

# Package ‘ENmix’

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**Title** Data preprocessing and quality control for Illumina  
HumanMethylation450 and MethylationEPIC BeadChip

**Type** Package

**Description** Illumina Methylation BeadChip array measurements have intrinsic levels of background noise that degrade methylation measurement. The ENmix package provides an efficient data pre-processing tool designed to reduce background noise and improve signal for DNA methylation estimation. Several efficient novel methods were incorporated in the package: ENmix is a model based background correction method that can significantly improve accuracy and reproducibility of methylation measures; RCP taking advantage of the high spatial correlation of DNA methylation levels between nearby type I and II probe pairs to reduce probe type bias and improve data quality on type II probe measures. The data structure used by the ENmix package is compatible with several other related R packages, such as minfi, wateRmelon and ChAMP, providing straightforward integration of ENmix-corrected datasets for subsequent data analysis. The software is designed to support large scale data analysis, and provides multi-processor parallel computing wrappers for some commonly used but computation intensive data preprocessing methods. In addition ENmix package has selectable complementary functions for efficient data visualization (such as data distribution plotting), quality control (identification and filtering of low quality data points, samples, probes, and outliers, along with imputation of missing values), inter-array normalization (3 different quantile normalizations), identification of probes with multimodal distributions due to SNPs and other factors, and exploration of data variance structure using principal component regression analysis plots. Together these provide a set of flexible and transparent tools for preprocessing of EWAS data in a computationally-efficient and user-friendly package.

**Depends** minfi,parallel,doParallel,Biobase (>= 2.17.8),foreach

**Imports** MASS,preprocessCore,wateRmelon,sva,geneploader,impute,grDevices,graphics,stats

**Suggests** minfiData (>= 0.4.1), RPMM, RUnit, BiocGenerics

**biocViews** DNAMethylation, Preprocessing, QualityControl, TwoChannel,  
Microarray, OneChannel, MethylationArray, BatchEffect,  
Normalization, DataImport, Regression, PrincipalComponent

**License** Artistic-2.0

**NeedsCompilation** no

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bmiq.mc

*A multi-processor wrapper of BMIQ method*

---

### Description

A multi-processor wrapper of BMIQ method. BMIQ is an intra-sample normalization procedure to correct the bias of Infinium 2 probe methylation beta values.

### Usage

```
bmiq.mc(mdat, nCores = 1, ...)
```

### Arguments

mdat	An object of class MethylSet.
nCores	Number of cores used for computation.
...	See BMIQ in R package wateRmelon for more options.

### Value

A data matrix of Methylation beta value.

**Author(s)**

Zongli Xu

**References**

Teschendorff AE et. al. *A beta-mixture quantile normalization method for correcting probe design bias in Illumina Infinium 450 k DNA methylation data*. Bioinformatics. 2013

**See Also**

See BMIQ in R package watermelon for model details

**Examples**

```
if(FALSE){
  if (require(minfiData)) {
    mdat=preprocessENmix(RGsetEx,bgParaEst="oob",nCores=6)
    mdatq1=norm.quantile(mdat,method="quantile1")
    beta=bmiq.mc(mdatq1,nCores=10)
  }}
```

---

ComBat.mc

*A multi-processor wrapper for ComBat method.*

---

**Description**

A multi-processor wrapper for ComBat method. ComBat is a method to adjust batch effect where the batch covariate is known.

**Usage**

```
ComBat.mc(dat, batch, nCores = 1, ...)
```

**Arguments**

dat	A data matrix with column for samples and row for probe.
batch	Batch covariate (multiple batches allowed)
nCores	Number of cores will be used for computation
...	See ComBat in sva package for extra options

**Value**

A data matrix with the same dimension as input data, adjusted for batch effects. Warning: Values for multimodal distributed CpGs could be over-adjusted.

**Author(s)**

Zongli Xu

## References

Johnson, WE, Rabinovic, A, and Li, C (2007). *Adjusting batch effects in microarray expression data using Empirical Bayes methods. Biostatistics 8(1):118-127.*

## See Also

See ComBat in sva package for details.

## Examples

```
if(FALSE){
  if (require(minfiData)) {
    mdat=preprocessENmix(RGsetEx,bgParaEst="oob",nCores=6)
    mdat=norm.quantile(mdat,method="quantile1")
    beta=bmiq.mc(mdat,nCores=10)
    batch=factor(pData(mdat)$Slide)
    betaC=ComBat.mc(beta,batch,nCores=6,mod=NULL)
  }}

```

---

ctrlsva

*Non-negative control surrogate variables*

---

## Description

Surrogate variables derived from intensity data for non-negative internal control probes. These variables can be modeled in association analysis to adjust for experimental batch effects.

