Package ‘RefPlus’

November 22, 2016

Type  Package
Title  A function set for the Extrapolation Strategy (RMA+) and
       Extrapolation Averaging (RMA++) methods.
Version  1.44.0
Author  Kai-Ming Chang <kaiming@gmail.com>,
        Chris Harbron <Chris.Harbron@astrazeneca.com>,
        Marie C South <Marie.C.South@astrazeneca.com>
Maintainer  Kai-Ming Chang <kaiming@gmail.com>
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:

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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

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**

```r
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

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
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 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.
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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