

# Package ‘flowClean’

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**Version** 1.47.0

**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 | <i>clean. For cleaning flow cytometry data.</i> |
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## 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 percentile. 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 | <i>Synthetically Perturbed FCS.</i> |
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**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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