Package 'flowMeans'

April 10, 2024

Type Package

Title Non-parametric Flow Cytometry Data Gating

Version 1.62.0

Date 2010-05-10

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Description Identifies cell populations in Flow Cytometry data using non-parametric clustering and segmented-regression-based change point detection. Note: R 2.11.0 or newer is required.

Imports Biobase, graphics, grDevices, methods, rrcov, stats, feature, flowCore

Depends R (>= 2.10.0)

License Artistic-2.0

LazyLoad yes

biocViews ImmunoOncology, FlowCytometry, CellBiology, Clustering

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

git_branch RELEASE_3_18

git_last_commit 93d34a9

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-04-10

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`flowMeans-package` *flowMeans Package*

Description

Non-parametric Flow Cytometry Data Gating

Details

Package:	flowMeans
Type:	Package
Version:	1.0
Date:	2010-03-02
License:	Artistic-2.0 or newer
LazyLoad:	yes

Author(s)

Nima Aghaeepour <naghaeep@bccrc.ca>

Examples

```
library(flowMeans)
data(x)
res <- flowMeans(x, c("FL1.H", "FL2.H", "FL3.H", "FL4.H"), MaxN=10)
plot(x[,c(3,4)], res, c("FL1.H", "FL2.H"))
```

`changepointDetection` *Change-Point Detection*

Description

Fits a two-component piecewise linear regression to the minimum distance between merged clusters vs the number of clusters for a list of merged cluster solutions.

Usage

```
changepointDetection(vect, OrthagonalResiduals = FALSE, PlotFlag = FALSE)
```

Arguments

vect	A vector of minimum distances between clusters chosen to be merged at each iteration.
OrthagonalResiduals	Boolean value, indicates if the residuals must be transformed to orthagonal distance or not.
PlotFlag	Boolean value, indicating if the regression lines must be visualized.

Value

MinIndex	Index of the merging step that produced the final results.
l1	First regression line used for finding the changepoint for stopping the merging process.
l2	Second regression line used for finding the changepoint for stopping the merging process.

Author(s)

Nima Aghaeepour

Examples

```
library(flowMeans)
data(x)
res <- flowMeans(x, c("FL1.H", "FL2.H", "FL3.H", "FL4.H"), MaxN=10)
ft<-changepointDetection(res@Mins)
plot(res@Mins)
abline(ft$l1)
abline(ft$l2)
```

---

flowMeans *flowMeans*

Description

Finds a good fit to the data using k-means clustering algorithm. Then merges the adjacent dense spherical clusters to find non-spherical clusters.

Usage

```
flowMeans(x, varNames=NULL, MaxN = NA, NumC = NA, iter.max = 50, nstart = 10,
Mahalanobis = TRUE, Standardize = TRUE, Update = "Mahalanobis", OrthagonalResiduals=TRUE,
MaxCovN=NA, MaxKernN=NA, addNoise=TRUE)
```

Arguments

x	A matrix, data frame of observations, or object of class `flowFrame`. Rows correspond to observations and columns correspond to variables.
varNames	A character vector specifying the variables (columns) to be included in clustering. When it is left unspecified, all the variables will be used.
MaxN	Maximum number of clusters. If set to NA (default) the value will be estimated automatically.
NumC	Number of clusters. If set to NA (default) the value will be estimated automatically.
iter.max	The maximum number of iterations allowed.
nstart	The number of random sets used for initialization.
Mahalanobis	Boolean value. If TRUE (default) mahalanobis distance will be used. Otherwised, euclidean distance will be used.
Standardize	Boolean value. If TRUE (default) the data will be transformed to the [0,1] interval.
Update	String value. If set to "Mahalanobis" the distance function will be updated at each merging iteration with recalculating mahalanobis distances. If set to "Mean" the distance matrix will be updated after each merging step with averaging. If set to "None" the distance matrix will not be updated.
MaxCovN	Maximum number of points, used for calculating the covariance. If set to NA (default), all the points will be used.)
MaxKernN	Maximum number of points, used for counting the modes using kernel density estimation. If set to NA (default), all the points will be used.)
addNoise	Boolean value. Determines if uniform noise must be added to the data to prevent singularity issues or not.
OrthagonalResiduals	Boolean value, indicates if the residuals must be transformed to orthagonal distance or not.

Details

If Mahalanobis distance is not used (i.e., Mahalanobis=FALSE) then the Update value cannot be set to Mahalanobis (i.e., Update="Mahalanobis")

Value

Label	A vector of integers indicating the cluster to which each point is allocated.
Labels	A list of vectors of integers indicating the cluster to which each point is allocated at each merging iteration.
Mats	A list of distance matrixes between clusters at every merging iteration.
MaxN	Maximum number of clusters
Mins	A vector of integers indicating the distance between the two clusters chosen to be merged at every iteration.

MinIndex	Index of the merging step that produced the final results.
Line1	First regression line used for finding the changepoint for stopping the merging process.
Line2	Second regression line used for finding the changepoint for stopping the merging process.

Author(s)

Nima Aghaeepour

Examples

```
library(flowMeans)
data(x)
res <- flowMeans(x, c("FL1.H", "FL2.H", "FL3.H", "FL4.H"), MaxN=10)
plot(x[,c(3,4)], res, c("FL1.H", "FL2.H"))
```

---

plot *Scatterplot of Clustering Results*

Description

This method generates scatterplot revealing the cluster assignment.

Usage

```
## S4 method for signature 'ANY,Populations'
plot(x, y, varNames=NULL, ...)
## S4 method for signature 'flowFrame,Populations'
plot(x, y, varNames=NULL, ...)
```

Arguments

x	A matrix, data frame of observations, or object of class flowFrame. This is the object on which flowClust was performed.
y	Object returned from flowMeans.
varNames	A character vector specifying the variables (columns) to be included in the plot. When it is left unspecified, all the variables will be used.
...	Extra parameters that will be passed to the generic plot function

Author(s)

Nima Aghaeepour <<naghaeep@bccrc.ca>>

See Also

flowMeans

Examples

```
library(flowMeans)
data(x)
plot(data.frame(x))
```

---

show *Show Method for Populations Class*

Description

This method lists out the slots contained in a Populations object.

Usage

```
## S4 method for signature 'Populations'
show(object)
```

Arguments

object	Object returned from flowMeans

Author(s)

Nima Aghaeepour <<naghaeep@bccrc.ca>>

See Also

flowMeans

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summary *Summary Method for flowMeans Object*

Description

This method prints out various characteristics of the populations found by flowMeans.

Usage

```
## S4 method for signature 'Populations'
summary(object,...)
```

Arguments

object	Object returned from flowMeans.
...	Object returned from flowMeans.

Details

This method prints out various characteristics of the populations found by flowMeans.

Author(s)

Nima Aghaeepour <<naghaeep@bccrc.ca>>

See Also

flowMeans

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x *xSample*

Description

A flow cytometry sample produced for diagnosis of the Graft versus Host Disease (GvHD)

Usage

```
data(x)
```

Format

A matrix describing expression values of 6 markers and 14936 cells. Each column represents a marker and each row represents a cell.

Source

R.R. Brinkman, M. Gasparetto, S.J.J. Lee, A.J. Ribickas, J. Perkins, W. Janssen, R. Smiley, and C. Smith. High-content flow cytometry and temporal data analysis for defining a cellular signature of graft- versus-host disease. Biology of Blood and Marrow Transplantation, 13(6):691?700, 2007.

Examples

```
data(x)
## maybe str(x) ; plot(x) ...
```

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