Package 'flowClean'

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Title flowClean

Description A quality control tool for flow cytometry data based on compositional data analysis.

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Depends R (>= 2.15.0), flowCore

Imports bit, changepoint, sfsmisc

Suggests flowViz, grid, gridExtra

License Artistic-2.0

LazyLoad yes

biocViews FlowCytometry, QualityControl, ImmunoOncology

NeedsCompilation no

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clean *clean. For cleaning flow cytometry data.*

Description

This function uses compositional data analysis to identify errant collection events.

Usage

```
clean(fF, vectMarkers, filePrefixWithDir, ext, binSize=0.01,
  nCellCutoff=500, announce=TRUE, cutoff="median", diagnostic=FALSE, fcMax=1.3)
```

Arguments

fF	flowFrame object containing experimental data to be cleaned.
vectMarkers	A vector of indices representing flow parameters to be examined. These are considered as columns in the data matrix in which cells are rows and parameters are columns. Generally this vector excludes indices for various 'scatter' parameters (e.g. 'FSC-A')
filePrefixWithDir	A string containing at least the desired name for the output flow file generated. Can include directory structure and folder ('/' or '\') characters.
ext	The file extension for the output flow file.
binSize	A number in [0,1]; represents the fraction of duration of collection per bin.
nCellCutoff	An integer; represents the minimum number of cells a population must have to be included in analysis.
cutoff	Method for determining threshold for parameter. Can be "median" (default) or in [0, 1], which is interpreted as a perecntile. Integers > 1 will be interpreted as the fluorescence value to be used for a threshold.
announce	Print completion messages.
fcMax	Maximum allowable increase relative to presumed 'good' data.
announce	If TRUE, will print message to screen if errors detected.
diagnostic	If TRUE, will make PNG of populations in time bins, and save with same prefix as specified in filePrefixWithDir.
returnVector	If desired, only return vector indicating if a given cell is 'good' or 'bad'.
nstable	The number of stable populations required to be observed during the duration of an experiment. Default is 5.

Author(s)

Kipper Fletez-Brant

References

Fletez-Brant C, Spidlen J, Brinkman R, Roederer M and Chattopadhyay P. flowClean: Automated identification and removal of fluorescence anomalies in flow cytometry data. Cytometry Part A, 2016.

See Also

The package vignette.

Examples

```
data(synPerturbed)
synPerturbed.c <- clean(synPerturbed, vectMarkers=c(5:17),
  filePrefixWithDir="sampleName", ext="fcs")
```

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synPerturbed *Synthetically Perturbed FCS.*

Description

This is a FCS file in which a subset of one parameter was artificially perturbed so as to have a much higher fluorescent intensity than the remainder of the parameter's observations.

Format

A flowFrame with 17 observables and 76466 cells.

Details

Cells during a specific time period had their fluorescent intensities increased on channel <V705-A>.

Examples

```
data(synPerturbed)
```

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