spotSegmentation

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plotBlockImage Plot Microarray Image Block

Description

Displays a block of a microarray image.

Usage

plotBlockImage(z,title,one)

Arguments

- **z**
  - Intensities of the image pixels, in the form a of a matrix.
- **title**
  - A title for the image plot (optional).
- **one**
  - Sets appropriate graphics parameters for displaying individuals spots (default:FALSE).

Value

None, other than the displayed plot.

References

See Also

spotseg

Examples

```R
data(spotSegTest)

# columns of spotSegTest:
# 1 intensities from the Cy3 (green) channel
# 2 intensities from the Cy5 (red) channel

dataTransformation <- function(x) (256*256-1-x)^2*4.71542407E-05

chan1 <- matrix(dataTransformation(spotSegTest[,1]), 144, 199)
chan2 <- matrix(dataTransformation(spotSegTest[,2]), 144, 199)

plotBlockImage(chan1)
plotBlockImage(chan2)
```

Description

Plot method for the `spotseg` function. Displays the result obtained from microarray spot segmentation via model-based clustering.

Usage

```R
## S3 method for class 'spotseg':
plot(x,...)
```

Arguments

- `x` An object of class "spotseg", which is the output of the function `spotseg`
- `...` Unused but required by generic "plot" method.

Value

None, other than the displayed plot.

References


See Also

spotseg
Examples

data(spotSegTest)

# columns of spotSegTest:
# 1 intensities from the Cy3 (green) channel
# 2 intensities from the Cy5 (red) channel

dataTransformation <- function(x) (256*256-1-x)^2*4.71542407E-05

chan1 <- matrix(dataTransformation(spotSegTest[,1]), 144, 199)
chan2 <- matrix(dataTransformation(spotSegTest[,2]), 144, 199)

hivGrid <- spotgrid(chan1, chan2, rows = 4, cols = 6, show = TRUE)

library(mclust)

hivSeg <- spotseg(chan1, chan2, hivGrid$rowcut, hivGrid$colcut)

plot(hivSeg)

spotgrid

Gridding for Blocks of Microarray Spots

Description

Determines row or column delimiters for spot locations from blocks of microarray slide image data.

Usage

spotgrid(chan1, chan2, rows = NULL, cols = NULL, span = NULL, show = FALSE)

Arguments

- chan1: matrix of pixel intensities from the first channel.
- chan2: matrix of pixel intensities from the second channel.
- rows: number of spots in a row of the image block.
- cols: number of spots in a column of the image block.
- span: Window size for locating peak signals. This can be of length 2, in which case the first value is interpreted as a window size for the rows and the second as a window size for the columns. A default is estimated from the image dimension and number of spots.
- show: logical variable indicating whether or not to display the gridding result.

Value

A list with two elements, rowcut and colcut giving delimiters for the row and/or column gridding of the slide. The indexes indicate the start of a segment of the grid, except for the last one, which indicates the end of the grid.
References


See Also

spotseg

Examples

data(spotSegTest)

# columns of spotSegTest:
# 1 intensities from the Cy3 (green) channel
# 2 intensities from the Cy5 (red) channel

dataTransformation <- function(x) (256*256-1-x)^2*4.71542407E-05

chan1 <- matrix(dataTransformation(spotSegTest[,1]), 144, 199)
chan2 <- matrix(dataTransformation(spotSegTest[,2]), 144, 199)

Grid <- spotgrid( chan1, chan2, rows = 4, cols = 6, show = TRUE)

spotseg

Microarray Spot Segmentation

Description

Microarray spot segmentation via model-based clustering.

Usage

spotseg(chan1, chan2, rowcut, colcut, R=NULL, C=NULL,
        threshold=100, hc=FALSE, show=FALSE)

Arguments

chan1          matrix of pixel intensities from the first channel.
chan2          matrix of pixel intensities from the second channel.
rowcut         row delimiters for the spots. Entries are the starting row location in the close of each spot, with the last entry being one pixel beyond the border of the last spot. For example, from the output of spotgrid.
colcut         column delimiters for the spots. Entries are the starting column location in the close of each spot, with the last entry being one pixel beyond the border of the last spot. For example, from the output of spotgrid.
R              rows over which the spots are to be segmented. The default is to segment spots in all rows.
C              columns over which the spots are to be segmented. The default is to segment spots in all columns.
threshold connected components of size smaller than threshold are ignored. Default: threshold=100.

hc logical variable indicating whether or not EM should be initialized by hierarchical clustering or quantiles in model-based clustering. The default is to use quantiles hc = FALSE, which is more efficient both in terms of speed and memory usage.

show logical variable indicating whether or not to display the segmentation of each individual spot as it is processed. The default is not to display the spots show = FALSE.

