Package ‘flowPeaks’

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Title An R package for flow data clustering
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Enhances flowCore
Description A fast and automatic clustering to classify the cells into
subpopulations based on finding the peaks from the overall
density function generated by K-means.
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adjust.flowPeaks

Adjusting the smoothing and merging behavior of the flowPeaks results

Description

Adjusting the smoothing and merging behavior of the flowPeaks results by changing the multipliers of the covariance matrix and the tolerance level for joining two peaks

Usage

adjust.flowPeaks(object, tol, h0, h, ...)

Arguments

- object: The output from the function flowPeaks
- tol: See flowPeaks
- h0: See flowPeaks
- h: See flowPeaks
- ...: Optional additional arguments. At present no additional arguments are used.

Value

It returns an updated object of class flowPeaks, the detail definition of which can be seen in flowPeaks.

Author(s)

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See Also

flowPeaks

assign.flowPeaks

Obtain the flowPeaks cluster labels with the option of identifying outliers and applying to a new data set

Description

The function takes a flowPeaks output and a new data set (or could be the same dataset that generated the flowPeaks), and compute the cluster label assignment

Usage

assign.flowPeaks(fp, A, tol=0.01, fc=0.8)
Arguments

- **fp**: an object of class flowPeaks, the output from the function `flowPeaks` or `adjust.flowPeaks`.
- **A**: A data matrix with the same number of columns as the data that generated fp.
- **tol**: All points where the probability density is less than tol (default is 1%) of the peak density of that cluster are labeled as outliers. If tol is set to 0, no outliers according to this rule. The details can be seen in the first equation of Section 2.5 in the flowPeaks manuscript (Ge et al 2012).
- **fc**: All points where the classified cluster contributes less than fc (default is 80%) of overall density are labeled as outliers. If fc is set to 0%, no outliers can be found according to this rule. The details can be seen in the second equation of Section 2.5 in the flowPeaks manuscript (Ge et al 2012).

Value

It returns the class label assignment of each data point, where -1 indicates outliers. When A is the same data that generated fp, if tol is 1 and fc is 0, the returned labels are the same as fp$peaks.cluster.

Author(s)

Yongchao Ge <yongchao.ge@gmail.com>

References


See Also

- `flowPeaks`
References


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concave

A simulated flow cytometry data with two concave shapes

Usage
data(concave)

Format

An object (concave) of data frame with rows and 3 columns and a vector (concave.cid) for the true cluster labels.

References


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evalCluster
evaluate the result of a clustering algorithm by comparing it with the gold standard

Description

This function takes the cluster labels of the two clusterings, one is based on the gold standard, the other is a candidate clustering, and compute one of the three metrics to assess the candidate clustering performance.

Usage
evalCluster(gs, cand, method=c("Rand.index","Fmeasure","Vmeasure"),
rm.gs.outliers=TRUE)
Arguments

**gs**  
A integer-valued vector of length n for the cluster labels of the gold standard clustering, where negative numbers such as -1 is for the outliers

**cand**  
A integer-valued vector of length n for the cluster label of a candidate clustering, where -1 is for the outliers

**rm.gs.outliers**  
Determining whether the outliers of the gold standard clustering should be removed in the comparison

**method**  
A single character to indicate which one of three metrics should be used to evaluate the clustering. The details are described in Ge (2012) and references mentioned in that paper

- **Rand.index**  The adjusted Rand index
- **Fmeasure**  F-measure
- **Vmeasure**  V-measure

Author(s)

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References


See Also

flowPeaks

Description

This is the core function in the flowPeaks package. It generates the output of the cluster and information associated with each cluster, which can be used by the function `plot` for visualization

Usage

`flowPeaks(x, tol=0.1, h0=1, h=1.5)`

Arguments

- **x**  
a data matrix for the flow cytometry data, it needs to have at least two rows, and the names for each column should be unique. For a flowFrame data, its `expression` matrix slot should be used as x, where only channels of interest are selected (see the example below).

