Package ‘mimager’

April 26, 2017

Version  1.0.0
Type     Package
Title    mimager: The Microarray Imager
Description Easily visualize and inspect microarrays for spatial artifacts.
License  MIT + file LICENSE
LazyData TRUE
Depends  Biobase
Imports  BiocGenerics, S4Vectors, preprocessCore, grDevices, methods, grid, gtable, scales, DBI, affy, affyPLM, oligo, oligoClasses
Collate  'mimager-package.r' 'all-generics.r' 'mimage.r' 'marray.r'
          'mindex.r' 'build-legend.r' 'checks.r' 'transformations.r'
          'utils-affy.r' 'utils-arrays.r' 'utils-plot.r'
Suggests knitr, rmarkdown, BiocStyle, testthat, lintr, Matrix, abind, affydata, hgu95av2cdf, oligoData, pd.hugene.1.0.st.v1
VignetteBuilder knitr
URL      https://github.com/aaronwolen/mimager
BugReports https://github.com/aaronwolen/mimager/issues
RoxygenNote 5.0.1
biocViews Infrastructure, Visualization, Microarray
NeedsCompilation no
Author    Aaron Wolen [aut, cre, cph]
Maintainer Aaron Wolen <aaron@wolen.com>

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arank

Array rank

Description
Determines the rank of values within each matrix of a three-dimensional array.

Usage
arank(x, na.last = TRUE, ties.method = "first")

Arguments
- **x**: a three-dimensional array of matrices
- **na.last**: for controlling the treatment of NAs. If TRUE, missing values in the data are put last; if FALSE, they are put first; if NA, they are removed; if "keep" they are kept with rank NA.
- **ties.method**: a character string specifying how ties are treated, see 'Details'; can be abbreviated.

Value
an array with the same dimensions as x

See Also
- rank

Other array.transformations: arle

Examples

```r
# microarray visualization
if (require(affydata, quietly = TRUE)) {
  data("Dilution", package = "affydata")
  x <- arank(marray(Dilution, transpose = TRUE))
}
```

arle

Array relative log expression

Description
The relative log expression (RLE) quantifies the extent to which each sample in a dataset differs from a "reference" sample, which represents each probe's median value across all samples.

Usage
arle(x, log2 = TRUE, normalize = TRUE)
**marray**

**Arguments**

- **x** a three-dimensional array of matrices
- **log2** should values be \( \log_2 \) transformed
- **normalize** should values be quantile normalized

**Value**

an array with the same dimensions as x

**See Also**

RLE

Other array.transformations: arank

**Examples**

# microarray visualization
if (require(affydata, quietly = TRUE)) {
  data("Dilution", package = "affydata")
  x <- arle(marray(Dilution, transpose = TRUE))
}

---

**marray**  
*Microarray array*

**Description**

Convert S4 microarray data structures into a three-dimensional array of matrices, where each matrix corresponds to an individual sample’s microarray with values arranged to reflect the physical position of the corresponding feature (i.e., probe) on the microarray surface.

**Usage**

marray(object, type = NULL, select = NULL, transpose = NULL)

### S4 method for signature 'AffyBatch'
marray(object, type = "pm", select = NULL, 
transpose = FALSE)

### S4 method for signature 'PLMset'
marray(object, type = "residuals", select = NULL, 
transpose = FALSE)

### S4 method for signature 'FeatureSet'
marray(object, type = "pm", select = NULL, 
transpose = FALSE)

### S4 method for signature 'oligoPLM'
marray(object, type = "residuals", select = NULL, 
transpose = FALSE)
Arguments

object a valid Bioconductor microarray data structure
type for microarray objects type refers to probe type; for objects containing probe-level models (e.g., PLMsets) type refers to the value type (i.e., "residuals" or "weights"). See probe type section for more information.
select a numeric, character or logical vector indicating samples to include
transpose TRUE (the default), ensures the reconstructed microarrays are vertically oriented, as is typically expected. Set to FALSE to return an array in the orientation strictly specified by the platform coordinates

Value

three-dimensional array

Probe types

For microarray data structures the type argument determines the type of probe that should be included. The following table provides a list of valid values for each supported microarray class:

<table>
<thead>
<tr>
<th>Microarray Class</th>
<th>Type Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>AffyBatch</td>
<td>&quot;all&quot;, &quot;pm&quot;, &quot;mm&quot;</td>
</tr>
<tr>
<td>ExpressionFeatureSet</td>
<td>&quot;all&quot;, &quot;pm&quot;, &quot;mm&quot;</td>
</tr>
<tr>
<td>GeneFeatureSet</td>
<td>&quot;all&quot;, &quot;pm&quot;</td>
</tr>
<tr>
<td>ExonFeatureSet</td>
<td>&quot;all&quot;, &quot;pm&quot;, &quot;mm&quot;, &quot;bg&quot;</td>
</tr>
<tr>
<td>SnpFeatureSet</td>
<td>&quot;all&quot;, &quot;pm&quot;, &quot;mm&quot;</td>
</tr>
</tbody>
</table>

Examples

```r
if (require(affydata, quietly = TRUE)) {
  data("Dilution", package = "affydata")
  dilution.array <- marray(Dilution, select = c("20A", "10A"))
}
```

Description

Visualize microarray probe intensities arranged by their physical location on the array. A false color image is produced for each sample in the microarray object and arranged in a grid.

