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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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

R topics documented:

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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.
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)
**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
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
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
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.
  Ex@<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

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)

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References


See Also

PLMset-class, rma.para, rmaplus
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