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arrayCGH

Object of Class arrayCGH

Description

Description of the object arrayCGH.

Value

The object arrayCGH is a list with at least a data.frame named arrayValues and a vector named arrayDesign. The data.frame arrayValues must contain the following fields:

Col  Vector of columns coordinates.
Row Vector of rows coordinates.

... Other elements can be added.

The vector arrayDesign is composed of 4 values: c(arrayCol, arrayRow, SpotCol, SpotRow). The array CGH is represented by arrayRow*arrayCol blocs and each bloc is composed of SpotRow*SpotCol spots.

N.B. : Col takes the values in 1:arrayRow*SpotRow and Row takes the values in 1:arrayCol*SpotCol

Note

People interested in tools dealing with array CGH analysis can visit our web-page http://bioinfo.curie.fr.

Author(s)

Philippe Hupé, (glad@curie.fr).

See Also

glad.

Examples

data(arrayCGH)

# object of class arrayCGH

array <- list(arrayValues=array2, arrayDesign=c(4,4,21,22))
class(array) <- "arrayCGH"

arrayPersp Perspective image of microarray spots statistic

Description

The function arrayPersp creates perspective images of shades of gray or colors that correspond to the values of a statistic for each spot on the array. The statistic can be the intensity log-ratio, a spot quality measure (e.g. spot size or shape), or a test statistic. This function can be used to explore whether there are any spatial effects in the data, for example, print-tip or cover-slip effects.

Usage

```r
## Default S3 method:
arrayPersp(Statistic, Col, Row,
           ArrCol, ArrRow, SpotCol, SpotRow,
           mediancenter=FALSE,
           col=myPalette("green","red","yellow"),
           zlim=zlim, bar=TRUE, ...)
```

```r
## S3 method for class 'arrayCGH':
```
arrayPersp

arrayPersp(arrayCGH, variable,
mediancenter=FALSE,
col=myPalette("green","red","yellow"),
zlim=zlim, bar=TRUE, ...)

Arguments

arrayCGH  Object of class arrayCGH.
variable  Variable to be plotted
Statistic  Statistic to be plotted.
Col  Vector of columns coordinates.
Row  Vector of rows coordinates.
ArrCol  Number of columns for the blocs.
ArrRow  Number of rows for the blocs.
SpotCol  Number of column for each bloc.
SpotRow  Number of rows for each bloc.
mediancenter  If mediancenter=TRUE, values of Statistic are median-centered.
col  List of colors such as that generated by Palettes. In addition to these color palettes functions, a new function myPalette was defined to generate color palettes from user supplied low, middle, and high color values.
zlim  Numerical vector of length 2 giving the extreme values of z to associate with colors low and high of myPalette. By default zlim is the range of z. Any values of z outside the interval zlim will be truncated to the relevant limit.
bar  If bar=TRUE, a calibration color bar is shown to the right of the image.
...  Graphical parameters can be given as arguments to function persp.

N.B. : Col takes the values in 1:arrayRow*SpotRow and Row takes the values in 1:arrayCol*SpotCol

Value

An image is created on the current graphics device.

Note

People interested in tools dealing with array CGH analysis can visit our web-page http://bioinfo.curie.fr.

Author(s)

Philippe Hupé, (glad@curie.fr).

See Also

persp, arrayPlot, myPalette.
Examples

```
data(arrayCGH)

# object of class arrayCGH

array <- list(arrayValues=array2, arrayDesign=c(4,4,21,22))
class(array) <- "arrayCGH"

arrayPersp(array,"Log2Rat", main="Perspective image of array CGH", box=FALSE, theta=110,

arrayPlot

Spatial image of microarray spots statistic

Description

The function arrayPlot creates spatial images of shades of gray or colors that correspond to the
values of a statistic for each spot on the array. The statistic can be the intensity log-ratio, a spot
quality measure (e.g. spot size or shape), or a test statistic. This function can be used to explore
whether there are any spatial effects in the data, for example, print-tip or cover-slip effects.

Usage

## Default S3 method:
arrayPlot(Statistic, Col, Row,
ArrCol, ArrRow, SpotCol, SpotRow,
mediancenter=FALSE,
col=myPalette("green", "red", "yellow"),
contour=FALSE, nlevels=5,
zlim=NULL, bar=c("none", "horizontal", "vertical"),
layout=TRUE, ...)

## S3 method for class 'arrayCGH':
arrayPlot(arrayCGH, variable,
mediancenter=FALSE,
col=myPalette("green", "red", "yellow"),
contour=FALSE, nlevels=5,
zlim=NULL, bar=c("none", "horizontal", "vertical"),
layout=TRUE, ...)

Arguments

arrayCGH Object of class arrayCGH.
variable Variable to be plotted
Statistic Statistic to be plotted.
Col Vector of columns coordinates.
Row Vector of rows coordinates.
ArrCol Number of columns for the blocs.
ArrRow Number of rows for the blocs.
arrayPlot

SpotCol Number of column for each bloc.
SpotRow Number of rows for each bloc.
mediancenter If mediancenter=TRUE, values of Statistic are median-centered.
col List of colors such as that generated by Palettes. In addition to these color palettes functions, a new function myPalette was defined to generate color palettes from user supplied low, middle, and high color values.
contour If contour=TRUE, contour are plotted, otherwise they are not shown.
nlevels Numbers of levels added by contour if contour=TRUE.
zlim Numerical vector of length 2 giving the extreme values of z to associate with colors low and high of myPalette. By default zlim is the range of z. Any values of z outside the interval zlim will be truncated to the relevant limit.
bar If bar=='horizontal' (resp. ‘vertical’), an horizontal (resp. vertical) calibration color bar is shown to the right of the image.
layout If layout==TRUE plot layout is automatically set when a color bar is asked for

Graphical parameters can be given as arguments to function image.

N.B.: Col takes the values in 1:arrayRow*SpotRow and Row takes the values in 1:arrayCol*SpotCol

Details

This function is very similar to the maImage written by Sandrine Dudoit with added options zlim, mediancenter and layout.

Value

An image is created on the current graphics device.

Note

People interested in tools dealing with array CGH analysis can visit our web-page http://bioinfo.curie.fr.

Author(s)

Philippe Hupé, (glad@curie.fr).

See Also

image, contour, arrayPersp, myPalette.

Examples

data(arrayCGH)

pdf(file="arrayCGH.pdf",height=21/cm(1),width=29.7/cm(1))
arrayPlot(array2$Log2Rat, array2$Col, array2$Row, 4,4,21,22, main="Spatial Image of array CGH")
dev.off()

# object of class arrayCGH

array <- list(arrayValues=array2, arrayDesign=c(4,4,21,22))
class(array) <- "arrayCGH"
arrayPlot(array,"Log2Rat", main="Spatial Image of array CGH")

as.data.frame.profileCGH

profileCGH conversion

Description

Convert a profileCGH object into a data.frame.

Usage

## S3 method for class 'profileCGH':
as.data.frame(x, row.names = NULL, optional = FALSE, ...)

Arguments

x

The object to converted into data.frame.

row.names

NULL or a character vector giving the row names for the data frame. Missing values are not allowed.

optional

logical. If `TRUE`, setting row names and converting column names (to syntactic names) is optional.

...

Details

The attributes `profileValues` and `profileValuesNA` are binded into a data.frame.

Value

A data.frame object

Note

People interested in tools dealing with array CGH analysis can visit our web-page http://bioinfo.curie.fr.

Author(s)

Philippe Hupé, (glad@curie.fr)

See Also

as.profileCGH
### Creation of "profileCGH" object