## Usage

```
ctrlsva(rgSet,percvar=0.9,npc=1,flag=1)
```

## Arguments

rgSet	An object of class RGChannelSet.
percvar	Minimum percentage of data variations can be explained by surrogate variables, range from 0 to 1,default is 0.9
npc	Number of surrogate variables, default is 1
flag	1: select number of surrogate variables based on argument percvar; 2: select number of surrogate variables based on argument npc

## Value

ctrlsva: a matrix of surrogate variables (columns) with row corresponding to samples

## Author(s)

Zongli Xu

## References

Zongli Xu, Liang Niu, Leping Li and Jack A. Taylor, *ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip*. Nucleic Acids Research 2015.

**Examples**

```

if(FALSE){
  if (require(minfiData)) {
    sheet <- read.metharray.sheet(file.path(find.package("minfiData"),"extdata"), pattern = "csv$")
    rgSet <- read.metharray.exp(targets = sheet,extended = TRUE)
    sva<-ctrl(rgSet)
  }}

```

freqpoly

*Frequency polygon plot***Description**

Similar to histogram, frequency polygon plot can be used to display data distribution.

**Usage**

```

freqpoly(mat, nbreaks=15, col="black", xlab="", ylab="Frequency",
         type="l",append=FALSE,...)

```

**Arguments**

mat	A numeric vector
nbreaks	Number of bins for frequency counting
col	color code
xlab	x-axis lable
ylab	y-axis lable
type	character indicating the type of plotting; actually any of the 'type's as in 'plot.default'.
append	TRUE or FALSE, whether to create a new figure or append to the current figure.
...	Further arguments that get passed to the function "plot"

**Value**

Frequency polygon plot.

**Author(s)**

Zongli Xu

**References**

Zongli Xu, Liang Niu, Leping Li and Jack A. Taylor, *ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip*. Nucleic Acids Research 2015.

**Examples**

```

if(FALSE){
  if (require(minfiData)) {
    mdat <- preprocessRaw(RGsetEx)
    beta=getBeta(mdat, "Illumina")
    freqpoly(beta[,1])
  }}

```

---

multifreqpoly                      *Frequency polygon plot to display data distribution.*

---

### Description

Produce Frequency polygon plot for each column of a numeric data matrix.

### Usage

```
multifreqpoly(mat, nbreaks=100, col=1:ncol(mat), xlab="",
              ylab="Frequency", legend = list(x = "top", fill=col,
              legend = if(is.null(colnames(mat))) paste(1:ncol(mat))
              else colnames(mat)),...)
```

### Arguments

mat	A numeric matrix
nbreaks	The number of bins for frequency counting
col	Line plot color code, the length should be equal to the number of columns in mat
xlab	x-axis lable
ylab	y-axis lable
legend	A list of arguments that get passed to the function "legend"
...	Further arguments that get passed to the function "plot"

### Value

Frequency polygon plot.

### Author(s)

Zongli Xu

### References

Zongli Xu, Liang Niu, Leping Li and Jack A. Taylor, *ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip*. Nucleic Acids Research 2015.

### Examples

```
if(FALSE){
  if (require(minfiData)) {
    mdat <- preprocessRaw(RGsetEx)
    beta=getBeta(mdat, "Illumina")
    multifreqpoly(beta,col=rep("black",ncol(beta)))
  }
}
```

---

`nmode.mc`*Estimating number of mode in methylation data for each probe.*

---

## Description

Due to SNPs in CpG probe region or other unknown factors, methylation beta values for some CpGs have multimodal distribution. This function is to identify this type of probes with obvious multimodal distribution.

## Usage

```
nmode.mc(x, minN = 3, modedist=0.2, nCores = 1)
```

## Arguments

<code>x</code>	A methylation beta value matrix with row for probes and column for samples.
<code>minN</code>	Minimum number of data points at each cluster
<code>modedist</code>	Minimum mode distance
<code>nCores</code>	Number of cores used for computation

## Details

This function used an empirical approach to estimate number of mode in methylation beta value for each CpG probe. By default, the function requires the distance between modes have to be greater than 0.2 in methylation beta value, and each mode clusters should have at least 3 data points or 5% of data points whichever is greater.

## Value

A vector of integers

## Author(s)

Zongli Xu

## References

Zongli Xu, Liang Niu, Leping Li and Jack A. Taylor, *ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip*. Nucleic Acids Research 2015

## Examples

```
if(FALSE){
  if (require(minfiData)) {
    mdat <- preprocessRaw(RGsetEx)
    beta=getBeta(mdat, "Illumina")
    nmode=nmode.mc(beta, minN = 3,modedist=0.2, nCores = 5)
  }
}
```

---

norm.quantile	<i>Quantile normalization.</i>
---------------	--------------------------------

---

### Description

Quantile normalization of methylation intensity data across samples for Illumina Infinium Human-Methylation 450 and MethylationEPIC BeadChip.

