

# Package ‘flowPeaks’

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**Title** An R package for flow data clustering

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**Depends** R (>= 2.12.0)

**Suggests** 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.

**License** Artistic-1.0

**biocViews** ImmunoOncology, FlowCytometry, Clustering, Gating

**SystemRequirements** gsl

**NeedsCompilation** yes

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adjust.flowPeaks	<i>Adjusting the smoothing and merging behavior of the flowPeaks results</i>
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**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 <a href="#">flowPeaks</a>
tol	See <a href="#">flowPeaks</a>
h0	See <a href="#">flowPeaks</a>
h	See <a href="#">flowPeaks</a>
...	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](#)

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assign.flowPeaks	<i>Obtain the flowPeaks cluster labels with the option of identifying outliers and applying to a new data set</i>
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**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 <a href="#">flowPeaks</a> or <a href="#">adjust.flowPeaks</a>
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 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**

Ge Y. et al, flowPeaks: a fast unsupervised clustering for flow cytometry data via K-means and density peak finding, 2012, Bioinformatics, 8(15):2052-8

**See Also**

[flowPeaks](#)

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barcode

*The barcode dataset*

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**Description**

A flow cytometry data that is used barcode to measure many samples simultaneously

**Usage**

```
data(barcode)
```

**Format**

An object (barcode) of data frame with 180912 rows and 3 columns and a vector (barcode.cid) for the cluster labels according to the manual gating.

**Source**

The data is a random subset of the full data set for Figure 3A of the paper (Sugar et al 2010), This subset was used to do all comparisons in the paper (Ge et al 2012) with other clustering algorithms.

**References**

Sugar I. P. and Sealfon S. C., Misty Mountain clustering: application to fast unsupervised flow cytometry gating, *BMC Bioinformatics*, 2010, 11:502.

Ge Y. et al, flowPeaks: a fast unsupervised clustering for flow cytometry data via K-means and density peak finding, 2012, *Bioinformatics* 8(15):2052-8

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concave	<i>The concave dataset</i>
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**Description**

A simulated flowcytometry 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**

Ge Y. et al, flowPeaks: a fast unsupervised clustering for flow cytometry data via K-means and density peak finding, *Bioinformatics* 8(15):2052-8

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evalCluster	<i>evaluate the result of a clustering algorithm by comparing it with the gold standard</i>
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**Description**

This function takes the cluster labels of the two clusterings, one is based on the gold standard, the other is a candidate clusterign, 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 outerliers
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)**

Yongchao Ge <yongchao.ge@gmail.com>

**References**

Ge Y. et al, flowPeaks: a fast unsupervised clustering for flow cytometry data via K-means and density peak finding, 2012, Bioinformatics 8(15):2052-8

**See Also**

[flowPeaks](#)

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flowPeaks

*Doing the flowPeaks analysis*

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**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: <ul style="list-style-type: none"> <li>• cid: cluster labels, should always be 1:K;</li> <li>• w: the weights of the K clusters;</li> <li>• mu: The mean of all cells in the K clusters;</li> <li>• S: The variance matrix of the K clusters. Note that each variance matrix for each cluster has been stacked as a column vector</li> </ul>
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

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**References**

Ge Y. et al, flowPeaks: a fast unsupervised clustering for flow cytometry data via K-means and density peak finding, 2012, Bioinformatics 8(15):2052-8

**See Also**

[plot.flowPeaks](#)

**Examples**

```
##demonstrate how to use a flowFrame
## Not run:
require(flowCore)
samp <- read.FCS(system.file("extdata","0877408774.B08",
package="flowCore"))
##do the clustering based on the asinh transformtion 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)
```

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plot.flowPeaks

*Plot the results generated by flowPeaks*


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**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**

```
## 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**

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

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**See Also**

[flowPeaks](#)

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`print.flowPeaks`

*The display of the flowPeaks results*

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**Description**

The display of the `flowPeaks` results

**Usage**

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

**Arguments**

<code>x</code>	The output from the function <a href="#">flowPeaks</a>
<code>...</code>	Optional additional arguments. At present no additional arguments are used.



**Author(s)**

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**See Also**

[flowPeaks](#)

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summary.flowPeaks      *The summary of the flowPeaks results*

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**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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