Usage

```r
mimage(object, type = NULL, select = NULL, colors = NULL, legend.label = NULL, nrow = NULL, ncol = NULL, fixed = FALSE, empty.rows = "fill", empty.thresh = 0.6, transform = NULL, trim = 0.01, fontsize = 12)
```

## S4 method for signature 'AffyBatch'
mimage(object, type = "pm", select = NULL,
       colors = NULL, legend.label = "Intensity", nrow = NULL, ncol = NULL,
       fixed = FALSE, empty.rows = "fill", empty.thresh = 0.6,
       transform = log2, trim = 0.01, fontsize = 12)

## S4 method for signature 'PLMset'
mimage(object, type = "residuals", select = NULL,
       colors = NULL, legend.label = type, nrow = NULL, ncol = NULL,
       fixed = FALSE, empty.rows = "fill", empty.thresh = 0.6,
       transform = identity, trim = 0.01, fontsize = 12)

## S4 method for signature 'FeatureSet'
mimage(object, type = "pm", select = NULL,
       colors = NULL, legend.label = "Intensity", nrow = NULL, ncol = NULL,
       fixed = FALSE, empty.rows = "fill", empty.thresh = 0.6,
       transform = log2, trim = 0.01, fontsize = 12)

## S4 method for signature 'oligoPLM'
mimage(object, type = "residuals", select = NULL,
       colors = NULL, legend.label = type, nrow = NULL, ncol = NULL,
       fixed = FALSE, empty.rows = "fill", empty.thresh = 0.6,
       transform = identity, trim = 0.01, fontsize = 12)

## S4 method for signature 'array'
mimage(object, type = NULL, select = NULL,
       colors = NULL, legend.label = "Values", nrow = NULL, ncol = NULL,
       fixed = FALSE, empty.rows = "ignore", empty.thresh = 1,
       transform = identity, trim = 0, fontsize = 12)

Arguments

object a valid Bioconductor microarray data structure

type for microarray objects type refers to probe type; for objects containing probe-
       level models (e.g., PLMsets) type refers to the value type (i.e, "residuals" or
       "weights"). See probe type section for more information.

select a numeric, character or logical vector indicating samples to include

colors a vector of colors used to represent probe values

legend.label Legend label

nrow optional, number of rows in grid layout

ncol optional, number of columns in grid layout

fixed Force images to assume a fixed aspect ratio corresponding to their physical di-

empty.rows Should empty rows be filled with values from neighboring rows (the default,
       "fill"), should they be dropped ("drop") entirely, or should they be left alone
       ("ignore")

empty.thresh what proportion of features must be missing from a row to consider that row empty

transform a function to be applied to the values prior to visualization

trim a percentile (default = 0.02) or range or 2 values see trimming section for
details

fontsize font size for labels and legend
Value

invisibly a gtable matrix of grobs

Trimming

By default, a 98% winsorization is performed prior to visualization, pulling in values outside of the 1st and 99th percentiles to their respective endpoints. This can be modified using the trim argument to provide either a new percentile, or a range of 2 values defining the min/max of the trimmed endpoints. Set trim = 0 to avoid trimming entirely.

Empty Rows

As a result of platform design, the presence unindexed probes or probe selection by the user (e.g., including only "pm" probes), the matrix-representation of a microarray can contain numerous rows comprised entirely (or mostly) of missing values, which may produce undesirable rasterization artifacts in the microarray image. To avoid this, empty rows are filled with values from a neighboring row. The threshold for what constitutes an empty row can be tweaked with the empty.thresh argument.

Probe types

For microarray data structures the type argument determines the type of probe that should be included. The following table provides a list of valid values for each supported microarray class:

<table>
<thead>
<tr>
<th>Class</th>
<th>all</th>
<th>pm</th>
<th>mm</th>
<th>bg</th>
</tr>
</thead>
<tbody>
<tr>
<td>AffyBatch</td>
<td>&quot;all&quot;</td>
<td>&quot;pm&quot;</td>
<td>&quot;mm&quot;</td>
<td>-</td>
</tr>
<tr>
<td>ExpressionFeatureSet</td>
<td>&quot;all&quot;</td>
<td>&quot;pm&quot;</td>
<td>&quot;mm&quot;</td>
<td>-</td>
</tr>
<tr>
<td>GeneFeatureSet</td>
<td>&quot;all&quot;</td>
<td>&quot;pm&quot;</td>
<td>-</td>
<td>&quot;bg&quot;</td>
</tr>
<tr>
<td>ExonFeatureSet</td>
<td>&quot;all&quot;</td>
<td>&quot;pm&quot;</td>
<td>&quot;mm&quot;</td>
<td>&quot;bg&quot;</td>
</tr>
<tr>
<td>SnpFeatureSet</td>
<td>&quot;all&quot;</td>
<td>&quot;pm&quot;</td>
<td>&quot;mm&quot;</td>
<td>-</td>
</tr>
</tbody>
</table>

Examples

# standard array visualization
mimage(iris3)

# microarray visualization
if (require(affydata, quietly = TRUE)) {
  data("Dilution", package = "affydata")
  mimage(Dilution, select = c("20A", "10A"))
}

mimager

mimager: The Microarray Imager

Description

mimager simplifies the creation of microarray images (sometimes called "pseudo-images") for the purpose of identifying problematic regional aberrations. Notable features include support for many of Bioconductor’s core microarray data structures, providing compatibility with a variety of common microarray platforms, and the ability to visualize multiple microarrays simultaneously.
Details

The following Bioconductor microarray data structures are currently supported:

- **AffyBatch-class** for Affymetrix GeneChip probe level data
- **PLMset-class** for probe-level linear models fitted to Affymetrix GeneChip probe level data
- **FeatureSet-class** for storing Expression/Exon/SNP data from a variety of oligonucleotide platforms
- **oligoPLM-class** for probe-level linear models fitted to any of the FeatureSet-like classes
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