```r
profileCGH <- as.profileCGH(gm13330)
```

```r
res <- glad(profileCGH, mediancenter=FALSE,
            smoothfunc="lawsglad", bandwidth=10, round=2,
            model="Gaussian", lkern="Exponential", qlambda=0.999,
            base=FALSE,
            lambdabreak=8, lambdacluster=8, lambdaclusterGen=40,
            type="tricubic", param=c(d=6),
            alpha=0.001, msize=5,
            method="centroid", nmax=8,
            verbose=FALSE)
```

```r
res <- as.data.frame(res)
```

---

**as.profileCGH**  
*Create an object of class profileCGH*

---

**Description**

Create an object of class profileCGH.

**Usage**

```r
as.profileCGH(object,...)
```

---

**Arguments**

- **object**  
  A data.frame to be convert into profileCGH.

- **infection**  
  If "value" then the LogRatio with infinite values (-Inf, Inf) are replace by + or - value according to the sign. If "empty" then NAs are put instead.

- **value**  
  replace Inf by value if infection is "value".

- **...**
Details

The data.frame to be convert must at least contain the following fields: LogRatio, PosOrder, and Chromosome. If the field Chromosome is of mode character, it is automatically converted into a numeric vector (see \texttt{ChrNumeric}); a field ChromosomeChar contains the character labels. The data.frame to be converted into a profileCGH objet is split into two data.frame: profileValuesNA contains the rows for which there is at least a missing value for either LogRatio, PosOrder or Chromosome; profileValues contains the remaining rows.

Value

A list with the following attributes

\begin{itemize}
  \item \texttt{profileValues} A data.frame
  \item \texttt{profileValuesNA} A data.frame
\end{itemize}

Note

People interested in tools dealing with array CGH analysis can visit our web-page \url{http://bioinfo.curie.fr}.

Author(s)

Philippe Hupé, \textit{⟨glad@curie.fr⟩}

See Also

\texttt{as.data.frame.profileCGH}

Examples

\begin{verbatim}
data(snijders)
### Creation of "profileCGH" object
profileCGH <- as.profileCGH(gm13330)
attributes(profileCGH)
\end{verbatim}

array 

\textit{Bladder cancer CGH data}

Description

Bladder cancer data from 3 arrays CGH (Comparative Genomic Hybridyzation). Arrays dimension are 4 blocs per column, 4 blocs per row, 21 columns per bloc and 22 rows by blocs.

Usage

\begin{verbatim}
data(arrayCGH)
\end{verbatim}
Format

A data frame composed of the following elements:

- **Log2Rat** Log 2 ratio.
- **Position** BAC position on the genome.
- **CHROMOSOME** Chromosome.
- **Col** Column location on the array.
- **Row** Row location on the array.

Source

Institut Curie, (glad@curie.fr).

Examples

data(arrayCGH)
data <- array1 #array1 to array3

ChrNumeric

**Convert chromosome into numeric values**

Description

Convert chromosome into numeric values.

Usage

ChrNumeric(Chromosome)

Arguments

- **Chromosome** A vector with chromosome labels.

Details

For sexual chromosome, labels must contains X or Y which are coded by 23 and 24 respectively.

Note

People interested in tools dealing with array CGH analysis can visit our web-page [http://bioinfo.curie.fr](http://bioinfo.curie.fr).

Author(s)

Philippe Hupé, (glad@curie.fr)

Examples

Chromosome <- c("1", "X", "Y", "chrX", "ChrX", "chrX", "Chr Y")
ChrNumeric(Chromosome)
ColorBar

Calibration bar for color images

Description
This function produces a color image (color bar) which can be used for the legend to another color image obtained from the functions `image` or `arrayPlot`.

Usage
```r
ColorBar(x, horizontal=TRUE, col=heat.colors(50), scale=1:length(x), k=10, ...)```

