Package ‘MmPalateMiRNA’

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MmPalateMiRNA-package  R package compendium for the analysis of murine palate two-color miRNA expression data

Description

R package compendium for the analysis of two-color miRNA expression data, during the period of murine embryonic palate development (gestational days (GD) 12, 13, and 14). Samples were hybridized to Miltenyi Biotech miRXplore Microarrays. The compendium covers a wide range of steps which occur in a typical miRNA microarray data analysis, including pre-processing, normalization, differential expression analysis, clustering, target identification, and gene-set enrichment analysis.

Details

Package: MmPalateMiRNA
Type: Package
Version: 1.0
Date: 2011-09-14
License: LGPL
LazyLoad: yes

The package contains several functions which are helpful during the pre-processing steps of array data, which are specific to RGList objects and, in the case of the fixOutliers and fixMVs functions, depend on the replicated structure of Miltenyi Biotech miRXplore Microarrays. Additionally, methods are available to produce diagnostic plots for RGList objects and lists of normalized data sets (MAList and/or NChannelSet objects), which build on the generic functions in lattice. Lastly, the main focus of the package is the package vignette "MmPalateMiRNA", which contains an extended example covering the typical steps in an miRNA microarray data analysis.
Author(s)
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References

checkMVs

Check an RGList object for missing values

Description
Checks each of the red and green foreground and background channels in an RGList object for missing values.

Usage
checkMVs(obj)
## S4 method for signature 'RGList'
checkMVs(obj)

Arguments
obj An RGList object

Value
Returns a list with the following components

R.na index of missing values in the red channel (obj$R)
Rb.na index of missing values in the red background channel (obj$Rb)
G.na index of missing values in the green channel (obj$G)
Gb.na index of missing values in the green background channel (obj$Gb)

Methods
signature(obj = "RGList")
checkOutliers

See Also

fixMVs, checkOutliers, fixOutliers

Examples

data(PalateData)
mvs <- checkMVs(PalateData)

Arguments

obj An RList object

Details

Checks each of the red and green foreground and background channels in an RList for outlying values.

Value

Returns a list with the following components

- Rout: index of outliers in the red channel (obj$R)
- Rbout: index of outliers in the red background channel (obj$Rb)
- Gout: index of outliers in the green channel (obj$G)
- Gbout: index of outliers in the green background channel (obj$Gb)

Methods

signature(obj = "RList")

See Also

fixOutliers, checkMVs, fixMVs
**Examples**

```r
data(PalateData)
outliers <- checkOutliers(PalateData)
```

---

**clustPlot**

*Plot expression profiles*

**Description**

Produces plots of clustered expression profiles, with separate plots for each cluster. The average expression profile for each cluster is superimposed as well.

**Usage**

```r
clustPlot(cl, mat, nrow, ncol)
```

**Arguments**

- `cl`: integer vector giving the cluster membership for each item
- `mat`: matrix of values to be plotted
- `nrow`: number of rows to use for plotting
- `ncol`: number of columns to use for plotting

**Details**

The figure region will be subdivided into `nrow` by `ncol` separate plots, using `mfrow`. The average expression profile and the number of genes belonging to each cluster is superimposed on each of the plots.

**References**


**See Also**

See the package vignette for illustration on usage

**Examples**

```r
## generate some fake data and cluster
set.seed(101)
mat <- matrix(rnorm(500), nrow=100, ncol=5)
clusts <- hclust(dist(mat))
cl <- cutree(clusts, 6)
clustPlot(cl, mat, 3, 2)
```
densityplot

Density plots of log2 intensity values

Description

Plots the estimated density of log2 intensity values for two-color microarrays

Usage

```r
## S4 method for signature 'RGList,missing'
densityplot(
  x,
  channel=c("G", "R"),
  group=NULL,
  subset=NULL,
  ...)
```

```r
## S4 method for signature 'list,missing'
densityplot(
  x,
  channel=c("G", "R"),
  group=NULL,
  subset=NULL,
  ...)
```

Arguments

- `x`: Either an `RGList` object, or a list containing `MAList` and/or `NChannelSet` objects
- `channel`: The channel to use for calculating distances, one of either "G" (green or control channel) or "R" (red or experimental channel)
- `group`: An optional character string specifying the name of a factor to create separate panel displays, which must be in `x$genes` (for `RGList` objects)
- `subset`: An optional character vector specifying the which levels of `group` to use in creating separate panel displays
- `...`: arguments to pass to `densityplot`

