Package 'flowPloidy'

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Title Analyze flow cytometer data to determine sample ploidy

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Description Determine sample ploidy via flow cytometry histogram analysis. Reads Flow Cytometry Standard (FCS) files via the flowCore bioconductor package, and provides functions for determining the DNA ploidy of samples based on internal standards.

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`browseFlowHist` *browseFlowHist*

Description

Visually assess and correct histogram fits

Usage

```
browseFlowHist(flowList, debug = FALSE)
```

Arguments

`flowList`	either a `FlowHist` object, or a list of `FlowHist` objects
`debug`	boolean, turns on debugging messages

Details

Visually assess histogram fits, correcting initial values, and selecting model components.

This function will open a browser tab displaying the first `FlowHist` object from the argument `flowList`. Using the interface, the user can modify the starting values for the histogram peaks, select different debris model components, toggle the linearity option, select which peak to treat as the standard, and, if multiple standard sizes are available, select which one to apply.

See the "Getting Started" vignette for a tutorial introduction.

Value

Returns the list of `FlowHist` objects, updated by any changes made in the GUI.

Author(s)

Tyler Smith

Examples

```
library(flowPloidyData)
batch1 <- batchFlowHist(flowPloidyFiles(), channel = "FL3.INT.LIN")
## Not run:
batch1 <- browseFlowHist(batch1)

## End(Not run)
```

`DebrisModels` *Histogram Debris Models*

Description

Implementation of debris models described by Bagwell et al. (1991).

Usage

```
getSingleCutValsBase(intensity, xx, first.channel)

getMultipleCutVals(intensity, first.channel)
```

Arguments

`intensity`	a numeric vector, the histogram intensity in each channel
`xx`	an integer vector, the ordered channels corresponding to the values in 'intensity'.
`first.channel`	integer, the lowest bin to include in the modelling process. Determined by the internal function `fhStart`.

Value

`getSingleCutVals`, the vectorized function built from getSingleCutValsBase, returns the fixed `SCvals` for the histogram.

`getMultipleCutVals`, a vectorized function, returns the fixed `MCvals` for the histogram.

Single Cut Model

This is the theoretical probability distribution of the size of pieces formed by a single random cut through an ellipsoid. In other words, we assume that the debris is composed of nuclei pieces generated by cutting a subset of the nuclei in a sample into two pieces.

The model is:

$$S(x) = a \sum_{j=x+1}^{n} \sqrt[3]{j} Y_j P_s(j, x)$$

1. `x` the histogram channel that we're estimating the debris value for.
2. `SCaP` the amplitude parameter.
3. `Y_j` the histogram intensity for channel j.

where P_s(j, x) is the probability of a nuclei from channel j falling into channel x when cut. That is, for j > x, the probability that fragmenting a nuclei from channel j with a single cut will produce a fragment of size x. This probability is calculated as:

$$P_s(j, x) = \frac{2}{(\pi j \sqrt{(x/j)(1 - x/j)}}$$

This model involves a recursive calculation, since the fitted value for channel x depends not just on the intensity for channel x, but also the intensities at all channels > x. I deal with this by pre-calculating the raw values, which don't actually depend on the only parameter, `SCaP`. These raw values are stored in the `histData` matrix (which is a slot in the `FlowHist` object). This must be accomodated by treating `SCvals` as a 'special parameter' in the `ModelComponent` definition. See that help page for details.

Multiple-Cut Model

The Multiple-Cut model extends the Single-Cut model by assuming that a single nuclei may be cut multiple times, thus creating more than two fragments.

The model is:

$$S(x) = MCaPe^{-kx} \sum_{j=x+1}^{n} Y_j$$

1. `x` the histogram channel that we're estimating the debris value for.
2. `k` an exponential fitting parameter
3. `MCaP` the amplitiude parameter
4. `Y_j` the histogram intensity for channel j.

This model involves another recursive or "histogram-dependent" component. Again, the sum is independent of the fitted parameters, so we can pre-compute that and add it to the `histData` slot, in the column `MCvals`. This is treated as a 'special parameter' when the Multiple-Cut model is applied, so we only need to fit the parameters k and MCaP.

Debris Models and Gating

The debris models assume that all debris is composed of nuclei (G1 and G2), that have been cut into 2 or more fragments. In actual practice, at least when working with plant cells, the debris likely also includes other cellular debris, including secondary compounds. This non-nuclear debris may take up, and interact with, the stain in unpredictable ways. In extreme cases, such as the Vaccinium

example in the "flowPloidy Getting Started" vignette, this cellular debris can completely obscure the G1 and G2 peaks, requiring gating.

The ideal gate would be one that excludes all of the non-nuclear debris, and none of the nuclear debris (i.e., the nuclei fragments). If we could accomplish this, then gating would improve our model-fitting. Leaving non-nuclear debris in the data will result in it getting fit by some combination of the model components, with a negative impact on their accuracy. On the other hand, excluding nuclear debris will reduce the information used to fit the SC or MC components, which will also reduce model accuracy.

Of course, we can't define an ideal gate, anymore than we can optimize our sample preparation such that our histograms are completely free of debris. As a practical approach, we recommend avoiding gating whenever possible, and taking a conservative approach when it is unavoidable.