Arguments
- **x**: If "numeric", a vector containing the "z" values in the color image, i.e., the values which are represented in the color image. Otherwise, a "character" vector representing colors.
- **horizontal**: If TRUE, the values of x are represented as vertical color strips in the image, else, the values are represented as horizontal color strips.
- **col**: Vector of colors such as that generated by rainbow, heat.colors, topo.colors, terrain.colors, or similar functions. In addition to these color palette functions, a new function `myPalette` was defined to generate color palettes from user supplied low, middle, and high color values.
- **scale**: A "numeric" vector specifying the "z" values in the color image. This is used when the argument x is a "character" vector representing color information.
- **k**: Object of class "numeric", for the number of labels displayed on the bar.
- **...**: Optional graphical parameters, see `par`.

Author(s)
Sandrine Dudoit, Yee Hwa (Jean) Yang.

See Also
`image`, `arrayPlot`, `myPalette`.

Examples
```r
par(mfrow=c(3,1))
Rcol <- myPalette(low="white", high="red", k=10)
Gcol <- myPalette(low="white", high="green", k=50)
RGcol <- myPalette(low="green", high="red", k=100)
ColorBar(Rcol)
ColorBar(Gcol, scale=c(-5,5))
ColorBar(1:50, col=RGcol)

par(mfrow=c(1,3))
x<-seq(-1, 1, by=0.01)
ColorBar(x, col=Gcol, horizontal=FALSE, k=11)
ColorBar(x, col=Gcol, horizontal=FALSE, k=21)
```
**cytoband**

```
ColorBar(x, col=Gcol, horizontal=FALSE, k=51)
```

---

**cytoband**

*Cytogenetic banding*

**Description**

Cytogenetic banding

**Usage**

```
data(cytoband)
```

**Examples**

```
data(cytoband)
cytoband
```

---

**daglad**

*Analysis of array CGH data*

**Description**

This function allows the detection of breakpoints in genomic profiles obtained by array CGH technology and affects a status (gain, normal or lost) to each clone.

**Usage**

```c
## S3 method for class 'profileCGH':
daglad(profileCGH, mediancenter=FALSE, normalrefcenter=FALSE, genomestep=FALSE, smoothfunc="lawsglad", lkern="Exponential", model="Gaussian", qlambda=0.999, bandwidth=10, sigma=NULL, base=FALSE, round=1, lambdabreak=8, lambdaclusterGen=40, param=c(d=6), alpha=0.001, method="centroid", nmin=1, nmax=8, amplicon=1, deletion=-5, deltaN=0.10, forceGL=c(-0.15,0.15), MinBkpWeight=0.35, CheckBkpPos=TRUE, assignGNLOut=TRUE, breaksFdrQ = 0.0001, haarStartLevel = 1, haarEndLevel = 5, verbose=FALSE, ...)
```
Arguments

profileCGH Object of class `profileCGH`

mediancenter If TRUE, LogRatio are centered on their median.

genomestep If TRUE, a smoothing step over the whole genome is performed and a "clustering throughout the genome" allows to identify a cluster corresponding to the Normal DNA level. The threshold used in the `daglad` function (deltaN, forceGL, amplicon, deletion) and then compared to the median of this cluster.

normalrefcenter
If TRUE, the LogRatio are centered through the median of the cluster identified during the `genomestep`.

smoothfunc Type of algorithm used to smooth LogRatio by a piecewise constant function. Choose either `lawsglad`, `haarseg`, `aws` or `laws`.

lkern lkern determines the location kernel to be used (see `laws` for details).

model model determines the distribution type of LogRatio (see `laws` for details).

qlambda qlambda determines the scale parameter qlambda for the stochastic penalty (see `laws` for details).

base If TRUE, the position of clone is the physical position onto the chromosome, otherwise the rank position is used.

sigma Value to be passed to either argument `sigma2` of `aws` function or `shape` of `laws`. If NULL, sigma is calculated from the data.

bandwidth Set the maximal bandwidth `hmax` in the `aws` or `laws` function. For example, if `bandwidth=10` then the hmax value is set to `10*X_N` where `X_N` is the position of the last clone.

round The smoothing results of either `aws` or `laws` function are rounded or not depending on the `round` argument. The `round` value is passed to the argument `digits` of the `round` function.

lambdabreak Penalty term (λ') used during the "Optimization of the number of breakpoints" step.

lambdaclusterGen Penalty term (λ*) used during the "clustering throughout the genome" step.

param Parameter of kernel used in the penalty term.

alpha Risk alpha used for the "Outlier detection" step.

msize The outliers MAD are calculated on regions with a cardinality greater or equal to msize.

method The agglomeration method to be used during the "clustering throughout the genome" steps.

nmin Minimum number of clusters (N*max) allowed during the "clustering throughout the genome" clustering step.

nmax Maximum number of clusters (N*max) allowed during the "clustering throughout the genome" clustering step.

amplicon Level (and outliers) with a smoothing value (log-ratio value) greater than this threshold are considered as amplicon. Note that first, the data are centered on the normal reference value computed during the "clustering throughout the genome" step.
$\texttt{daglad}$ Level (and outliers) with a smoothing value (log-ratio value) lower than this threshold are considered as deletion. Note that first, the data are centered on the normal reference value computed during the "clustering throughout the genome" step.

