

# Package ‘RefPlus’

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**Type** Package

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

**Version** 1.46.0

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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*

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## 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*


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**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](#)

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