Author(s)

Tyler Smith

References

Bagwell, C. B., Mayo, S. W., Whetstone, S. D., Hitchcox, S. A., Baker, D. R., Herbert, D. J., Weaver, D. L., Jones, M. A. and Lovett, E. J. (1991), DNA histogram debris theory and compensation. Cytometry, 12: 107-118. doi: 10.1002/cyto.990120203

Examples

```
## This is an internal function, called from setBins()
## Not run:
  ## ...
  SCvals <- getSingleCutVals(intensity, xx, startBin)
  MCvals <- getMultipleCutVals(intensity, startBin)
  ## ...
  fhHistData(fh) <- data.frame(xx = xx, intensity = intensity,
                           SCvals = SCvals, MCvals = MCvals,
                           DBvals = DBvals, TRvals = TRvals,
                           QDvals = QDvals, gateResid = gateResid)
  ## ...

## End(Not run)
```

`fhAccessors` *FlowHist Accessors*

Description

Functions to access slot values in `FlowHist` objects

Usage

```
fhGate(fh)

fhLimits(fh)

fhSamples(fh)
```

```
fhTrimRaw(fh)

fhPeaks(fh)

fhInit(fh)

fhComps(fh)

fhModel(fh)

fhSpecialParams(fh)

fhArgs(fh)

fhNLS(fh)

fhCounts(fh)

fhCV(fh)

fhRCS(fh)

fhFile(fh)

fhName(fh)

fhChannel(fh)

fhBins(fh)

fhLinearity(fh)

fhDebris(fh)

fhHistData(fh)

fhRaw(fh)

fhStandards(fh)

fhStdPeak(fh)

fhStdSelected(fh)

fhStdSizes(fh)

fhOpts(fh)

fhG2(fh)

fhAnnotation(fh)
```

```
fhFail(fh)
```

Arguments

fh	a FlowHist

Details

For normal users, these functions aren't necessary. Overly curious users, or those wishing to hack on the code, may find these useful for inspecting the various bits and pieces inside a FlowHist object.

The versions of these functions that allow modification of the FlowHist object are not exported. Functions are provided for users to update FlowHist objects in a safe way.

Value

Used to access a slot, returns the value of the slot. Used to update the value of a slot, returns the updated FlowHist object.

Author(s)

Tyler Smith

Examples

```
library(flowPloidyData)
fh1 <- FlowHist(file = flowPloidyFiles()[1], channel = "FL3.INT.LIN")
fhModel(fh1) ## prints the model to screen
```

---

fhAnalyze *fhAnalyze*

Description

Complete non-linear regression analysis of FlowHist histogram data

Usage

```
fhAnalyze(fh, verbose = TRUE)
```

Arguments

fh	a FlowHist object
verbose	boolean, set to FALSE to turn off logging messages

Details

Completes the NLS analysis, and calculates the modelled events and CVs for the result.

Value

a FlowHist object with the analysis (nls, counts, cv, RCS) slots filled.

Author(s)

Tyler Smith

See Also

FlowHist

Examples

```
library(flowPloidyData)
fh1 <- FlowHist(file = flowPloidyFiles()[1], channel = "FL3.INT.LIN")
fh1 <- fhAnalyze(fh1)
```

---

fhDoCounts *Calculcate* FlowHist *nuclei counts*

Description

Uses the fitted NLS model for a FlowHist object to calculate the cell counts for the G1 peak, G2 peak, and S-phase model components. The actual values are generated by numerical integration of the model components.

Usage

```
fhDoCounts(fh)
```

Arguments

fh	a FlowHist object

Value

The updated FlowHist object with the counts slot updated.

Author(s)

Tyler Smith

See Also

integrate, fhDoCV fhDoNLS, fhDoRCS.

fhDoCV *Calculate CVs from a* FlowHist *object*

Description

Extracts the model parameters (G1 peak means and standard deviations) and calculates the CVs. It also calculates the standard errors for the peak ratios.

Usage

```
fhDoCV(fh)
```

Arguments

fh	a FlowHist object

Details

Note that the standard errors here are in fact the SE for the model fit to the particular data set, NOT the SE for the DNA content ratio. In other words, it's a measure of how well the model has fit the data, not a measure of confidence in the actual amount of DNA in the original samples. It's almost always very small, even with very noisy data.

Value

The updated FlowHist object.

Author(s)

Tyler Smith

See Also

deltaMethod, fhDoCounts, fhDoNLS, fhDoRCS.

fhDoNLS *Fit the NLS model for a* FlowHist *model*

Description

Constructs the call to nlsLM for the FlowHist object.

Usage

```
fhDoNLS(fh)
```

Arguments

fh	a FlowHist object

Value

The FlowHist object with the NLS slot updated to include the results of the analysis

Author(s)

Tyler Smith

See Also

nlsLM, fhDoCV, fhDoRCS, fhDoCounts

---

fhDoRCS *Calculate the Residual Chi-Square for a FlowHist object*

Description

Calculate the Residual Chi-Square value for a FlowHist model fit.

Usage

```
fhDoRCS(fh)
```

Arguments

fh	a FlowHist object

Value

The updated FlowHist object.

Overview

The algorithm used to fit the non-linear regression model works by adjusting the model parameters to minimize the Chi-Square value for the resulting fit. The Chi-Square value calculates the departure of observed values from the values predicted by the fitted model:

$$\mathrm{X}^2 = \sum \frac{(observed(x) - predicted(x))^2}{observed(x)}$$

This would make the Chi-Square value a natural choice for an index to determine the overall goodness-of-fit of the model. However, the Chi-Square value is sensitive to the number of data points in our histogram. We could aggregate the same data into 256, 512 or 1024 bins. All else being equal, the analysis based on 256 bins would give us a lower Chi-Square value than the analyses that use more bins, despite providing essentially identical results.

Bagwell (1993) suggested using the Reduced Chi-Square (RCS) value as an superior alternative. It is defined as:

$$RCS = \frac{\mathrm{X}^2}{n - m}$$

Where n is the number of data points (bins), and m is the number of model parameters. Thus, we correct for the inflation of the Chi-Square value that obtains for higher numbers of bins. At

the same time, we introduce a penalty for increasing model complexity, increasing the Chi-Square value proportional to the number of model parameters. This helps us protect against over-fitting the model.

Guidelines

As a rule of thumb, RCS values below 0.7 suggest over-fitting, and above 4.0 suggest a poor fit.

These are guidelines only, and should not be treated as significance tests. From a statistical perspective, there is limited value to a 'goodness-of-fit' index for a single model. In other contexts we'd compare several competing models to determine which is better. For this application, the RCS is serving as a rough sanity check.

Additionally, the absolute value of the RCS is influenced by particular design decisions I made in writing the model-fitting routines. Consequently, other, equally valid approaches may yield slightly different values (Rabinovitch 1994).

