Package ‘RefPlus’

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Type Package

Title A function set for the Extrapolation Strategy (RMA+) and
       Extrapolation Averaging (RMA++) methods.

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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

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RefPlus-package

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.

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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<-Para[[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
colMedians(mat)

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

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)
rma.para

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]
```

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.

Author(s)

Kai-Ming Chang (kaiming@gmail.com)

References


See Also

rmaplus, rmaref.predict

Examples

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

## Background correct, estimate the probe effects, and calculate the
## RMA intensities using rma.par 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

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

Arguments

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

Value

The RMA+ intensities of Future.

Author(s)

Kai-Ming Chang (kaiming@gmail.com)

References


See Also

PLMset-class, rma.para, rmaref.predict

Examples

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<-Para[[3]]

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

---

**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**

```r
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**

`PLMset-class`, `rma.para`, `rmaplus`
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