$\texttt{deltaN}$ Region with smoothing values in between the interval $[-\texttt{deltaN},+\texttt{deltaN}]$ are supposed to be normal.

$\texttt{forceGL}$ Level with smoothing value greater (lower) than $\texttt{rangeGL}[1]$ ($\texttt{rangeGL}[2]$) are considered as gain (lost). Note that first, the data are centered on the normal reference value computed during the "clustering throughout the genome" step.

$\texttt{nbsigma}$ For each breakpoints, a weight is calculated which is a function of absolute value of the Gap between the smoothing values of the two consecutive regions. $\texttt{Weight} = 1 - \text{kernelpen}(\text{abs}(\text{Gap}), \text{param}=c(d=\text{nbsigma}*\text{Sigma}))$ where $\text{Sigma}$ is the standard deviation of the LogRatio.

$\texttt{MinBkpWeight}$ Breakpoints which $\texttt{GNLchange}==0$ and $\texttt{Weight}$ less than $\texttt{MinBkpWeight}$ are discarded.

$\texttt{CheckBkpPos}$ If TRUE, the accuracy position of each breakpoints is checked.

$\texttt{assignGNLOut}$ If FALSE the status (gain/normal/loss) is not assigned for outliers.

$\texttt{breaksFdrQ}$ breaksFdrQ for HaarSeg algorithm.

$\texttt{haarStartLevel}$ haarStartLevel for HaarSeg algorithm.

$\texttt{haarEndLevel}$ haarEndLevel for HaarSeg algorithm.

$\texttt{verbose}$ If TRUE some information are printed.

... 

Details

The function $\texttt{daglad}$ implements a slightly modified version of the methodology described in the article : Analysis of array CGH data: from signal ratio to gain and loss of DNA regions (Hupé et al., Bioinformatics, 2004). For smoothing, it is possible to use either the AWS algorithm (Polzehl and Spokoiny, 2002) or the HaarSeg algorithm (Ben-Yaacov and Eldar, Bioinformatics, 2008). The $\texttt{daglad}$ function allows to choose some threshold to help the algorithm to identify the status of the genomic regions. The thresholds are given in the following parameters:

- $\texttt{deltaN}$
- $\texttt{forceGL}$
- $\texttt{deletion}$
- $\texttt{amplicon}$

Value

An object of class "profileCGH" with the following attributes:

**\texttt{profileValues}**

- a data.frame with the following added information:
  - **Smoothing** The smoothing values correspond to the median of each Level
  - **Breakpoints** The last position of a region with identical amount of DNA is flagged by 1 otherwise it is 0. Note that during the "Optimization of the number of breakpoints" step, removed breakpoints are flagged by -1.
Level Each position with equal smoothing value are labelled the same way with an integer value starting from one. The label is incremented by one when a new level occurs or when moving to the next chromosome.

OutliersAws Each AWS outliers are flagged by -1 (if it is in the $\alpha/2$ lower tail of the distribution) or 1 (if it is in the $\alpha/2$ upper tail of the distribution) otherwise it is 0.

OutliersMad Each MAD outliers are flagged by -1 (if it is in the $\alpha/2$ lower tail of the distribution) or 1 (if it is in the $\alpha/2$ upper tail of the distribution) otherwise it is 0.

OutliersTot OutliersAws + OutliersMad.

NormalRef Clusters which have been used to set the normal reference during the "clustering throughout the genome" step are code by 0. Note that if genomestep=FALSE, all the value are set to 0.

ZoneGNL Status of each clone: Gain is coded by 1, Loss by -1, Amplicon by 2, deletion by -10 and Normal by 0.

\textbf{BkpInfo} a data.frame sum up the information for each breakpoint:

\begin{itemize}
  \item Chromosome Chromosome name.
  \item Smoothing Smoothing value for the breakpoint.
  \item Gap absolute value of the gap between the smoothing values of the two consecutive regions.
  \item Sigma The estimation of the standard-deviation of the chromosome.
  \item Weight $1 - \text{kernelpen}(\text{Gap}, \text{type}, \text{param}=c(d=nbsigma*Sigma))$
  \item ZoneGNL Status of the level where is the breakpoint.
  \item GNLchange Takes the value 1 if the ZoneGNL of the two consecutive regions are different.
  \item LogRatio Test over Reference log-ratio.
\end{itemize}

\textbf{NormalRef}

\begin{itemize}
  \item If genomestep=TRUE and normalrefcenter=FALSE, then NormalRef is the median of the cluster which has been used to set the normal reference during the "clustering throughout the genome" step. Otherwise NormalRef is 0.
\end{itemize}

\textbf{Note}

People interested in tools dealing with array CGH analysis can visit our web-page \url{http://bioinfo.curie.fr}.

\textbf{Author(s)}

Philippe Hupé, \{glad@curie.fr\}.

\textbf{References}

Hupé et al. (Bioinformatics, 2004) Analysis of array CGH data: from signal ratio to gain and loss of DNA regions.


Ben-Yaacov and Eldar (Bioinformatics, 2008) A fast and flexible method for the segmentation of aCGH data.

