curvHDRfilter

Filtering via the curvHDR method.

Description

Filter univariate or bivariate data using the curvHDR method. The motivating application is flow
cytometry, where the filters endeavour to mimic human-perceived gates.

Usage

curvHDRfilter(x, HDRlevel, growthFac = NULL, signifLevel = 0.05,
    bwFac = 1, gridsize = NULL, removeDebri = TRUE,
    minSampSize = NULL, HpiGridSize = NULL, quiet = TRUE,
    graphChk = FALSE)

Arguments

x
    array containing the input data, typically corresponding to flow cytometric mea-
    surements. x should either be a numerical vector (univariate input data) or a
    matrix or data frame having 1-3 columns.

HDRlevel
    number between 0 and 1 corresponding to the level of the highest density region
    within each high curvature region.

growthFac
    growth factor parameter. High curvature regions are grown to have ‘volume’
growthFac times larger than the original region. The default value of growthFac is
    5^(d/2) where d is the dimension of the input data.

signifLevel
    number between 0 and 1 corresponding to the significance level for curve region
determination. The default value of signifLevel is 0.05.

bwFac
    bandwidth factor. The default bandwidth is multiplied by bwFac. The default
    value of bwFac is 1.

gridsize
    vector of number of grid points in each direction

removeDebri
    Boolean flag for removal of ‘debri’ points in the input data. The default value of
    removeDebri is true.

minSampSize
    curvHDR regions with less than minSampSize are excluded. The default value of
    minSampSize is 50^(d-1)) where d is the dimension of the input data.

HpiGridSize
    gridsize used for plug-in bandwidth selection in the case where the input data is
    trivariate. The default value of HpiGridSize is rep(21,3).

quiet
    Boolean flag for ‘quiet’ running. If quiet is FALSE then progress reports on
    during filter determination are given. The default value of quiet is TRUE

graphChk
    Boolean flag for graphical checking. If graphChk is TRUE then graphical dis-
    plays for each stage of the curvHDRfilter() are sent to the screen. At the first
    stage, the input data are plotted. Then the high negative curvature regions are
    shown in purple. This is followed by a display, in green, of the growthFac-
magnifications of the convexified high negative curvature regions. The final
    gates, corresponding to highest density regions for each green region, are shown
    in blue. The default value of graphChk is FALSE.
Value

- **data**: the input data (for use in plotting).
- **insideFilter**: logical variable indicating the rows of the input data matrix corresponding to points inside the curvHDR filter.
- **polys**: the curvHDR filter. Depending on the dimension d this is a list of intervals (d=1), polygons (d=2) or polyhedra (d=3).
- **HDRlevel**: highest density region level

Author(s)

G. Luta, U. Naumann and M.P. Wand

References


See Also

- `plot.curvHDRfilter`

Examples

```r
library(curvHDR)

# Univariate curvHDR examples:
xUniv <- c(rnorm(1000,-2),rnorm(1000,2))
gate1a <- curvHDRfilter(xUniv)
plot(gate1a)
print(gate1a$poly)  # List of intervals that define gate1a.
## Not run: print(gate1a$insideFilter)  # Indicators of inclusion of
   # xUniv inside gate1a.

## End(Not run)

gate1b <- curvHDRfilter(xUniv,HDRlevel=0.5)
plot(gate1b)
print(gate1b$poly)  # List of intervals that define gate1b.
## Not run: print(gate1b$insideFilter)  # Indicators of inclusion of
   # xUniv inside gate1b.

## End(Not run)

# Bivariate curvHDR examples:
xBiva <- cbind(c(rnorm(1000,-2),rnorm(1000,2)),
                c(rnorm(1000,-2),rnorm(1000,2)))
```
curvHDR vignette

Display the package’s vignette.

Description

The vignette of the curvHDR package is displayed using the default PDF file browser. It provides a detailed description of use of the package for gating flow cytometry data using the curvHDR method.
Usage

```
curvHDRvignette()
```

Author(s)

Matt Wand (matt.wand@uts.edu.au), G. Luta (gl77@georgetown.edu) and U. Naumann (ulrike.naumann1@gmail.com)

Examples

```
curvHDRvignette()
```

---

**plot.curvHDRfilter**  
*Plot a curvHDR filter.*

Description

Takes an object of class `curvHDR`, produced by `curvHDRfilter()`, and then plots it together with (a subset of) the data.

Usage

```
## S3 method for class 'curvHDRfilter'
plot(x, removeDebri = TRUE, pch = NULL, cex = NULL, bty = NULL, col = NULL, main = NULL, ...)
```

Arguments

- `x`: an object of class `curvHDRfilter` produced by `curvHDRfilter()`.
- `removeDebri`: a boolean flag for removal of 'debri' points in the input data. Default is `TRUE`.
- `pch`: plotting character specification.
- `cex`: character expansion factor.
- `bty`: box-type for the plotting frame.
- `col`: colour of the points.
- `main`: main label on the plot.
- `...`: other graphical parameters.

Value

The function generates a plot.

Author(s)

G. Luta, U. Naumann and M.P. Wand
References


See Also

curvHDRfilter

Examples

```r
library(curvHDR)

# Univariate curvHDR example:

xUniv <- c(rnorm(1000,-2),rnorm(1000,2))
gate1 <- curvHDRfilter(xUniv)
plot(gate1)

# Bivariate curvHDR example:

xBiva <- cbind(c(rnorm(1000,-2),rnorm(1000,2)),
               c(rnorm(1000,-2),rnorm(1000,2)))
gate2 <- curvHDRfilter(xBiva)
plot(gate2)

# Trivariate curvHDR example:

## Not run:
xTriv <- cbind(c(rnorm(1000,-2),rnorm(1000,2)),
               c(rnorm(1000,-2),rnorm(1000,2)),
               c(rnorm(1000,-2),rnorm(1000,2)))
gate3 <- curvHDRfilter(xTriv)
plot(gate3)

## End(Not run)
```
Index

*Topic **density estimation**
  curvHDRfilter, 2
  plot.curvHDRfilter, 5

*Topic **feature significance**
  curvHDRfilter, 2
  plot.curvHDRfilter, 5

*Topic **flow cytometry**
  curvHDRfilter, 2
  plot.curvHDRfilter, 5
  curvHDRfilter, 2, 6
  curvHDRvignette, 4

plot.curvHDRfilter, 3, 5