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

NeedsCompilation no

R topics documented:

RefPlus-package .......................................................... 1
colMedians ............................................................... 2
normalize.quantiles2 .................................................. 3
rma.para ................................................................. 4
rmaplus ................................................................. 5
rmaref.predict ......................................................... 6

Index 8

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.
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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)
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References

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)
}

---
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)
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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)

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.
rma.para

**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.

**Examples**

```r
A<-matrix(rnorm(30),10,3)
core<1:10
An<-normalize.quantiles2(A,core)
rank(A[,1])==An[,1]
```
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.
  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 the 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.
The RMA+ intensities of `Future`.

Kai-Ming Chang (kaiming@gmail.com)


See Also

`PLMset-class`, `rma.para`, `rmaref.predict`

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)
}
```

---

**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
Index

*Topic `manip`
  colMedians, 2
  normalize.quantiles2, 3
  rma.para, 4
  rmaplus, 5
  rmaref.predict, 6

*Topic `package`
  RefPlus-package, 1
  colMedians, 2
  normalize.quantiles, 4
  normalize.quantiles2, 3
  RefPlus (RefPlus-package), 1
  RefPlus-package, 1
  rma.para, 4, 6, 7
  rmaplus, 5, 5, 7
  rmaref.predict, 5, 6, 6
  rowQ, 3