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

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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**

```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

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.
Fitting a RMA model

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
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.
Value

The RMA+ intensities of Future.

Author(s)

Kai-Ming Chang(kaiming@gmail.com)

References


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)**

Kai-Ming Chang(kaiming@gmail.com)

**References**


**See Also**

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