Methods

signature(x = "RGList", data = "missing") For `RGList` objects, separate panel displays can be produced for different types of probes, as determined by the group argument.

signature(x = "list", data = "missing") The method for list objects is intended to work with lists of normalized data sets, as either `MAList` or `NChannelSet` objects. This method will produce separate panel displays for each normalized data set, additionally subsetted by the group argument if supplied. The `useOuterStrips` function in the `latticeExtra` package can be used for 'outer' strip labels in the latter case.
References


See Also

levelplot for pairwise distance plots between arrays, MADvsMedianPlot for median absolute deviation versus median plots, and Maplot for MA plots

Examples

data(PalateData)
res < M densityplot(PalateData, channel="G", group="probe.type",
subset = c("Other miRNAs", "MMU miRNAs", "Control"),
col=rep(1:3, each=3), lty=rep(1:3, 3),
key = list(lines=list(col=rep(1:3, each=3), lty=rep(1:3, 3)),
columns=3))
print(res)

filterArray

Filter an RGList object to remove probes

Description

Filters an RGList object to remove probes with foreground intensities not sufficiently above the background intensity. Additionally can filter probes based on character strings, to remove e.g. control probes.

Usage

filterArray(obj, ...)  
## S4 method for signature 'RGList'
filterArray(obj, keep, frac, number, reps)

Arguments

obj  
An RGList object

keep  
Character vector to be used as a text filter. Only gene names (as contained in obj$genes$Name) which contain these text strings will be retained.

frac  
Fraction to use as a background filter. Only those probes with foreground values (both red and green) greater than 'frac' times the background values pass the filter.

number  
The number of samples required to pass the background filter for each probe.

reps  
The number of replicates for each probe required to pass the filtering step.

...  
allows additional arguments to be passed to specific methods
fixMVs

Value

Returns an RGList object identical in structure to the input object, but with reduced dimension according to the filtering steps.

Methods

signature(obj = "RGList")

See Also

checkMVs, fixMVs, checkOutliers, fixOutliers

Examples

data(PalateData)
reducedSet <- filterArray(PalateData, keep=c("MIR", "LET", "POCON", "CALIB"),
frac=1.1, number=3, reps=4)

fixMVs(mat, idx, gene.id)

Arguments

mat One of the red foreground (R), red background (Rb), green foreground (G), or green background (Gb) matrices in an RGList object, which contains missing values.
idx Index of missing values, as returned by the checkMVs function. See examples for usage.
gene.id Vector of gene IDs for each probe. See examples for usage.

Details

The function is specific to RGList objects which were created from Miltenyi Biotech miRXplore Microarrays, since it depends on the replicated structure of that array (probes spotted in quadruplicate) to impute the missing probe values.
Value

Returns a matrix with the missing probe values imputed.

See Also

checkMVs, checkOutliers, fixOutliers

Examples

data(PalateData)
mvs <- checkMVs(PalateData)
PalateData$rB <- fixMVs(PalateData$rB, mvs$rB, na, PalateData$genes$Gene)

Description

Imputes outlying values in one of the red foreground, red background, green foreground, or green background matrices of an RGList object created from Miltenyi Biotech miRXplore Microarrays. Uses the replicate structure of the array to impute the outlying values. Implicit assumption is that only one of the four replicated values for a probe is an outlying value.

Usage

fixOutliers(mat, idx, gene.ids)

Arguments

mat

One of the red foreground (R), red background (Rb), green foreground (G), or green background (Gb) matrices in an RGList object, which contains outlying values.

idx

Index of outlying values, as returned by the checkOutliers function. See examples for usage.

gene.ids

Vector of gene IDs for each probe. See examples for usage.

Details

The function is specific to RGList objects which were created from Miltenyi Biotech miRXplore Microarrays, since it depends on the replicated structure of that array (probes spotted in quadruplicate) to impute the outlying probe values.

Value

Returns a matrix with the outlying probe values imputed.
See Also

checkoutliers, checkMVs, fixMVs

Examples

data(PalateData)
  outliers <- checkoutliers(PalateData)
  PalateData$R <- fixOutliers(PalateData$R, outliers$Rout, PalateData$genes$Gene)

Description

Imputes missing values in a data matrix using the K-nearest neighbor algorithm.