With this in mind, as long as the values are close to the ideal range 0.7-4.0, we can be reasonably confident that our anlaysis is acceptable. If we get values outside this range, it is a caution that we ought to carefully inspect our model fit, to make sure it appears sensible; the results may still be fine.

The most common issue identified by extreme RCS values is poor fitting of the debris component. Occassionally, an otherwise sensible looking model fit will produce extremely high RCS values. Switching from Single-Cut to Multiple-Cut, or vice versa, will often provide a much better fit, with a corresondingly lower RCS value. Visually, the fit may not look much different, and usually the model parameters don't change much either way.

Author(s)

Tyler Smith

References

Bagwell, C.B., 1993. Theoretical aspects of flow cytometry data analysis. pp.41-61 in Clinical flow cytometry: principles and applications. Baltimore: Williams & Wilkins.

Rabinovitch, P. S. 1994. DNA content histogram and cell-cycle analysis. Methods in Cell Biology 41:263-296.

See Also

`fhDoCV`, `fhDoNLS`, `fhDoCounts`, `DebrisModels`

`fhMetadata` *Display metadata present in an FCS file*

Description

Displays a selection of potentially useful metadata fields from the FCS data file, and a summary of the data channels. Useful for selecting the the `channel` argument in `FlowHist`, finding a starting value for `trimRaw` (when needed), and identifying the parameter to use for the sample name.

Usage

```
viewFlowChannels(file, emptyValue = TRUE, truncate_max_range = TRUE)

fhMetadata(file, emptyValue = TRUE, truncate_max_range = TRUE)
```

Arguments

file	character, the name of an FCS data file; or the name of a FlowHist object.
emptyValue	boolean, passed to read.FCS, needed to deal with unusual FCS file formats. Default is TRUE - if your file loads without errors, then don't change this value
truncate_max_range	boolean, passed to read.FCS.

Details

The 'top' column in the Flow Channels table displays the 99th percentile value for that parameter. For flow cytometers that require the trimRaw argument, this may be a reasonable starting place. See FlowHist.

The 'metadata' table includes a selection of parameters stored in the FCS file. Different machines include different fields here. I've tried to select ones that are most likely to be useful. You can always all the metadata with fhRaw, i.e., 'fhRaw(fh)@description'.

Value

A list of

Author(s)

Tyler Smith

See Also

FlowHist

Examples

```
library(flowPloidyData)
fhMetadata(flowPloidyFiles()[1])

## retained for now, but viewFlowChannels will be removed from future
## relases:
viewFlowChannels(flowPloidyFiles()[1])
```

fhModels *Building Flow Histogram Models*

Description

Functions for assembling non-linear regression models for FlowHist objects.

Usage

```
addComponents(fh)

dropComponents(fh, components)

setLimits(fh)

makeModel(fh, env = parent.frame())
```

Arguments

fh	a FlowHist object
components	character, a vector of ModelComponent names.
env	an R environment. Don't change this, it's R magic to keep the appropriate environment in scope when building our model.

Details

addComponents examines the model components in fhComponents and includes the ones that pass their includeTest.

dropComponents removes a component from the FlowHist model

setLimits collates the parameter limits for the model components included in a FlowHist object. (could be called automatically from addComponents, as it already is from dropComponents?)

makeModel creates a model out of all the included components.

Value

The updated FlowHist object.

Author(s)

Tyler Smith

fhStart — *Calculate the where to start analysis for a* FlowHist *histogram*

Description

We exclude the first five bins at the outset (as part of the function setBins. For some flow cytometers, these values contain very high spikes that are an artifact of compensation, and are not useful data.

Usage

```
fhStart(intensity)
```

Arguments

intensity	numeric, the fluorescence intensity channel bins

Details

After that, we call fhStart to skip to the highest value in the first 10 non-zero bins, and ignore everything below that. The motivation here is the same - to get out beyond the noisy bins and into the actual data we're trying to fit.

Value

an integer, the index of the first intensity element to include in the actual model fitting. That is, everything from startBin to the end of intensity gets fit in the model, everything below startBin is ignored.

Author(s)

Tyler Smith

findPeaks — *findPeaks*

Description

Locate potential peaks in histogram data

Usage

```
findPeaks(fh, window = 20, smooth = 20)

cleanPeaks(fh, window = 20, debrisLimit = 40)
```

Arguments

fh	a FlowHist object
window	an integer, the width of the moving window to use in identifying local maxima via runmax
smooth	an integer, the width of the moving window to use in removing noise via runmean
debrisLimit	an integer value. Peaks with fluorescence values less than debrisLimit will be ignored by the automatic peak-finding algorithm.

Details

Peaks are defined as local maxima in the vector of values, using a moving window. Note that these are used in the context of finding starting values - accuracy isn't important, we just need something 'close-enough' that the nls algorithm will be able to find the correct value.

Utility functions for use internally by flowPloidy; not exported and won't be visible to users. Usually invoked from within FlowHist.

Note that there is a trade-off between accuracy in detected peaks, and avoiding noise. Increasing the value of smooth will reduce the amount of 'noise' that is included in the peak list. However, increasing smoothing shifts the location of the actual peaks. Most of the time the default values provide an acceptable compromise, given we only need to get 'close enough' for the NLS optimization to find the true parameter values. If you'd like to explore this, the internal (unexported) function fhPeakPlot may be useful.

cleanPeaks filters the output of findPeaks to:

- remove duplicates, ie., peaks with the same intensity that occur within window positions of each other. Otherwise, findPeaks will consider noisy peaks without a single highest point to be multiple distinct peaks.
- drop G2 peaks. In some cases the G2 peak for one sample will have greater intensity than the G1 peak for another sample. We correct for this by removing detected peaks with means close to twice that of other peaks. This step is skipped for endopolyploidy analysis (i.e., when G2 == FALSE).
- ignore noise, by removing peaks with fluorescence < debrisLimit. The default is 40, which works well for moderate-to-large debris fields. You may need to reduce this value if you have clean histograms with peaks below 40. Note that this value does not affect peaks selected manually.