\textbf{See Also}

\texttt{glad}.
Examples

data(snijders)
gm13330$Clone <- gm13330$BAC
profileCGH <- as.profileCGH(gm13330)

#daglad function

res <- daglad(profileCGH, mediancenter=FALSE, normalrefcenter=FALSE, genomestep=FALSE, smoothfunc="lawsglad", lkern="Exponential", model="Gaussian", qlambda=0.999, bandwidth=10, base=FALSE, round=1.5, lambdabreak=8, lambdaclusterGen=40, param=c(d=6), alpha=0.001, msize=5, method="centroid", nmin=1, nmax=8, amplicon=1, deletion=-5, deltaN=0.10, forceGL=c(-0.15,0.15), nbsigma=3, MinBkpWeight=0.35, CheckBkpPos=TRUE)

### Genomic profile on the whole genome
plotProfile(res, unit=3, Bkp=TRUE, labels=FALSE, Smoothing="Smoothing", main="Breakpoints detection: DAGLAD analysis")

###Genomic profile for chromosome 1
plotProfile(res, unit=3, Bkp=TRUE, labels=TRUE, Chromosome=1, Smoothing="Smoothing", main="Chromosome 1: DAGLAD analysis")

### The standard-deviation of LogRatio are:
res$SigmaC

### The list of breakpoints is:
res$BkpInfo

---

**GLAD-internal**

**Description**

Internal functions

**Usage**

```
```

**Value**

```
```

**Author(s)**

Philippe Hupé, glad@curie.fr
See Also

- ""

---

**glad**

*Analysis of array CGH data*

**Description**

This function allows the detection of breakpoints in genomic profiles obtained by array CGH technology and affects a status (gain, normal or lost) to each clone.

**Usage**

```r
## S3 method for class 'profileCGH':
glad(profileCGH, mediancenter=FALSE, 
      smoothfunc="lawsglad", bandwidth=10, round=1.5, 
      model="Gaussian", lkern="Exponential", qlambda=0.999, 
      base=FALSE, sigma, 
      lambdabreak=8, lambdacluster=8, lambdaclusterGen=40, 
      type="tricubic", param=c(d=6), 
      alpha=0.001, msize=5, 
      method="centroid", nmax=8, assignGNLOut=TRUE, 
      breaksFdrQ = 0.0001, haarStartLevel = 1, haarEndLevel = 5, 
      verbose=FALSE, ...)
```

**Arguments**

- **profileCGH**: Object of class `profileCGH`
- **mediancenter**: If TRUE, LogRatio are center on their median.
- **smoothfunc**: Type of algorithm used to smooth LogRatio by a piecewise constant function. Choose either `lawsglad`, `haarseg`, `aws` or `laws`.
- **bandwidth**: Set the maximal bandwidth hmax in the `aws` or `laws` function. For example, if `bandwidth=10` then the hmax value is set to 10*X_N where X_N is the position of the last clone.
- **round**: The smoothing results are rounded or not depending on the `round` argument. The `round` value is passed to the argument `digits` of the `round` function.
- **model**: Determines the distribution type of the LogRatio. Keep always the model as "Gaussian" (see `laws`).
- **lkern**: Determines the location kernel to be used (see `aws` or `laws`).
- **qlambda**: Determines the scale parameter for the stochastic penalty (see `aws` or `laws`).
- **base**: If TRUE, the position of clone is the physical position onto the chromosome, otherwise the rank position is used.
- **sigma**: Value to be passed to either argument `sigma2` of `aws` function or shape of `laws`. If NULL, sigma is calculated from the data.
- **lambdabreak**: Penalty term (\(\lambda\))' used during the Optimization of the number of breakpoints step.
The function `glad` implements the methodology which is described in the article: Analysis of array CGH data: from signal ratio to gain and loss of DNA regions (Hupé et al., Bioinformatics, 2004).

The principle of the GLAD algorithm: First, the detection of breakpoints is based on the estimation of a piecewise constant function with the Adaptive Weights Smoothing (AWS) procedure (Polzehl and Spokoiny, 2002). Alternatively, it is possible to use the HaarSeg algorithm (Ben-Yaacov and Eldar, Bioinformatics, 2008). Thus, a procedure based on penalized maximum likelihood optimizes the number of breakpoints allows the undesirable breakpoints to be removed. Finally, based on the regions previously identified, a two-step unsupervised classification (MSHR clustering by chromosome and the HCSR clustering throughout the genome) with model selection criteria allows a status to be assigned for each region (gain, loss or normal).

Main parameters to be tuned:

- `qlambda` if you want the smoothing to fit some very local effect, choose a smaller `qlambda`.
- `bandwidth` choose a bandwidth not to small otherwise you will have a lot of little discontinuities.
- `lambdabreak` More the parameter is high more the number of undesirable breakpoints is high.
- `lambdacluster` More the parameter is high more the regions within a chromosome are supposed to belong to the same cluster.
- `lambdaclusterGen` More the parameter is high more the regions over the whole genome are supposed to belong to the same cluster.

Details

An object of class "profileCGH" with the following attributes:
profileValues:
 a data.frame with the following added information:

   **Smoothing**  The smoothing values correspond to the median of each MSHR (i.e. Region).

   **Breakpoints**  The last position of a region with identical amount of DNA is flagged by 1 otherwise it is 0. Note that during the "Optimization of the number of breakpoints" step, removed breakpoints are flagged by -1.

   **Region**  Each position between two breakpoints are labelled the same way with an integer value starting from one. The label is incremented by one when a new breakpoints occurs or when moving to the next chromosome. The variable region is what we call MSHR.

   **Level**  Each position with equal smoothing value are labelled the same way with an integer value starting from one. The label is incremented by one when a new level occurs or when moving to the next chromosome.