- **tol**  
The tolerance (between 0 and 1) when neighboring clusters should be considered to be merged

- **h0**  
The multiplier of the variance matrix $S_0$

- **h**  
The multiplier of the variance matrix $S$
Value

It returns an object of class flowPeaks, which is a list of the following variables:

- **peaks.cluster**: An integer shows the cluster labels (between 1 and K for K clusters) for each cell. The clustering is based on the flowPeaks algorithm.
- **peaks**: A summary of the cluster information. It is a list with the following three variables:
  - cid: cluster labels, should always be 1:K;
  - w: the weights of the K clusters;
  - mu: The mean of all cells in the K clusters;
  - S: The variance matrix of the K clusters. Note that each variance matrix for each cluster has been stacked as a column vector.
- **kmeans.cluster**: An integer shows the cluster labels for the initial kmeans clustering.
- **kmeans**: A summary of the initial kmeans clustering. The meaning of the variables can be seen in the description of peaks above.
- **info**: The information that can be used for plot, and how the initial kmeans clustering and the final flowPeaks clustering are connected.
- **x**: The input data x.

Author(s)

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References


See Also

plot.flowPeaks

Examples

```r
## demonstrate how to use a flowFrame
## Not run:
require(flowCore)
samp <- read.FCS(system.file("extdata","0877488774.B08",
package="flowCore")
## do the clustering based on the asinh transformation of
## the first two FL channels
fp<-flowPeaks(asinh(samp@exprs[,3:4]))
plot(fp)

## End(Not run)
data(barcode)
fp<-flowPeaks(barcode[,c(1,3)])
plot(fp)

## to compare it with the gold standard
evalCluster(barcode.cid,fp$peaks.cluster,method="Vmeasure")
```
#to remove the outliers
fpc<-assign.flowPeaks(fp,fp$x)
plot(fp,classlab=fpc,drawboundary=FALSE,
     drawvor=FALSE,drawkmeans=FALSE,drawlab=TRUE)

#to adjust the cluster by increasing the tol,h0, h, which results
#in a smaller number of clusters
fp2<-adjust.flowPeaks(fp,tol=0.5,h0=2,h=2)
summary(fp2)
print(fp) #an alternative of using summary(fp)

---

**plot.flowPeaks**  
Plot the results generated by flowPeaks

**Description**

This function takes the results generated from flowPeaks as an input, and plot the data in 2D. These plots display the clustering structure.

**Usage**

```r
## S3 method for class 'flowPeaks'
plot(x,idx=c(1,2),drawlab=FALSE,
     cols=c("red","green3","blue","cyan","magenta","yellow","gray"),drawvor=TRUE,
     drawlocalpeaks=FALSE,drawkmeans=TRUE,drawboundary=TRUE,
     classlab, negcol, negpch,...)
```

**Arguments**

- `x`  
  An object of class flowPeaks, e.g., the output from the functions flowPeaks or adjust.flowPeaks
- `idx`  
  The index of the columns will be used to plot the clustering. idx needs to be at least length 2, and have no duplicate elements, and the values can only take from 1 to d, where d is the number of columns for the input matrix x that is used as an input of the function flowPeaks
- `drawlab`  
  The option to decide whether we should draw the cluster labels
- `cols`  
  The color specification for plotting the points in each cluster. Please note, "white" and "black" are not allowed, which are reserved for other purpose
- `drawvor`  
  Deciding whether the voronoi diagram should be drawn, only good for 2D data
- `drawlocalpeaks`  
  Deciding whether the local peaks with a triangle symbol should be drawn
- `drawkmeans`  
  Deciding whether the kmeans center with a filled circle should be drawn
- `drawboundary`  
  Deciding whether the boundary between clusters should be drawn, only good for 2D data
- `classlab`  
  Use this to replace the default class labels from x$peak.cluster, for example, the classlab may come from assign.flowPeaks
- `negcol`  
  Deciding the color of the negative, which are outliers
- `negpch`  
  Deciding the symbols for the outliers
- `...`  
  Optional additional arguments. At present no additional arguments are used.
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See Also
flowPeaks

print.flowPeaks  The display of the flowPeaks results

Description
The display of the flowPeaks results

Usage
## S3 method for class 'flowPeaks'
print(x,...)

Arguments
x  The output from the function flowPeaks
...  Optional additional arguments. At present no additional arguments are used.

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See Also
flowPeaks

summary.flowPeaks  The summary of the flowPeaks results

Description
The summary of the flowPeaks results

Usage
## S3 method for class 'flowPeaks'
summary(object,...)

Arguments
object  The output from the function flowPeaks
...  Optional additional arguments. At present no additional arguments are used.
Author(s)

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See Also

flowPeaks
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