Value

Returns a matrix with two columns:

mean the index position of each potential peak

height the height (intensity) of the peak at that index position

Author(s)

Tyler Smith

Examples

```
## Not run:
set.seed(123)
test.dat <-(cumsum(runif(1000, min = -1)))
plot(test.dat, type = 'l')
test.peaks <- flowPloidy::findPeaks(test.dat, window = 20)
points(test.peaks, col = 'red', cex = 2)

## End(Not run)
```

FlowHist *FlowHist*

Description

Creates a FlowHist object from an FCS file, setting up the histogram data for analysis.

Usage

```
FlowHist(
  file,
  channel,
  bins = 256,
  analyze = TRUE,
  linearity = "variable",
  debris = "SC",
  samples = 2,
  pick = FALSE,
  standards = 0,
  g2 = TRUE,
  debrisLimit = 40,
  truncate_max_range = TRUE,
  trimRaw = 0,
  nameField = "GUID",
  ...
)

batchFlowHist(files, channel, verbose = TRUE, ...)
```

Arguments

file	character, the name of the single file to load
channel	character, the name of the data column to use
bins	integer, the number of bins to use to aggregate events into a histogram
analyze	logical, if TRUE the model will be analyzed immediately
linearity	character, either "variable", the default, or "fixed". If "fixed", linearity is fixed at 2; if "variable", linearity is fit as a model parameter.
debris	character, either "SC", the default, "MC", or "none", to set the debris model component to the Single-Cut or Multi-Cut models, or to not include a debris component (such as for gated data).

samples	integer; the number of samples in the data. Default is 2 (unknown and standard), but can be set to 3 if two standards are used, or up to 6 for endopolyploidy analysis.
pick	logical; if TRUE, the user will be prompted to select peaks to use for starting values. Otherwise (the default), starting values will be detected automatically.
standards	numeric; the size of the internal standard in pg. When loading a data set where different samples have different standards, a vector of all the standard sizes. If set to 0, calculation of pg for the unknown sample will not be done.
g2	a logical value, default is TRUE. Should G2 peaks be included in the model?
debrisLimit	an integer value, default is 40. Passed to cleanPeaks. Peaks with fluorescence values less than debrisLimit will be ignored by the automatic peak-finding algorithm. Used to ignore the debris often found at the left side of the histogram.
truncate_max_range	logical, default is TRUE. Can be turned off to avoid truncating extreme positive values from the instrument. See read.FCS for details.
trimRaw	numeric. If not 0, truncate the raw intensity data to below this threshold. Necessary for some cytometers, which emit a lot of (nearly) empty data channels.
nameField	string, default is "GUID", which field to use for the sample name. Check fhMetadata for other likely options.
...	additional arguments passed from batchFlowHist to FlowHist, or to assorted helper functions. See findPeaks (arguments window and smooth)
files	character, a vector of file names to load, or a single character value giving the path to a directory; if the latter, all files in the directory will be loaded
verbose	logical; if TRUE, batchFlowHist will list files as it processes them.

Details

For most uses, simpling calling FlowHist with a file, channel, and standards argument will do what you need. The other arguments are provided for optional tuning of this process. In practice, it's easier to correct the model fit using browseFlowHist than to determine 'perfect' values to pass in as arguments to FlowHist.

Similarly, batchFlowHist is usually used with only the files, channel, and standards arguments.

NOTE: the raw data emitted by some Flow Cytometers includes a small proportion of very high values in some channels. This generates histograms that are strongly skewed to the left, and mostly empty in the central and right side. We deal with that in flowPloidy by trimming off these upper bins manually. Which means you need to set the threshold via the trimRaw argument. The output of fhMetadata, particularly the top column of the FlowChannel table, may provide a useful starting point for this.

The flow cytometers we use don't do this, so I don't have direct experience. From analyzing files submitted by flowPloidy users, the empty upper channels are clearly distinct from the actual data. The analysis output does not appear to be sensitive to the specific value of trimRaw, so long as the retained data fills the histogram without being clipped at the right side.

In operation, FlowHist starts by reading an FCS file (using the function read.FCS internally). This produces a flowFrame object, which we extend to a FlowHist object as follows:

1. Extract the fluorescence data from channel.
2. Remove the top bin, which contains off-scale readings we ignore in the analysis.

3. Remove negative fluorescence values, which are artifacts of instrument compensation
4. Removes the first 5 bins, which often contain noisy values, probably further artifacts of compensation.
5. aggregates the raw data into the desired number of bins, as specified with the `bins` argument. The default is 256, but you may also try 128 or 512. Any integer is technically acceptable, but I wouldn't stray from the default without a good reason. (I've never had a good reason!)
6. identify model components to include. All `FlowHist` objects will have the single-cut debris model and the G1 peak for sample A, and the broadened rectangle for the S-phase of sample A. Depending on the data, additional components for the G2 peak and sample B (G1, G2, s-phase) may also be added. The `debris` argument can be used to select the Multi-Cut debris model instead, or this can be toggled in `browseFlowHist`
7. Build the NLS model. All the components are combined into a single model.
8. Identify starting values for Gaussian (G1 and G2 peaks) model components. For reasonably clean data, the built-in peak detection is ok. You can evaluate this by plotting the `FlowHist` object with the argument `init = TRUE`. The easiest way to fix bad peak detection is via the `browseFlowHist` interface. You can also play with the `window` and `smooth` arguments (which is tedious!), or pick the peaks visually yourself with `pick = TRUE`.
9. Finally, we fit the model and calculate the fitted parameters. Model fitting is suppressed if the `analyze` argument is set as `FALSE`

Value

`FlowHist` returns a `FlowHist` object.

`batchFlowHist` returns a list of `FlowHist` objects.

Slots

`raw` a flowFrame object containing the raw data from the FCS file

`name` character, the name of the sample, used in plots and other summaries

`channel` character, the name of the data column to use

`bins` integer, the number of bins to use to aggregate events into a histogram

`linearity` character, either "fixed" or "variable" to indicate if linearity is fixed at 2 or fit as a model parameter

`debris` character, either "SC" or "MC" to indicate if the model should include the single-cut or multi-cut model

`gate` logical, a vector indicating events to exclude from the analysis. In normal use, the gate will be modified via interactive functions, not set directly by users.