   **OutliersAws**  Each AWS outliers are flagged by -1 or 1 otherwise it is 0.

   **OutliersMad**  Each MAD outliers are flagged by -1 (if it is in the $\alpha/2$ lower tail of the distribution) or 1 (if it is in the $\alpha/2$ upper tail of the distribution) otherwise it is 0.

   **OutliersTot**  OutliersAws + OutliersMad.

   **ZoneChr**  Clusters identified after MSHR (i.e. Region) clustering by chromosome.

   **ZoneGen**  Clusters identified after HCSR clustering throughout the genome.

   **ZoneGNL**  Status of each clone : Gain is coded by 1, Loss by -1 and Normal by 0.

BkpInfo:  the data.frame attribute BkpInfo which gives the list of breakpoints:

   **PosOrder**  The rank position of each clone on the genome.

   **PosBase**  The base position of each clone on the genome.

   **Chromosome**  Chromosome name.

SigmaC:  the data.frame attribute SigmaC gives the estimation of the LogRatio standard-deviation for each chromosome:

   **Chromosome**  Chromosome name.

   **Value**  The estimation is based on the Inter Quartile Range.

**Note**

People interested in tools dealing with array CGH analysis can visit our web-page [http://bioinfo.curie.fr](http://bioinfo.curie.fr).

**Author(s)**

Philippe Hupé. (glad@curie.fr).

**References**

Hupé et al. (Bioinformatics, 2004)  Analysis of array CGH data: from signal ratio to gain and loss of DNA regions.


Ben-Yaacov and Eldar (Bioinformatics, 2008)  A fast and flexible method for the segmentation of aCGH data.

**See Also**

profileCGH, as.profileCGH, plotProfile.
Examples

data(snijders)

### Creation of "profileCGH" object
gm13330$Clone <- gm13330$BAC
profileCGH <- as.profileCGH(gm13330)

###########################################################
### glad function as described in Hupé et al. (2004)###
###########################################################
res <- glad(profileCGH, mediancenter=FALSE,
            smoothfunc="lawsglad", bandwidth=10, round=1.5,
            model="Gaussian", lkern="Exponential", qlambda=0.999,
            base=FALSE,
            lambdabreak=8, lambdacluster=8, lambdaclusterGen=40,
            type="tricubic", param=c(d=6),
            alpha=0.001, msize=5,
            method="centroid", nmax=8,
            verbose=FALSE)

### Genomic profile on the whole genome
plotProfile(res, unit=3, Bkp=TRUE, labels=FALSE, Smoothing="Smoothing",
            main="Breakpoints detection: GLAD analysis")

### Genomic profile for chromosome 1
plotProfile(res, unit=3, Bkp=TRUE, labels=TRUE, Chromosome=1,
            Smoothing="Smoothing", main="Chromosome 1: GLAD analysis")

### The standard-deviation of LogRatio are:
res$SigmaC

### The list of breakpoints is:
res$BkpInfo

hclustglad

Hierarchical Clustering

Description

Hierarchical cluster analysis on a set of dissimilarities and methods for analyzing it.

Usage

hclustglad(d, method = "complete", members=NULL)
Arguments

d
- a dissimilarity structure as produced by dist.

method
- the agglomeration method to be used. This should be (an unambiguous abbreviation of) one of "ward", "single", "complete", "average", "mcquitty", "median" or "centroid".

members
- NULL or a vector with length size of d.

Details

This function performs a hierarchical cluster analysis using a set of dissimilarities for the n objects being clustered. Initially, each object is assigned to its own cluster and then the algorithm proceeds iteratively, at each stage joining the two most similar clusters, continuing until there is just a single cluster. At each stage distances between clusters are recomputed by the Lance–Williams dissimilarity update formula according to the particular clustering method being used.

A number of different clustering methods are provided. Ward's minimum variance method aims at finding compact, spherical clusters. The complete linkage method finds similar clusters. The single linkage method (which is closely related to the minimal spanning tree) adopts a ‘friends of friends’ clustering strategy. The other methods can be regarded as aiming for clusters with characteristics somewhere between the single and complete link methods.

If members!=NULL, then d is taken to be a dissimilarity matrix between clusters instead of dissimilarities between singletons and members gives the number of observations per cluster. This way the hierarchical cluster algorithm can be “started in the middle of the dendrogram”, e.g., in order to reconstruct the part of the tree above a cut (see examples). Dissimilarities between clusters can be efficiently computed (i.e., without hclustglad itself) only for a limited number of distance/linkage combinations, the simplest one being squared Euclidean distance and centroid linkage. In this case the dissimilarities between the clusters are the squared Euclidean distances between cluster means.

In hierarchical cluster displays, a decision is needed at each merge to specify which subtree should go on the left and which on the right. Since, for n observations there are n−1 merges, there are \(2^{(n-1)}\) possible orderings for the leaves in a cluster tree, or dendrogram. The algorithm used in hclustglad is to order the subtree so that the tighter cluster is on the left (the last, i.e. most recent, merge of the left subtree is at a lower value than the last merge of the right subtree). Single observations are the tightest clusters possible, and merges involving two observations place them in order by their observation sequence number.