Usage

imputeKNN(data, k = 10, distance = "euclidean", rm.na = TRUE, rm.nan = TRUE, rm.inf = TRUE)

Arguments

data a data matrix
k number of neighbors to use
distance distance metric to use, one of "euclidean" or "correlation"
rm.na should NA values be imputed?
rm.nan should NaN values be imputed?
rm.inf should Inf values be imputed?

Details

Uses the K-nearest neighbor algorithm, as described in Troyanskaya et al., 2001, to impute missing values in a data matrix. Elements are imputed row-wise, so that neighbors are selected based on the rows which are closest in distance to the row with missing values. There are two choices for a distance metric, either Euclidean (the default) or a correlation 'metric'. If the latter is selected, matrix values are first row-normalized to mean zero and standard deviation one to select neighbors. Values are 'un'-normalized by applying the inverse transformation prior to returning the imputed data matrix.

Value

A data matrix with missing values imputed.

Author(s)

Guy Brock
levelplot

References


See Also

See the package vignette for illustration on usage.

Examples

```r
## generate some fake data and impute MVs
set.seed(101)
mat <- matrix(rnorm(500), nrow=100, ncol=5)
idx.mv <- sample(1:length(mat), 50, replace=FALSE)
mat[idx.mv] <- NA
imputed <- imputeKNN(mat)
```

levelplot  

Pairwise distance between arrays

Description

Calculates and plots the pairwise distance between arrays, as measured by the median of the absolute differences in log2 intensity values.

Usage

```r
## S4 method for signature 'RGLlist,missing'
levelplot(
  x,
  channel=c("G", "R"),
  group=NULL,
  subset=NULL,
  ...
)

## S4 method for signature 'list,missing'
levelplot(
  x,
  channel=c("G", "R"),
  order=NULL,
  ...
)
```
Arguments

x
Either an RGList object, or a list containing MAList and/or NChannelSet objects

channel
The channel to use for calculating distances, one of either "G" (green or control channel) or "R" (red or experimental channel)

group
An optional character string specifying the name of a factor to create separate panel displays, which must be in x$genes (for RGList objects)

subset
An optional character vector specifying the which levels of group to use in creating separate panel displays

order
An optional numeric vector specifying the order of the arrays to use in producing the distance plots, i.e. for grouping certain arrays together

... arguments to pass to levelplot

Methods

signature(x = "RGList", data = "missing") For RGList objects, separate panel displays can be produced for different types of probes, as determined by the group argument.

signature(x = "list", data = "missing") The method for list objects is intended to work with lists of normalized data sets, as either MAList or NChannelSet objects. This method will produce separate panel displays for each normalized data set.

References


See Also
densityplot for density plots of log2 intensity values, MADvsMedianPlot for median absolute deviation versus median plots, and Maplot for MA plots

Examples

data(PalateData)
res <- levelplot(PalateData[, c(1,5,9,2:4,6:8)],
                 channel="G", group="probe.type",
                 subset=c("MMJ miRNAs", "Other miRNAs", "Control", "Empty"),
                 scales = list(rot=c(45, 45)))
print(res)
Description

Plots of the spread (median absolute deviation) versus the location (median) of probe intensity levels.

Usage

MADvsMedianPlot(x, ...)

## S4 method for signature 'list'
MADvsMedianPlot(
  x,
  channel=c("G", "R"),
  group=NULL,
  subset=NULL,
  ...)

Arguments

- **x**: A list containing MAList and/or NChannelSet objects.
- **channel**: The channel to use for calculating distances, one of either "G" (green or control channel) or "R" (red or experimental channel).
- **group**: An optional character string specifying the name of a factor to create separate panel displays, which must be in x$genes (for RList objects).
- **subset**: An optional character vector specifying the which levels of group to use in creating separate panel displays.
- **...**: arguments to pass to densityplot.

Methods

signature(x = "list") The method for list objects is intended to work with lists of normalized data sets, as either MAList or NChannelSet objects. This method will produce separate panel displays for each normalized data set, additionally color-coded by the group argument if supplied.

References

MAplot

See Also

levelplot for pairwise distance plots between arrays, densityplot for density plots of log2 intensity values, and MAplot for MA plots.