`trimRaw` numeric, the threshold for trimming/truncating raw data before binning. The default, 0, means no trimming will be done.

`histdata` data.frame, the columns are the histogram bin number (xx), florescence intensity (intensity), and the raw single-cut and multi-cut debris model values (SCvals and MCvals), and the raw doublet, triplet and quadruplet aggregate values (DBvals, TRvals, and QDvals). The debris and aggregate values are used in the NLS fitting procedures.

`peaks` matrix, containing the coordinates used for peaks when calculcating initial parameter values.

`opts` list, currently unused. A convenient place to store flags when trying out new options.

`comps` a list of `ModelComponent` objects included for these data.

`model` the function (built from `comps`) to fit to these data.

`limits` list, a list of lower and upper bounds for model parameters

`init` a list of initial parameter estimates to use in fitting the model.

`nls` the nls object produced by the model fitting

`counts` a list of cells counted in each peak of the fitted model

`CV` a list of the coefficients of variation for each peak in the fitted model.

`RCS` numeric, the residual chi-square for the fitted model.

`samples` numeric, the number of samples included in the data. The default is 2 (i.e., unknown and standard), but if two standards are used it should be set to 3. It can be up to 6 for endopolyploidy analysis, and can be interactively increased (or decreased) via `browseFlowHist`

`standards` a `FlowStandards` object.

`g2` logical, if TRUE the model will include G2 peaks for each sample (as long as the G1 peak is less than half-way across the histogram). Set to FALSE to drop the G2 peaks for endopolyploidy analyses.

`annotation` character, user-added annotation for the sample.

`fail` logical, set by the user via the `browseFlowHist` interface to indicate the sample failed and no model fitting should be done.

Author(s)

Tyler Smith

Examples

```
library(flowPloidyData)
fh1 <- FlowHist(file = flowPloidyFiles()[1], channel = "FL3.INT.LIN")
fh1
batch1 <- batchFlowHist(flowPloidyFiles(), channel = "FL3.INT.LIN")
batch1
```

`flowPloidy` *flowPloidy: A package for analyzing Flow Cytometry Histograms*

Description

The flowPloidy package provides functions for reading and analyzing flow cytometry histograms. Specifically, it builds and fits a non-linear regression model, from which peak parameters (mean, CV) can be estimated. In normal use, samples will include a co-chopped size standard. Comparing the unknown peak mean to the standard peak mean, we determine the genome content for the unknown sample.

Details

Please see the vignettes for an overview: `histogram-tour` and `flowPloidy-gettingStarted`. To follow along with the examples in the vignettes, and also in the documentation listed below, you'll need to install the `flowPloidyData` package from Bioconductor.

Primary Functions

Most users will need only the functions:

1. `fhMetadata`, to determine the name of the primary data channel to use.
2. `batchFlowHist`, to load a list of FCM files into R.
3. `browseFlowHist`, to review and correct the model-fitting for the files, using an interactive graphical browser.
4. `tabulateFlowHist`, to extract the results and save them to a file.

Additional User Tools

Additional functions for inspecting and manipulating `FlowHist` objects and analyses:

1. `FlowHist`, to load a single FCM file into R.
2. `plot.FlowHist`, for plotting the data and fitted model using base R graphics.
3. `pickInit`, to interactively select initial peak estimates, using base R graphics (this is more easily accomplished via `browseFlowHist`.
4. `setBins`, to reset the bins, selecting the number of bins to use.
5. `fhAnalyze`, to (re-)analyze the FCM data, presumably after updating the settings for a file. Most functions that make changes that would require reanalysis provide the option to do this automatically, and this option is usually the default.
6. `updateFlowHist`, to update the settings for an FCM file.

Internal Functions

These functions aren't necessary for regular use, and are not exported for direct access by users. They may be useful to those interested in modifying or extending the package, or just curious about details:

1. `fhAccessors`, for inspecting the slots of a `FlowHist` object
2. `findPeaks`, the functions which perform the initial peak detection
3. `ModelComponent`, the S4 class for the various model components used in constructing the non-linear regression model.
4. `GaussianComponents`, a description of the Gaussian model component that is fit to cell peaks.
5. `DebrisModels`, a description of the debris model components.
6. `FlowStandards`, the S4 class for the size standard data.
7. `plotFH`, a low-level plotting function for displaying raw histogram data.
8. `resetFlowHist`, a function for safely resetting various portions of a `FlowHist` object.
9. `flowModels`, functions for assembling `ModelComponent` into a complete model.
10. `fhDoNLS`, `fhDoCounts`, `fhDoCV`, `fhDoRCS`: the functions which actually complete the model fitting and extract the parameters of interest.
11. `setGate`, the function for applying a gate to a `FlowHist` object.

Author(s)

Tyler Smith

See Also

Useful links:

- https://github.com/plantarum/flowPloidy
- Report bugs at https://github.com/plantarum/flowPloidy/issues

---

FlowStandards *An S4 class to represent internal standard details for* FlowHist *objects*

Description

The sizes slot is set in FlowHist or batchFlowHist. The other values are updates through interaction with the browseFlowHist GUI.

Usage

```
stdSizes(std)

stdSelected(std)

stdPeak(std)
```

Arguments

std	a FlowStandards object

Value

stdSizes, stdSelected and stdPeak return the corresponding slot values

Slots

sizes numeric, the size (in pg) of the internal size standard. Can be a vector of multiple values, if the sample is part of a set that included different standards for different samples.

selected numeric, the size (in pg) of the internal size standard actually used for this sample. Must be one of the values in the sizes slot.

peak character, "A" or "B", indicating which of the histogram peaks is the size standard.