Value

An object of class hclust which describes the tree produced by the clustering process. The object is a list with components:

merge
- an n−1 by 2 matrix. Row i of merge describes the merging of clusters at step i of the clustering. If an element j in the row is negative, then observation −j was merged at this stage. If j is positive then the merge was with the cluster formed at the (earlier) stage j of the algorithm. Thus negative entries in merge indicate agglomerations of singletons, and positive entries indicate agglomerations of non-singletons.

height
- a set of n−1 non-decreasing real values. The clustering height: that is, the value of the criterion associated with the clustering method for the particular agglomeration.
order a vector giving the permutation of the original observations suitable for plotting, in the sense that a cluster plot using this ordering and matrix merge will not have crossings of the branches.

labels labels for each of the objects being clustered.

call the call which produced the result.

method the cluster method that has been used.

dist.method the distance that has been used to create d (only returned if the distance object has a "method" attribute).

Author(s)

The hclustglad function is based an Algorithm contributed to STATLIB by F. Murtagh.

References


See Also

hclustglad kmeans.

Examples

data(USArrests)
hc <- hclustglad(dist(USArrests), "ave")
plot(hc)
plot(hc, hang = -1)

## Do the same with centroid clustering and squared Euclidean distance,
## cut the tree into ten clusters and reconstruct the upper part of the
## tree from the cluster centers.
hc <- hclustglad(dist(USArrests)^2, "cen")
memb <- cutree(hc, k = 10)
cent <- NULL
for(k in 1:10){
  cent <- rbind(cent, colMeans(USArrests[memb == k, , drop = FALSE]))
}
hc1 <- hclustglad(dist(cent)^2, method = "cen", members = table(memb))
par <- par(mfrow = c(1, 2))
plot(hc, labels = FALSE, hang = -1, main = "Original Tree")
plot(hc1, labels = FALSE, hang = -1, main = "Re-start from 10 clusters")
par(opar)
**Kernelpen function**

**Description**

Kernel function used in the penalty term.

**Usage**

```r
kernelpen(x, type="tricubic", param)
```

**Arguments**

- `x`: Real Value.
- `type`: Type of kernelpen to be used
- `param`: a named vector.

**Details**

The only kernel available is the "tricubic" kernel which takes the values 

\[(1 - (x/d)^3)^3\]

The value of d is given by `param=c(d=6)` for example.

**Note**

People interested in tools dealing with array CGH analysis can visit our web-page [http://bioinfo.curie.fr](http://bioinfo.curie.fr).

**Author(s)**

Philippe Hupé, (glad@curie.fr)

---

**myPalette**

**Microarray color palette**

**Description**

This function returns a vector of color names corresponding to a range of colors specified in the arguments.

**Usage**

```r
myPalette(low = "white", high = c("green", "red"), mid=NULL, k =50)
```
**Arguments**

- **low**: Color for the lower end of the color palette, specified using any of the three kinds of R colors, i.e., either a color name (an element of `colors`), a hexadecimal string of the form "#rrggbb", or an integer i meaning `palette()[i]`.

- **high**: Color for the upper end of the color palette, specified using any of the three kinds of R colors, i.e., either a color name (an element of `colors`), a hexadecimal string of the form "#rrggbb", or an integer i meaning `palette()[i]`.

- **mid**: Color for the middle portion of the color palette, specified using any of the three kinds of R colors, i.e., either a color name (an element of `colors`), a hexadecimal string of the form "#rrggbb", or an integer i meaning `palette()[i]`.

- **k**: Number of colors in the palette.

**Value**

A "character" vector of color names. This can be used to create a user-defined color palette for subsequent graphics by `palette`, in a `col=` specification in graphics functions, or in `par`.

**Author(s)**

Sandrine Dudoit, Yee Hwa (Jean) Yang.

**See Also**

`palette`, `rgb`, `colors`, `col2rgb`, `image`, `ColorBar`, `arrayPlot`.

**Examples**

```r
par(mfrow=c(1,4))
pal <- myPalette(low="red", high="green")
ColorBar(seq(-2, 2, 0.2), col=pal, horizontal=FALSE, k=21)
pal <- myPalette(low="red", high="green", mid="yellow")
ColorBar(seq(-2, 2, 0.2), col=pal, horizontal=FALSE, k=21)
pal <- myPalette()
ColorBar(seq(-2, 2, 0.2), col=pal, horizontal=FALSE, k=21)
pal <- myPalette(low="purple", high="purple", mid="white")
ColorBar(seq(-2, 2, 0.2), col=pal, horizontal=FALSE, k=21)
```

---

**plotProfile**

**Plot genomic profile and cytogenetic banding**

**Description**

Plot genomic profile with breakpoints, outliers, smoothing line and cytogenetic banding.
## Usage

```r
## S3 method for class 'profileCGH':
plotProfile(profileCGH, variable="LogRatio", Chromosome=NULL,
            Smoothing=NULL, GNL="ZoneGNL", Bkp=FALSE,
            labels=TRUE, plotband=TRUE, unit=0,
            colDAGLAD=c("black","blue","red","green","yellow"),
            pchSymbol=c(20,13),
            colCytoBand=c("white","darkblue"),
            colCentro="red", text=NULL, main="", ylim=NULL, ...)
```

