RefPlus
November 11, 2009

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colMedians

Derive column medians of a numerical matrix

Description

Form column medians of a numerical array.

Usage

```
colMedians(mat)
```

Arguments

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Details

Form column medians of a numerical array.

Value

A vector of column medians is returned.

Author(s)

Kai-Ming Chang(kaiming@gmail.com)
normalize.quantiles2

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

See Also
normalize.quantiles

dnorm.quantiles
RefPlus-package

Examples

A<-matrix(rnorm(30),10,3)
core<-1:10
An<-normalize.quantiles2(A,core)
rank(A[,1])==An[,1]

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


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)
## 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.

### Author(s)

Kai-Ming Chang (kaiming@gmail.com)

### References


### See Also

- `rmaplus`, `rmaref.predict`
Examples

```r
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

```r
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`.

Value

The RMA+ intensities of `Future`.

Author(s)

Kai-Ming Chang(kaiming@gmail.com)
References

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

See Also
PLMset-class, rma.para, rmaplus
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