Examples

data(PalateData)
reducedSet <- filterArray(PalateData, keep=c("MIR", "LET", "POCON", "CALIB"),
                         frac=1.1, number=3, reps=4)
ndata.none <- normalizeWithinArrays(reducedSet, method="none")
ndata.median <- normalizeWithinArrays(reducedSet, method="median")
ndata.loess <- normalizeWithinArrays(reducedSet, method="loess")
ndata.quantile <- normalizeBetweenArrays(reducedSet, method="quantile")
ndata.all <- list(ndata.none, ndata.median, ndata.loess,
                   ndata.quantile)
res <- MADvsMedianPlot(ndata.all, channel="R", group="probe.type",
                        subset=c("MMJ miRNAs", "Other miRNAs", "Control"))
print(res)

Description

Plots of the log2 expression ratios (M values) versus the mean log2 expression values (A values) for each probe for each array.

Usage

MAplot(x, ...)

## S4 method for signature 'MAList'
MAplot(
  x,
  ...
)

## S4 method for signature 'NChannelSet'
MAplot(
  x,
  ...
)

Arguments

x Either an MAList object or an NChannelSet object
...

arguments to pass to xyplot
Details

The so-called "MA" plot can be used to evaluate whether there is a bias associated with overall intensity level for each array. Loess smoothed regression lines are superimposed on each plot to demonstrate the trend.

Methods

signature(x = "MAlist") M and A values are stored as matrices in x
signature(x = "NChannelSet") M and A values are calculated from the R and G matrices returned by assayData(x)

See Also
densityplot for density plots of log2 intensity values, levelplot for pairwise distance plots between arrays, and MADvsMedianPlot for median absolute deviation versus median plots.

Examples

data(PalateData)
reducedSet <- filterArray(PalateData, keep=c("MIR", "LET", "POSCON", "CALIB"),
frac=1.1, number=3, reps=4)
ndata.quantile <- normalizeBetweenArrays(reducedSet, method="quantile")
res <- MAplot(ndata.quantile)
print(res)

---

PalateData Murine Secondary Palate Development miRNA Expression Data

Description

This data set contains two-color miRNA microarray expression data obtained from mouse embryonic tissue during gestational days (GD) 12, 13, and 14, which represents the critical period of palate development in the mouse.

Usage

data(PalateData)

Format

The data are in the format of an "RGList", which in this case is a list with the following 9 elements:

- R matrix of dimension 6336 x 9 which contains the red channel foreground measurements
- G matrix of dimension 6336 x 9 which contains the green channel foreground measurements
- Rb matrix of dimension 6336 x 9 which contains the red channel background measurements
- Gb matrix of dimension 6336 x 9 which contains the green channel background measurements
- source source of the images, here "imagene"
Field Dimensions numeric vector giving the field dimensions of the array (Metarows, Metacols, Rows and Cols)

weights matrix of dimension 6336 x 9 which contains the quality weights associated with each spot on the arrays

printer list containing information on the process used to print the spots on the arrays (number of grid rows / columns and number of spot rows / columns per grid - coincides with Field Dimensions)

genes A data.frame containing information on each probe. Has the following columns:

  Field field position for the probe
  Meta Row meta row position for the probe
  Meta Column meta column position for the probe
  Row row position for the probe
  Column column position for the probe
  Gene ID unique gene identifier provided by Miltenyi Biotec
  ID unique probe identifier constructed by concatenating the "Gene ID" with "Meta Row", "Meta Column", "Row", and "Column" information
  Name name of the microRNA
  Name.stem base name of the microRNA
  probe.type type of probe, "MMU miRNAs", "Other miRNAs", "Control", "Empty", and "Other"

Details

RNA samples were isolated from mouse embryonic orofacial tissues (GD-12 - GD-14) and fluorescently labeled with Hy5 (red). Control samples (miRXplore Universal Reference) were labeled with Hy3 (green). The two sets of samples were hybridized to miRXplore Microarrays (Miltenyi Biotec) using the a-Hyb Hybridization Station (Miltenyi Biotec). Probes for a total of 1336 mature miRNAs (from human, mouse, rat and virus), including positive control and calibration probes, were spotted in quadruplicate on each microarray. Each array included probes for 588 murine miRNAs.

Source


Examples

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