Examples

```
library(flowPloidyData)
fh1 <- FlowHist(file = flowPloidyFiles()[1], channel = "FL3.INT.LIN",
                standards = c(1.96, 5.43))
fhStandards(fh1)  ## display standards included in this object
stdSizes(fhStandards(fh1))  ## list standard sizes
```

gauss *Gaussian model components*

Description

Components for modeling Gaussian features in flow histograms

Arguments

a1, a2, b1, b2, c1, c2	area parameters
Ma, Mb, Mc	curve mean parameter
Sa, Sb, Sc	curve standard deviation parameter
xx	vector of histogram intensities
linearity	numeric, the ratio of G2/G1 peak means. When linearity is fixed, this is set to 2. Otherwise, it is fit as a model parameter bounded between flowPloidy:::linL and flowPloidy:::linH.

Details

Typically the complete models will contain fA1 and fB1, which model the G1 peaks of the sample and the standard. In many cases, they will also contain fA2 and fB2, which model the G2 peaks. The G2 peaks are linked to the G1 peaks, in that they require some of the parameters from the G1 peaks as well (mean and standard deviation).

If the linearity parameter is set to "fixed", the G2 peaks will be fit as exactly 2 times the mean of the G1 peaks. If linearity is set to "variable", the ratio of the G2 peaks to the G1 peaks will be fit as a model parameter with an initial value of 2, and constrained to the range 1.5 – 2.5. (The range is coded as linL and linH. If in doubt, check the values of those, i.e., flowPloidy:::linL, flowPloidy:::linH, to be sure Tyler hasn't changed the range without updating this documentation!!)

Additionally, for each set of peaks (sample and standard(s)), a broadened rectangle component is included to model the S-phase. At present, this is component has a single parameter, the height of the rectangle. The standard deviation is fixed at 1. Allowing the SD to vary in the model fitting doesn't make an appreciable difference in my tests so far, so I've left it simple.

Value

NA

Author(s)

Tyler Smith

ModelComponent *An S4 class to represent model components*

Description

ModelComponent objects bundle the actual mathematical function for a particular component with various associated data necesarry to incorporate them into a complete NLS model.

Details

To be included in the automatic processing of potential model components, a ModelComponent needs to be added to the variable fhComponents.

Slots

name character, a convenient name with which to refer to the component

desc character, a short description of the component, for human readers

color character, the color to use when plotting the component

includeTest function, a function which takes a single argument, a FlowHist object, and returns TRUE if the component should be included in the model for that object.

function function, a single-line function that returns the value of the component. The function can take multiple arguments, which usually will include xx, the bin number (i.e., x value) of the histogram. The other arguments are model parameters, and should be included in the initParams function.

initParams function, a function with a single argument, a FlowHist object, which returns named list of model parameters and their initial estimates.

specialParams list, a named list. The names are variables to exclude from the default argument list, as they aren't parameters to fit in the NLS procedure, but are actually fixed values. The body of the list element is the object to insert into the model formula to account for that variable. Note that this slot is not set directly, but should be provided by the value returned by specialParamSetter (which by default is list(xx = substitute(xx))).

specialParamSetter function, a function with one argument, the FlowHist object, used to set the value of specialParams. This allows parameters to be declared 'special' based on values in the FlowHist object. The default value for this slot is a function which returns list(xx = substitute(xx))

paramLimits list, a named list with the upper and lower limits of each parameter in the function.

doCounts logical, should cell counts be evaluated for this component? Used to exclude the debris models, which don't work with R's Integrate function.

Coding Concepts

See the source code file models.R for the actual code used in defining model components. Here are a few examples to illustrate different concepts.

We'll start with the G1 peaks. They are modelled by the components fA1 and fB1 (for the A and B samples). The includeTest for fA1 is simply function(fh) TRUE, since there will always be at least one peak to fit. fB1 is included if there is more than 1 detected peak, and the setting samples is more than 1, so the includeTest is

```
function(fh) nrow(fhPeaks(fh)) > 1 && fhSamples(fh) > 1
```

The G1 component is defined by the function

```
(a1 / (sqrt(2 * pi) * Sa) * exp(-((xx - Ma)^2)/(2 *
  Sa^2)))
```

with the arguments `a1`, `Ma`, `Sa`, `xx`. `xx` is treated specially, by default, and we don't need to deal with it here. The initial estimates for the other parameters are calculated in `initParams`:

```
function(fh){
  Ma <- as.numeric(fhPeaks(fh)[1, "mean"])
  Sa <- as.numeric(Ma / 20)
  a1 <- as.numeric(fhPeaks(fh)[1, "height"] * Sa / 0.45)
  list(Ma = Ma, Sa = Sa, a1 = a1)
}
```

`Ma` is the mean of the distribution, which should be very close to the peak. `Sa` is the standard distribution of the distribution. If we assume the CV is 5%, that means the `Sa` should be 5% of the distribution mean, which gives us a good first estimate. `a1` is a scaling parameter, and I came up with the initial estimate by trial-and-error. Given the other two values are going to be reasonably close, the starting value of `a1` doesn't seem to be that crucial.

The limits for these values are provided in `paramLimits`.

```
paramLimits = list(Ma = c(0, Inf), Sa = c(0, Inf), a1 =
  c(0, Inf))
```

They're all bound between 0 and Infinity. The upper bound for `Ma` and `Sa` could be lowered to the number of bins, but I haven't had time or need to explore this yet.

The G2 peaks include the `d` argument, which is the ratio of the G2 peak to the G1 peak. That is, the linearity parameter:

```
func = function(a2, Ma, Sa, d, xx){
  (a2 / (sqrt(2 * pi) * Sa * 2) *
    exp(-((xx - Ma * d)^2)/(2 * (Sa * 2)^2)))
}
```

`d` is the ratio between the G2 and G1 peaks. If `linearity = "fixed"`, it is set to 2. Otherwise, it is fit as a model parameter. This requires special handling. First, we check the `linearity` value in `initParams`, and provide a value for `d` if needed:

```
res <- list(a2 = a2)
if(fhLinearity(fh) == "variable")
    res <- c(res, d = 2)
```

Here, `a2` is always treated as a parameter, and `d` is appended to the initial paramter list only if needed.

We also need to use the `specialParamSetter` function, in this case calling the helper function `setLinearity(fh)`. This function checks the value of `linearity`, and returns the appropriate object depending on the result.

