

Package ‘RefPlus’

October 12, 2016

Type Package

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

Version 1.42.0

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:

RefPlus-package	2
colMedians	3
normalize.quantiles2	4
rma.para	5
rmaplus	6
rmaref.predict	7

Index	9
--------------	----------

 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.

Details

Package: RefPlus
 Type: Package
 Version: 1.13.2
 Date: 2009-03-11
 License: GPL version 2 or newer

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

Chang,K.M., Harbron,C., South,M.C. (2006) An Exploration of Extensions to the RMA Algorithm. Available with the RefPlus package.Avaliable with the package.

Harbron, C, Chang, K.M., South,M.C.(2007) RefPlus : an R package extending the RMA Algorithm. *Bioinformatics* 23, 2493-2494.

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)
```

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.

Author(s)

Kai-Ming Chang(kaiming@gmail.com)

References

Chang,K.M., Harbron,C., South,M.C. (2006) An Exploration of Extensions to the RMA Algorithm. Available with the RefPlus package.

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 <code>bg.correct.rma</code> .
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

Chang,K.M., Harbron,C., South,M.C. (2006) An Exploration of Extensions to the RMA Algorithm. Available with the RefPlus package.

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

Chang,K.M., Harbron,C., South,M.C. (2006) An Exploration of Extensions to the RMA Algorithm. Available with the RefPlus package.

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)

Kai-Ming Chang(kaiming@gmail.com)

References

Chang,K.M., Harbron,C., South,M.C. (2006) An Exploration of Extensions to the RMA Algorithm. Available with the RefPlus package.

See Also

[PLMset-class,rma.para](#), [rmaplus](#)

Index

*Topic **manip**

- colMedians, 3
- normalize.quantiles2, 4
- rma.para, 5
- rmaplus, 6
- rmaref.predict, 7

*Topic **package**

- RefPlus-package, 2

colMedians, 3

normalize.quantiles, 4
normalize.quantiles2, 4

RefPlus (RefPlus-package), 2

RefPlus-package, 2

rma.para, 5, 7, 8

rmaplus, 5, 6, 8

rmaref.predict, 5, 7, 7

rowQ, 3