Package 'flowMeans'

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Type Package

Title Non-parametric Flow Cytometry Data Gating

Version 1.32.0

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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 FlowCytometry, CellBiology, Clustering

NeedsCompilation no

R topics documented:

`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)

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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`

`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`

`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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