Details

There are plot and summary methods that can be applied to the result.

Value

An array of the same dimensions as the image in which the pixels are labeled according to their group within the spot area: 1=background, 2=uncertain, 3=sample.

Note

The mclust package is required for clustering.

References


See Also

summary.spotseg, plot.spotseg, spotgrid

Examples

data(spotSegTest)

# columns of spotSegTest:
# 1 intensities from the Cy3 (green) channel
# 2 intensities from the Cy5 (red) channel

dataTransformation <- function(x) (256*256-1-x)^2*4.71542407E-05

chan1 <- matrix(dataTransformation(spotSegTest[,1]), 144, 199)
chan2 <- matrix(dataTransformation(spotSegTest[,2]), 144, 199)

Grid <- spotgrid( chan1, chan2, rows = 4, cols = 6, show = TRUE)

library(mclust)

Seg <- spotseg( chan1, chan2, Grid$rowcut, Grid$colcut)

plot(Seg)

spotSummary <- summary(Seg)
spotSegTest <- spotseg(chan1, chan2, Grid$rowcut, Grid$colcut,
                      R = 1, C = 1, show = TRUE)

| spotSegTest | Spot Segmentation Test Data |

**Description**

The two columns of this data set represent the Cy3 (green) absorption intensities for channel 1, and the Cy5 (red) absorption intensities for channel 2 for part of a dye-swap experiment with replicates. They measure expression levels of cellular RNA transcripts assessed in CD4+ T cell lines at different times after infection with HIV-1BRU using DNA microarrays.

**Usage**

data(spotSegTest)

**Format**

Each column is a vector of intensities of 24 spots arranged in 4 rows and 6 columns, encoded for compact (16-bit TIFF) storage. For processing each column of `spotSegTest` should first be converted to a 144x199 matrix, then applying the transformation described below.

**Details**

The intensities can be obtained from this data by first subtracting them from 65535 (256*256-1), then squaring, then multiplying by a scale factor 4.71542407E-05. In other words, a number \( x \) in the `spotSegTest` data set corresponds to intensity

\[
(256 \times 256 - 1 - x)^2 \times 0.0000471542407
\]

**Source**

Dr. Angelique van’t Wout, Department of Microbiology, University of Washington. The data is a subset the first block of a 12 block array image (‘001030_08_1.GEL’) in the first data set (‘2000095918 A’) in the first experiment (‘CEM LAI vs HI-LAI 24hr’) of the following data archive: http://expression.microslu.washington.edu/expression/vantwoutjvi2002.html

**References**

Microarray Spot Segmentation Summary

Description

Summary method for the `spotseg` function. Gives the estimates of foreground and background intensity obtained from microarray spot segmentation via model-based clustering.

Usage

```r
## S3 method for class 'spotseg':
summary(object, ...)
```

Arguments

- `object` An object of class "spotseg", which is the output of the function `spotseg`.
- `...` Unused, but required by generic "summary" method.

Value

A list with two components, "channel1" and "channel2" each of which has subcomponents "background" and "foreground", each of which in turn has subcomponents "mean" and "median", giving the mean and median estimates of background and foreground for each channel. There will be missing entries (value NA) whenever no foreground is detected.

References


See Also

`spotseg`

Examples

```r
data(spotSegTest)

# columns of spotSegTest:
# 1 intensities from the Cy3 (green) channel
# 2 intensities from the Cy5 (red) channel

dataTransformation <- function(x) (256*256-1-x)^2*4.71542407E-05

chan1 <- matrix(dataTransformation(spotSegTest[,1]), 144, 199)
chan2 <- matrix(dataTransformation(spotSegTest[,2]), 144, 199)

hivGrid <- spotgrid( chan1, chan2, rows = 4, cols = 6, show = TRUE)
library(mclust)

hivSeg <- spotseg( chan1, chan2, hivGrid$rowcut, hivGrid$colcut)
```
hivSummary <- summary(hivSeg)
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