### Arguments

- **profileCGH**: Object of class `profileCGH`
- **variable**: The variable to be plot.
- **Chromosome**: A numeric vector with chromosome number to be plotted. Use 23 and 24 for chromosome X and Y respectively. If `NULL`, all the genome is plotted.
- **Smoothing**: The variable used to plot the smoothing line. If `NULL`, nothing is plotted.
- **GNL**: The variable used to plot the Gain, Normal and Loss color code.
- **Bkp**: If `TRUE`, the breakpoints are represented by a vertical red dashed line.
- **labels**: If `TRUE`, the labels of the cytogenetic banding are written.
- **plotband**: If `TRUE`, the cytogenetic banding are plotted.
- **unit**: Give the unit of the PosBase. For example if `unit=3`, PosBase are in Kb, if `unit=6`, PosBase are in Mb, ...
- **colDAGLAD**: Color code to plot Deletion, Amplification, Gain, Lost and Normal status.
- **pchSymbol**: A vector of two elements to specify the symbol tu be used for plotting point. `pchSymbol[2]` is the symbol for outliers.
- **colCytoBand**: Color code for cytogenetic banding.
- **colCentro**: Color code for centromere.
- **text**: A list with the parameters to be passed to the function `text`.
- **main**: title of the plot.
- **ylim**: range of the y-axis

### Details

```
```

### Value

A plot

### Note

People interested in tools dealing with array CGH analysis can visit our web-page [http://bioinfo.curie.fr](http://bioinfo.curie.fr).
Author(s)  
Philippe Hupé, (glad@curie.fr).

See Also  

Examples

```r
### Cytogenetic banding information
data(cytoband)

###
data(snijders)

### Creation of "profileCGH" object
profileCGH <- as.profileCGH(gm13330)

### glad function as described in Hupé et al. (2004)
res <- glad(profileCGH, mediancenter=FALSE, smoothfunc="lawsglad", bandwidth=10, round=2, model="Gaussian", lkern="Exponential", qlambda=0.999, base=FALSE, lambdabreak=8, lambdacluster=8, lambdaclusterGen=40, type="tricubic", param=c(d=6), alpha=0.001, msize=5, method="centroid", nmax=8, verbose=FALSE)

### Genomic profile on the whole genome
plotProfile(res, unit=3, Bkp=TRUE, labels=FALSE, Smoothing="Smoothing", plotband=FALSE)

### Genomic profile on the whole genome and cytogenetic banding
plotProfile(res, unit=3, Bkp=TRUE, labels=FALSE, Smoothing="Smoothing")

### Genomic profile for chromosome 1
text <- list(x=c(90000,200000), y=c(0.15,0.3), labels=c("NORMAL","GAIN"), cex=2)
plotProfile(res, unit=3, Bkp=TRUE, labels=TRUE, Chromosome=1, Smoothing="Smoothing", plotband=FALSE, text=text)

### Genomic profile for chromosome 1 and cytogenetic banding with labels
plotProfile(res, unit=3, Bkp=TRUE, labels=TRUE, Chromosome=1, Smoothing="Smoothing", text=text, main="Chromosome 1")
```
Objects of Class `profileCGH` and `profileChr`

**Description**

Description of the objects `profileCGH` and `profileChr`. The last object corresponds to data of only one chromosome.

**Details**

LogRatio, Chromosome and PosOrder are compulsory.

**Value**

Objects `profileCGH` and `profileChr` are composed of a list with the first element `profileValues` which is a `data.frame` with the following columns names:

<table>
<thead>
<tr>
<th>Column</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>LogRatio</td>
<td>Test over Reference log-ratio.</td>
</tr>
<tr>
<td>PosOrder</td>
<td>The rank position of each clone on the genome.</td>
</tr>
<tr>
<td>PosBase</td>
<td>The base position of each clone on the genome.</td>
</tr>
<tr>
<td>Chromosome</td>
<td>Chromosome name.</td>
</tr>
<tr>
<td>Clone</td>
<td>The name of the corresponding clone.</td>
</tr>
<tr>
<td>...</td>
<td>Other elements can be added.</td>
</tr>
</tbody>
</table>

**Note**

People interested in tools dealing with array CGH analysis can visit our web-page [http://bioinfo.curie.fr](http://bioinfo.curie.fr).

**Author(s)**

Philippe Hupé, (glad@curie.fr).

**See Also**

`glad`, `as.profileCGH`.

**Examples**

```r
data(snijders)
gm13330$Clone <- gm13330$BAC
profileCGH <- as.profileCGH(gm13330)
class(profileCGH) <- "profileCGH"

profileChr <- as.profileCGH(gm13330[which(gm13330$Chromosome==1),])
class(profileChr) <- "profileChr"
```
snijders  

Public CGH data of Snijders

Description

The data consist of 15 human cell strains with known karyotype (12 fibroblast cell strains, 2 chorionic villus cell strains, 1 lymphoblast cell strain) from the NIGMS Human Genetics Cell Repository (http://locus.umdnj.edu/nigms). Each cell strain has been hybridized onto a CGH-array of 2276 BAC’s spotted in triplicate.

Usage

data(snijders)

Source

http://www.nature.com/ng/journal/v29/n3/suppinfo/ng754_S1.html

References


Examples

data(snijders)
array <- gm13330

tkdaglad  

Graphical interface for GLAD package

Description

A graphical interface to analyse array CGH data.

Arguments

list  
A character vector with the array to be analysed

Note

People interested in tools dealing with array CGH analysis can visit our web-page http://bioinfo.curie.fr.

Author(s)

Philippe Hupé, (glad@curie.fr).
See Also

glad, daglad, plotProfile.

Examples

data(snijders)
array1 <- as.profileCGH(gm13330)
array2 <- as.profileCGH(gm04435)

## tkdaglad(c("array1","array2"))
## tkglad(c("array1","array2"))

veltman

Public CGH data of Veltman

Description


Usage

data(veltman)

Source

http://cancerres.aacrjournals.org/cgi/content/full/63/11/2872

References


Examples

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