Note that we use the arguments `Ma` and `Sa` appear in the `function` slot for `fA2`, but we don't need to provide their initial values or limits. These values are already supplied in the definition of `fA1`, which is always present when `fA2` is.

NB.: This isn't checked in the code! I know fA1 is always present, but there is no automated checking of this fact. If you create a ModelComponent that has parameters that are not defined in that component, and are not defined in other components (like Ma is in this case), you will cause problems. There is also nothing to stop you from defining a parameter multiple times. That is, you could define initial estimates and limits for Ma in fA1 and fA2. This may also cause problems. It would be nice to do some sanity-checking to protect against using parameters without defining initial estimates or limits, or providing multiple/conflicting definitions.

The Single-Cut Debris component is unusual in two ways. It doesn't include the argument xx, but it uses the pre-computed values SCvals. Consequently, we must provide a function for specialParamSetter to deal with this:

```
specialParamSetter = function(fh){ list(SCvals =
substitute(SCvals)) }
```

The Multi-Cut Debris component MC is similar, but it needs to include xx as a special parameter. The aggregate component AG also includes several special parameters.

For more discussion of the debris components, see DebrisModels.

The code responsible for this is in the file models.R. Accessor functions are provided (but not exported) for getting and setting ModelComponent slots. These functions are named mcSLOT, and include mcFunc, mcColor, mcName, mcDesc, mcSpecialParams, mcSpecialParamSetter, mcIncludeTest, mcInitParams.

Examples

```
## The 'master list' of components is stored in fhComponents:
flowPloidy:::fhComponents ## outputs a list of component summaries

## adding a new component to the list:
## Not run:
fhComponents$pois <-
  new("ModelComponent", name = "pois", color = "bisque",
      desc = "A poisson component, as a silly example",
      includeTest = function(fh){
          ## in this case, we check for a flag in the opt slot
          ## We could also base the test on some feature of the
          ## data, perhaps something in the peaks or histData slots
          "pois" %in% fh@opt
      },
      func = function(xx, plam){
          ## The function needs to be complete on a single line, as it
          ## will be 'stitched' together with other functions to make
          ## the complete model.
          exp(-plam)*plam^xx/factorial(xx)
      },
      initParams = function(fh){
          ## If we were to use this function for one of our peaks, we
          ## could use the peak position as our initial estimate of
          ## the Poisson rate parameter:
          plam <- as.numeric(fhPeaks(fh)[1, "mean"])
      },
      ## bound the search for plam between 0 and infinity. Tighter
      ## bounds might be useful, if possible, in speeding up model
      ## fitting and avoiding local minima in extremes.
      paramLimits = list(plam = c(0, Inf))
  )
```

```
  ## specialParamSetter is not needed here - it will default to a
  ## function that returns "xx = xx", indicating that all other
  ## parameters will be fit. That is what we need for this example. If
  ## the component doesn't include xx, or includes other fixed
  ## parameters, then specialParamSetter will need to be provided.

  ## Note that if our intention is to replace an existing component with
  ## a new one, we either need to explicitly change the includeTest for
  ## the existing component to account for situations when the new one
  ## is used instead. As a temporary hack, you could add both and then
  ## manually remove one with \code{dropComponents}.

## End(Not run)
```

`pickInit` *Interactively select model starting values*

Description

Prompts the user to select the peaks to use as initial values for non-linear regression on a plot of the histogram data.

Usage

```
pickInit(fh)
```

Arguments

`fh`	A `FlowHist` object

Details

The raw histogram data are plotted, and the user is prompted to select the peak positions to use as starting values in the NLS procedure. This is useful when the automated peak-finding algorithm fails to discriminate between overlapping peaks, or is confused by noise.

Note that the A peak must be lower (smaller mean, further left) than the B peak. If the user selects the A peak with a higher mean than the B peak, the peaks will be swapped to ensure A is lower.

Value

`pickInit` returns the `FlowHist` object with its initial value slot updated.

Author(s)

Tyler Smith

Examples

```
library(flowPloidyData)
fh2 <- FlowHist(file = flowPloidyFiles()[2], channel = "FL3.INT.LIN")
plot(fh2, init = TRUE) ## automatic peak estimates
## Not run:
fh2 <- pickInit(fh2)   ## hand-pick peak estimates

## End(Not run)
plot(fh2, init = TRUE) ## revised starting values
```

`plot.FlowHist` *Plot histograms for FlowHist objects*

Description

Plot histograms for FlowHist objects

Usage

```
## S3 method for class 'FlowHist'
plot(x, init = FALSE, nls = TRUE, comps = TRUE, main = fhName(x), ...)
```

Arguments

`x`	a `FlowHist` object
`init`	boolean; if TRUE, plot the regression model using the initial parameter estimates over the raw data.
`nls`	boolean; if TRUE, plot the fitted regression model over the raw data (i.e., using the final parameter values)
`comps`	boolean; if TRUE, plot the individual model components over the raw data.
`main`	character; the plot title. Defaults to the filename of the `FlowHist` object.
`...`	additional arguments passed on to plot()

Value

Not applicable

Author(s)

Tyler Smith

plotFH *Plot the raw data for a FlowHist object*

Description

Creates a simple plot of the raw histogram data. Used as a utility for other plotting functions, and perhaps useful for users who wish to create their own plotting routines.

Usage

```
plotFH(fh, main = fhName(fh), ...)
```

Arguments

fh	a FlowHist object
main	character; the plot title. Defaults to the filename of the FlowHist object.
...	additional parameters passed to plot

Value

Not applicable, used for plotting

Author(s)

Tyler Smith

Examples

```
library(flowPloidyData)
fh1 <- FlowHist(file = flowPloidyFiles()[1], channel = "FL3.INT.LIN")
plotFH(fh1)
```

resetFlowHist *Reset the values in a FlowHist object*

Description

NB: This function isn't required for normal use, and isn't exported for general use. It's provided as a convenience for anyone interested in tweaking model construction and associated parameters. Regular users don't need to do this!

