[[2]], "FL2-Height LOG", parent.fitting@parentPeakPosition, parent.fit

  # generations as vector
  my.fit@generations
  # generations as list
  getGenerations(my.fit)

  # CFSE, CPD and CTV data
  data(QuahAndParish)
  parent.fitting.cfse <- parentFitting(QuahAndParish[[1]], "<FITC-A>")
 fitting.cfse <- proliferationFitting(QuahAndParish[[2]], "<FITC-A>", parent.fitting.cfse@parentPeakPosition,

  summary(fitting.cfse)
  confint(fitting.cfse)
  coef(fitting.cfse)
  Data(fitting.cfse)

  plot(parent.fitting.cfse)
  plot(fitting.cfse)

 # for CPD samples we use a Fixed Model: we keep fixed in the model the Parent Peak Position
  parent.fitting.cpd <- parentFitting(QuahAndParish[[1]], "<APC-A>")
 fitting.cpd <- proliferationFitting(QuahAndParish[[3]], "<APC-A>", parent.fitting.cpd@parentPeakPosition, par

  parent.fitting.ctv <- parentFitting(QuahAndParish[[1]], "<Alexa Fluor 405-A>")
 fitting.ctv <- proliferationFitting(QuahAndParish[[4]], "<Alexa Fluor 405-A>", parent.fitting.ctv@parentPeakPo
```

```
  # lets compare the generations across the 3 samples:
  plot(parent.fitting.cfse, main="CFSE Non Stimulated")
  plot(fitting.cfse, which=3, main="CFSE")
  plot(fitting.cfse, which=4, main="CFSE")
  plot(fitting.cfse, which=5, main="CFSE")
  plot(parent.fitting.cpd, main="CPD Non Stimulated")
  plot(fitting.cpd, which=3, main="CPD")
  plot(fitting.cpd, which=4, main="CPD")
  plot(fitting.cpd, which=5, main="CPD")
  plot(parent.fitting.ctv, main="CTV Non Stimulated")
  plot(fitting.ctv, which=3, main="CTV")
  plot(fitting.ctv, which=4, main="CTV")
  plot(fitting.ctv, which=5, main="CTV")
}
```

`proliferationFittingData-class`
Class "proliferationFittingData"

Description

Provides S4 data structure and basic infrastructure and functions to store proliferation tracking data of the Parent Population.

Objects from the Class

Objects can be created by calls of the form `new("proliferationFittingData", flowframe, channel, ...)`. This class is for internal use.

Slots

`data`: Object of class `"flowFrame"` ~~

`channel`: Object of class `"character"` ~~

`estimatedPeakPosition`: Object of class `"numeric"` ~~

`estimatedPeakSize`: Object of class `"numeric"` ~~

`dataRange`: Object of class `"numeric"` ~~

`logDecades`: Object of class `"numeric"` ~~

`estimatedDistance`: Object of class `"numeric"` ~~

`parentPeakPosition`: Object of class `"numeric"` ~~

`parentPeakSize`: Object of class `"numeric"` ~~

`fittingDeviance`: Object of class `"numeric"` ~~

`fixedModel`: Object of class `"logical"` ~~

`fixedPars`: Object of class `"list"` ~~

`generationsDistance`: Object of class `"numeric"` ~~

heights: Object of class "list" ~~
generations: Object of class "numeric" ~~
binning: Object of class "logical" ~~
breaks: Object of class "numeric" ~~
dataSmooth: Object of class "logical" ~~
smoothWindow: Object of class "numeric" ~~
parStart: Object of class "list" ~~
dataMatrix: Object of class "matrix" ~~
dataPoints: Object of class "data.frame" ~~
modelPoints: Object of class "data.frame" ~~
model: Object of class "function" ~~
residFun: Object of class "function" ~~
lmOutput: Object of class "nls.lm" ~~
numberOfPeaks: Object of class "numeric" ~~

Methods

plot Basic plots for proliferationFittingData objects. *Usage:* plot(proliferationFittingData, main="Original

show Display details about the proliferationFittingData object.

summary Return a descriptive summary about the proliferationFittingData object.

Data Return the flowFrame object.

coef Return coefficients of the model.

confint Return confidence intervals of the model.

Author(s)

Davide Rambaldi

See Also

proliferationFitting

Examples

```
showClass("proliferationFittingData")
if(require(flowFitExampleData)){
  data(PKH26data)
  parent.fitting <-  parentFitting(PKH26data[[1]], "FL2-Height LOG")
 my.fit <- proliferationFitting(PKH26data[[2]], "FL2-Height LOG", parent.fitting@parentPeakPosition, parent.fit
  my.fit
  summary(my.fit)
  confint(my.fit)
  coef(my.fit)
  plot(my.fit)
  Data(my.fit)
}
```

proliferationGrid *proliferationGrid function for plotting*

Description

This function draw a proliferation grid. The grid marks the distance between cell generations calculated with the function generationsDistance

Usage

```
proliferationGrid(parentPosition,
  fittedDistance = NA, dataRange = 1024, logDecades = 4,
  lwd=1, lty=3, col=rgb(0,0,0,0.5))
```

Arguments

parentPosition	Position of the parent Peak from parentFitting
fittedDistance	You can provide the distance estimated from the proliferationFitting function
dataRange	Range of your data (number of data points in the FACS)
logDecades	Number of log decades in the FACS
lwd	Grid line size. See par
lty	Grid line type. See par
col	Grid color. See par and rgb

Author(s)

Davide Rambaldi

Examples

```
plot(c(0,1023),c(0,1000), xlim=c(0,1023),ylim=c(0,1000),  xlab="FACS CHANNEL", ylab="# OF EVENTS", main="A flowF
 # create a grid with parent at 800
 proliferationGrid(1000, dataRange=1024, logDecades=4)
```

`proliferationIndex` *proliferation index calculator*

Description

Proliferation index calculator. Proliferation index is calculated as the sum of the cells in all generations including the parental divided by the computed number of original parent cells theoretically present at the start of the experiment. It is a measure of the fold increase in cell number in the culture over the course of the experiment.

Usage

```
proliferationIndex(object)
```

Arguments

`object`	An object of class `proliferationFittingData`

Details

The formula is: $\frac{\sum_0^i N_i}{\sum_0^i N^i/2^i}$ Where i is the generation number (parent generation = 0). In the absence of proliferation, that is, when all cells are in the parent generation, the formula gives: $\frac{N_0}{N_0/2^0} = 1$ defining the lower limit of the PI.

Value

return a `numeric`

Author(s)

Davide Rambaldi

References

1. Munson ME. An improved technique for calculating relative response in cellular proliferation experiments. Cytometry A. 2010 Oct;77(10):909-10. doi: 10.1002/cyto.a.20935. Erratum in: Cytometry A. 2010 Dec;77(12):1177. PubMed PMID: 21290464.

See Also

`proliferationFitting` `proliferationFittingData-class`

Examples

```
# load data
if(require(flowFitExampleData)){
  data(PKH26data)
  parent.fitting <-  parentFitting(PKH26data[[1]], "FL2-Height LOG")
 my.fit <- proliferationFitting(PKH26data[[2]], "FL2-Height LOG", parent.fitting@parentPeakPosition, parent.fit
  my.index <- proliferationIndex(my.fit)
}
```

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