Package ‘flowMeans’

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Type  Package
Title  Non-parametric Flow Cytometry Data Gating
Version  1.34.0
Date  2010-05-10
Author  Nima Aghaeepour
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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 ....................................................... 2
changepointDetection .................................................... 3
flowMeans ................................................................. 4
plot ................................................................. 6
show ............................................................... 6
summary ......................................................... 7
x ............................................................. 8

Index  9
flowMeans-package  

flowMeans Package 

Description

Non-parametric Flow Cytometry Data Gating

Details
changepointDetection

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)
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, OrthogonalResiduals = FALSE, PlotFlag = FALSE)

Arguments

vect A vector of minimum distances between clusters chosen to be merged at each iteration.
OrthogonalResiduals Boolean value, indicates if the residuals must be transformed to orthogonal 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.
11 First regression line used for finding the changepoint for stopping the merging process.
12 Second regression line used for finding the changepoint for stopping the merging process.
flowMeans

Author(s)
Nima Aghaeepour

Examples

```r
library(flowMeans)
data(x)
ft<-changepointDetection(res@Mins)
plot(res@Mins)
abline(ft$l1)
abline(ft$l2)
```

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", OrthogonalResiduals=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. Otherwise, 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.
flowMeans

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.

OrthogonalResiduals Boolean value, indicates if the residuals must be transformed to orthogonal 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

Label1 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)
plot(x[,c(3,4)], res, c("FL1.H", "FL2.H"))
**plot**  

*Scatterplot of Clustering Results*

**Description**

This method generates a scatterplot revealing the cluster assignment.

**Usage**

```r
## 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**

```r
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**

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

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.

Details

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

Author(s)

Nima Aghaeepour <naghaeep@bccrc.ca>

See Also

flowMeans
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


Examples

data(x)

## maybe str(x) ; plot(x) ...
Index

*Topic cluster
  flowMeans, 4
  flowMeans-package, 2

*Topic datasets
  x, 8

*Topic graphs
  plot, 6

*Topic multivariate
  flowMeans, 4
  flowMeans-package, 2

*Topic nonparametric
  flowMeans, 4
  flowMeans-package, 2

*Topic print
  show, 6
  summary, 7
  changepointDetection, 3

  flowMeans, 4, 6, 7
  flowMeans-package, 2

  plot, 6
  plot,ANY,Populations (plot), 6
  plot,ANY,Populations-method (plot), 6
  plot,flowFrame,Populations (plot), 6
  plot,flowFrame,Populations-method (plot), 6

  show, 6
  show,Populations (show), 6
  show,Populations-method (show), 6
  summary, 7
  summary,Populations (summary), 7
  summary,Populations-method (summary), 7

  x, 8