Usage

```
resetFlowHist(fh, from = "peaks")
```

Arguments

fh	a FlowHist object.
from	character, the point in the FlowHist process to reset from (see details).

Details

This function provides a safe way to reset the values in a FlowHist object. This is important because changing something early in the process will require updating all the dependent values in the appropriate order.

The dependency relationships are:

gate <- peaks <- comps <- limits

Consequently, changing the gate requires updating peaks, comps and limits. Changing components only requires updating the limits. Updating limits implicitly updates the model and subsequent analysis (i.e., NLS, CV, counts and RCS).

In practice, this means that if you change the components, you should call resetFlowHist to update the dependencies. i.e., resetFlowHist(fh, from = "limits").

Value

the updated FlowHist object.

Author(s)

Tyler Smith

---

setBins *setBins*

Description

(Re-)set the bins for a FlowHist object

Usage

```
setBins(fh, bins = 256)
```

Arguments

fh	a FlowHist object
bins	integer, the number of bins to use in aggregating FCS data

Details

This function sets (or resets) the number of bins to use in aggregating FCS data into a histogram, and generates the corresponding data matrix. Not exported for general use.

The histData matrix also contains the columns corresponding to the raw data used in calculating the single-cut and multiple-cut debris components, as well as the doublet, triplet, and quadruplet aggregate values. (i.e., SCvals, MCvals, DBvals, TRvals, and QDvals).

setBins includes a call to resetFlowHist, so all the model components that depend on the bins are updated in the process (as you want!).

Value

a FlowHist object, with the bins slot set to bins, and the corresonding binned data stored in a matrix in the histData slot. Any previous analysis slots are removed: peaks, comps, model, init, nls, counts, CV, RCS.

Author(s)

Tyler Smith

Examples

```
## defaults to 256 bins:
library(flowPloidyData)
fh1 <- FlowHist(file = flowPloidyFiles()[1], channel = "FL3.INT.LIN")
plot(fh1)
## reset them to 512 bins:
fh1 <- setBins(fh1, 512)
plot(fh1)
```

---

setGate *setGate*

Description

Apply a gate to a FlowHist object

Usage

```
setGate(fh, gate, refresh = TRUE)

isGated(fh)
```

Arguments

fh	a FlowHist object
gate	boolean, a vector indicating which rows in the raw data should be included (gated) in the analysis.
refresh	boolean, should the analysis be updated after applying the gate (default = TRUE)?

Details

This function is primarily book-keeping to make sure that histData and downstream calculations are appropriately updated when a gate is applied. The code for applying the gate is actually in the function setBins.

Value

setGate returns an updated FlowHist object, with the histData slot updated to account for the gate. With refresh = TRUE (default), it will also rebuild the model and complete the analysis.

isGated returns TRUE if the FlowHist object is gated.

Author(s)

Tyler Smith

See Also

setBins

tabulateFlowHist *exportFlowHist*

Description

Extract analysis results from a FlowHist object

Usage

```
tabulateFlowHist(fh, file = NULL)
```

Arguments

fh	a FlowHist object, or a list of FlowHist objects.
file	character, the name of the file to save data to

Details

A convenience function for extracting the results of the NLS curve-fitting analysis on a FlowHist object.

If fh is a single FlowHist object, a data.frame with a single row is returned. If fh is a list of FlowHist objects, a row for each object will be added to the data.frame.

If a file name is provided, the data will be saved to that file.

The columns of the returned data.frame may include:

StdPeak: which peak (A, B etc) was identified by the user as the internal standard

ratio: the ratio of the sample peak size to the standard peak size, if the standard size was set and the standard peak identified

StdSize: the size of the standard in pg, if set

pg: genome size estimate, if the sample peak was identified and the size of the standard was set

RCS: the residual Chi-Square for the model fit

a_mean, b_mean etc: the peak position for the G1 peak of each sample

a_stddev, b_stddev etc: standard devation for each G1 peak position

a1_count, b1_count etc: the cell counts for the G1 peak of each sample

a2_count, b2_count etc: the cell counts for the G2 peak of each sample

a_s_count, b_s_count etc: the cell counts for the S-phase for each sample

a_CV, b_CV etc: the coefficient of variation for each sample

linearity: the linearity value, if not fixed at 2

Note that columns are only produced for parameters that exist in your data. That is, if none of your samples have a G2 peak for the A sample, you won't get a2_count column. Similarly, if you didn't set the standard size, or identify which peak was the standard, you won't get StdPeak, ratio, StdSize, or pg columns.

Value

a data frame

Author(s)

Tyler Smith

Examples

```
library(flowPloidyData)
fh1 <- FlowHist(file = flowPloidyFiles()[1], channel = "FL3.INT.LIN")
fh1 <- fhAnalyze(fh1)
tabulateFlowHist(fh1)
```

---

updateFlowHist *updateFlowHist*

Description

Update, and optionally re-analyze, a FlowHist object

Usage

```
updateFlowHist(
  fh,
  linearity = NULL,
  debris = NULL,
  samples = NULL,
  analyze = TRUE
)
```

Arguments

fh	a FlowHist object
linearity	character, either "variable", the default, or "fixed". If "fixed", linearity is fixed at 2; if "variable", linearity is fit as a model parameter.
debris	character, either "SC", the default, or "MC", to set the debris model component to the Single-Cut or Multi-Cut models.
samples	integer, the number of samples in the data
analyze	logical, if TRUE the updated model will be analyzed immediately

Details

Allows users to switch the debris model from Single-Cut to Multi-Cut (or vice-versa), or to toggle linearity between fixed and variable.

Value

a FlowHist object with the modified values of linearity and/or debris, and, if analyze was TRUE, a new NLS fitting

Author(s)

Tyler Smith

Examples

```
## defaults to 256 bins:
library(flowPloidyData)
fh1 <- FlowHist(file = flowPloidyFiles()[1], channel = "FL3.INT.LIN")
## default is Single-Cut, change that to Multi-Cut:
fh1mc <- updateFlowHist(fh1, debris = "MC")
plot(fh1)
```

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