Package: flowPeaks (via r-universe)

November 24, 2026

Version 1.60.0

Date 1-12-2012

Title An R package for flow data clustering

Author Yongchao Ge<yongchao.ge@gmail.com>

Maintainer Yongchao Ge<yongchao.ge@gmail.com>

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

git_url https://git.bioconductor.org/packages/flowPeaks

git_branch RELEASE_3_15

git_last_commit da9fd47

git_last_commit_date 2022-04-26

Config/pak/sysreqs libgsl0-dev

Repository Bioconductor 3.24

Date/Publication 2026-11-23 22:31:51 UTC

RemoteUrl https://github.com/bioc/flowPeaks

RemoteRef RELEASE_3_24

RemoteSha 42d23226bf7a2312d04071916b26a03fef99dec6

Contents

adjust.flowPeaks . . . 2
assign.flowPeaks . . . 3
barcode . . . 4
concave . . . 4
evalCluster . . . 5
flowPeaks . . . 6
plot.flowPeaks . . . 7
print.flowPeaks . . . 9
summary.flowPeaks . . . 9

Index **11**

`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 defintion of which can be seen in `flowPeaks`.

Author(s)

Yongchao Ge <yongchao.ge@gmail.com>

See Also

`flowPeaks`

`assign.flowPeaks` *Obtain the flowPeaks cluster lables 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 geneterated fp
`tol`	All points where the probability density is less than tol (default is 1%) of the peak denisty of that cluster are labled 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 denstiy 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`

barcode *The barcode dataset*

Description

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

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 accoring 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 Bioinformatcs, 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

concave *The concave dataset*

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

`evalCluster` *evaulate the result of a clustering algorihm 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 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`

`flowPeaks` *Doing the flowPeaks analysis*

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 exprssion matrix slot should be used as x, where only channles 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 vaiarance matrix S0
`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 seens 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)

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

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 transforamtion 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

```
## 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	Anobject of class flowPeaks, e.g., t 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 legnth 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 purpse
drawvor	Deciding whether the voronoi diagram should be drawn, only good for 2D data
drawlocalpeaks	Decding 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 boudary 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	Deciing the symbols for the outliers
...	Optional additional arguments. At present no additional arguments are used.

Author(s)

Yongchao Ge <yongchao.ge@gmail.com>

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.

Author(s)

Yongchao Ge <yongchao.ge@gmail.com>

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)

Yongchao Ge <yongchao.ge@gmail.com>

See Also

flowPeaks

Index

∗ **adjust**
adjust.flowPeaks, 2
∗ **cluster,multivariate,smooth**
flowPeaks, 6
∗ **cluster,multivarite**
assign.flowPeaks, 3
∗ **cluster,utiliteis**
evalCluster, 5
∗ **datasets**
barcode, 4
concave, 4
∗ **plot,multivariate,smooth**
plot.flowPeaks, 7
∗ **print**
print.flowPeaks, 9
∗ **summary**
summary.flowPeaks, 9

adjust.flowPeaks, 2, *3*, *8*
assign.flowPeaks, 3, *8*

barcode, 4

concave, 4

evalCluster, 5

flowPeaks, *2, 3*, *5*, 6, *8–10*

plot.flowPeaks, 7, *7*
print.flowPeaks, 9

summary.flowPeaks, 9