Package ‘RefPlus’

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Type  Package
Title  A function set for the Extrapolation Strategy (RMA+) and Extrapolation Averaging (RMA++) methods.
Version 1.44.0
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Depends R (>= 2.8.0), Biobase (>= 2.1.0), affy (>= 1.20.0), affyPLM (>= 1.18.0), preprocessCore (>= 1.4.0)
Suggests affydata
Description The package contains functions for pre-processing Affymetrix data using the RMA+ and the RMA++ methods.
License GPL (>= 2)
biocViews Microarray, OneChannel, Preprocessing
NeedsCompilation no

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RefPlus-package  RMA based on reference microarrays: RMA+ and RMA++ methods

Description

RMA+ is an extension of the RMA algorithm that calculates the probeset intensities of a microarray using a pre-stored RMA model fitted on previously obtained microarrays, e.g. reference microarrays. RMA++ is a further extension based on the RMA+ method. This package depends on the affyPLM package.
Details

Package: RefPlus
Type: Package
Version: 1.13.2
Date: 2009-03-11
License: GPL version 2 or newer

Use `rma.para` to obtain the reference quantiles and the probe effects from a reference set, then use `rmaplus` to calculate the RMA+ intensities based on the fitted reference quantiles and probe effects.

Author(s)

By Kai-Ming Chang(kaiming@gmail.com)

References


Examples

```r
if (require(affydata)) {
  ## Use Dilution in affydata package
  data(Dilution)

  ## Calculate RMA intensities using the rma function.
  Ex0<-exprs(rma(Dilution))

  ## Background correct, estimate the probe effects, and calculate the
  ## RMA intensities using rma.para function.
  Para<-rma.para(Dilution, bg=TRUE, exp=TRUE)
  Ex1<-Par[3]

  ## Calculate the RMA+ intensity using rmaplus function.
  Ex2<-rmaplus(Dilution, rmapara=Para, bg = TRUE)
}
```

colMedians

Derive column medians of a numerical matrix

Description

Form column medians of a numerical array.

Usage

```r
colMedians(mat)
```
normalize.quantiles2

Arguments

*mat*  
A numerical matrix.

Details

Form column medians of a numerical array.

Value

A vector of column medians is returned.

Author(s)

Kai-Ming Chang(kaiming@gmail.com)

See Also

*rowQ*

Examples

```r
A<-matrix(rnorm(30),10,3)
colMedians(A)
```

---

**normalize.quantiles2**  
Reference quantile normalization

Description

Quantile normalization to a reference set.

Usage

`normalize.quantiles2(X, Reference.Quantiles)`

Arguments

*X*  
A matrix of probe intensity data to be reference quantile normalized.

*Reference.Quantiles*  
A vector of the reference quantiles that the probe intensities of a sample is normalized to.

Details

The function quantile normalized the probe intensities of a set of microarrays to a set of reference quantiles which are formed by a set of reference microarrays.

Value

The reference quantile normalized probe intensities.
Author(s)
Kai-Ming Chang(kaiming@gmail.com)

References

See Also

normalize.quantiles

Examples

```r
A <- matrix(rnorm(30), 10, 3)
core <- 1:10
An <- normalize.quantiles2(A, core)
rank(A[, 1]) == An[, 1]
```

---

rma.para  
*Fitting a RMA model*

Description

Obtain reference quantiles and reference probe effects based on reference set `Train`, and calculate the gene expression

Usage

```r
rma.para(Train, bg = TRUE, exp = FALSE)
```

Arguments

- **Train**
  An `AffyBatch` object of the reference set microarrays.
- **bg**
  A logical flag. If `TRUE` (by default), background correct `Train` using default `bg.correct.rma`.
- **exp**
  A logical flag. If `TRUE`, calculate the RMA measurements of `Train`. If `FALSE`, return 0.

Value

- **Reference.Quantiles**
  Reference quantiles derived from `Train`.
- **probe.effects**
  Estimated probe effects derived from `Train`.
- **expression**
  RMA measurements of `Train`.

Note

The RMA procedure requires a lot of computer memory.
**rmaplus**

**Author(s)**

Kai-Ming Chang(kaiming@gmail.com)

**References**


**See Also**

rmaplus, rmaref.predict

**Examples**

```r
if (require(affydata)) {
  ## Use Dilution in affydata package
  data(Dilution)

  ## Background correct, estimate the probe effects, and calculate the
  ## RMA intensities using rma.para function.
  Ex<-rma.para(Dilution, bg=TRUE,exp=TRUE)

  ## Calculate the rma intensities using rma function.
  Ex0<-exprs(rma(Dilution))

  plot(Ex$express[,1],Ex0[,1])
}
```

**rmaplus**

*Derive RMA+ intensities*

**Description**

Calculate the RMA+ intensities using pre-stored reference quantiles and probe effects. The reference quantiles and the probe effects are the estimated parameter values from RMAing a set of microarrays (e.g. a reference set).

**Usage**

```r
rmaplus(Future, rmapara, r.q, p.e, bg = TRUE)
```

**Arguments**

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Future</td>
<td>An affybatch object of the microarrays to be pre-processed using the RMA+ methods.</td>
</tr>
<tr>
<td>rmapara</td>
<td>Output of rma.para function that the contain reference quantiles and the reference probe effects.</td>
</tr>
<tr>
<td>r.q</td>
<td>The pre-stored vector of the quantiles that the probe intensity data of a microarray should be normalized to.</td>
</tr>
<tr>
<td>p.e</td>
<td>A pre-stored list of probe effects. It is a probe.coefs object of PLMset class in affyPLM package.</td>
</tr>
<tr>
<td>bg</td>
<td>A logical flag. If True(by default), background correct Train using default bg.correct.rma.</td>
</tr>
</tbody>
</table>
rmaref.predict

A function used by the rmaplus function

Description

Derive RMA+ expression. Used by rmaplus. The function does not background correct and normalize the probe-level data.

Usage

rmaref.predict(Future, p.e)

Arguments

Future

An affybatch object of the microarrays to be summarized by the RMA+ method.

p.e

The pre-stored list of the probe.effects. It is a probe.coefs object of PLMset class in affyPLM package.
Value

The RMA+ intensities of Future.

Note

Use the rmaplus function to normalize Future to pre-stored reference quantiles and correct the probe effects to obtain the RMA+ intensities.

Author(s)

Kai-Ming Chang(kaiming@gmail.com)

References


See Also

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