### Usage

```
norm.quantile(mdat, method = "quantile1")
```

### Arguments

mdat	An object of class MethylSet.
method	Quantile normalization method. This should be one of the following strings: "quantile1", "quantile2", or "quantile3".

### Details

By default, method = "quantile1" will separately quantile normalize Methylated or Unmethylated intensities for Infinium I or II probes. The "quantile2" will quantile normalize combined Methylated or Unmethylated intensities for Infinium I or II probes. The "quantile3" will quantile normalize combined Methylated or Unmethylated intensities for Infinium I and II probes together.

### Value

An object of class MethylSet.

### Author(s)

Zongli Xu

### References

Pidsley, R., CC, Y.W., Volta, M., Lunnon, K., Mill, J. and Schalkwyk, L.C. (2013) A data-driven approach to preprocessing Illumina 450K methylation array data. BMC genomics, 14, 293.

### Examples

```
if(FALSE){  
  if (require(minfiData)) {  
    mdat=preprocessENmix(RGsetEx,bgParaEst="oob",nCores=6)  
    mdatq1=norm.quantile(mdat,method="quantile1")  
  }  
}
```



---

`normalize.quantile.450k`*Quantile normalization.*

---

**Description**

Quantile normalization of methylation intensity data across samples for Illumina Infinium Human-Methylation 450 BeadChip.

**Usage**

```
normalize.quantile.450k(mdat, method = "quantile1")
```

**Arguments**

<code>mdat</code>	An object of class <code>MethylSet</code> .
<code>method</code>	Quantile normalization method. This should be one of the following strings: "quantile1", "quantile2", or "quantile3".

**Details**

By default, `method = "quantile1"` will separately quantile normalize Methylated or Unmethylated intensities for Infinium I or II probes. The "quantile2" will quantile normalize combined Methylated or Unmethylated intensities for Infinium I or II probes. The "quantile3" will quantile normalize combined Methylated or Unmethylated intensities for Infinium I and II probes together.

**Value**

An object of class `MethylSet`.

**Author(s)**

Zongli Xu

**References**

Pidsley, R., CC, Y.W., Volta, M., Lunnon, K., Mill, J. and Schalkwyk, L.C. (2013) A data-driven approach to preprocessing Illumina 450K methylation array data. *BMC genomics*, 14, 293.

**Examples**

```
if(FALSE){
  if (require(minfiData)) {
    mdat=preprocessENmix(RGsetEx,bgParaEst="oob",nCores=6)
    mdatq1=normalize.quantile.450k(mdat,method="quantile1")
  }}
```

oxBS.MLE

*oxBS-MLE.***Description**

Find the Maximum Likelihood Estimate (MLE) of 5-methylcytosine (5mC) and 5-hydroxymethylcytosine (5hmC) using sequencing/array data from paired bisulfite and oxidative bisulfite treated DNA experiments.

**Usage**

```
oxBS.MLE(beta.BS, beta.oxBS, N.BS, N.oxBS)
```

**Arguments**

beta.BS	A matrix of measurements (proportions of methylated signals in total signals) obtained from bisulfite (BS) experiments
beta.oxBS	A matrix of measurements obtained from oxidative bisulfite (oxBS) experiments
N.BS	A matrix of total signals from BS experiments
N.oxBS	A matrix of total signals from oxBS experiments

**Details**

For all the inputs (beta.BS, beta.oxBS, N.BS and N.oxBS), the rows should be corresponding to CpG loci and the columns should be corresponding to samples. The order of rows/columns in all four matrices should be consistent (otherwise oxBS.MLE will stop with error messages). Using a binomial model at each CpG locus in each sample, oxBS.MLE outputs a list with two matrices: a matrix of MLEs of 5mC levels and a matrix of MLEs of 5hmC levels. The rows and columns of both matrices are consistent with the rows and columns of the input matrices. For any CpG locus in any sample, if any of the four corresponding values (beta.BS, beta.oxBS, N.BS and N.oxBS) is NA, or N.BS is zero, or N.oxBS is zero, the MLE of both 5mC and 5hmC levels will be set as NA.

**Value**

A list with two elements:  
 5mC: a matrix of estimated 5mC levels.  
 5hmC: a matrix for estimated 5hmC levels.

**Author(s)**

Liang Niu and Zongli Xu

**References**

Zongli Xu, Jack A. Taylor, Yuet-Kin Leung, Shuk-Mei Ho and Liang Niu, *oxBS-MLE: An efficient method to estimate 5-methylcytosine and 5-hydroxymethylcytosine in paired bisulfite and oxidative bisulfite treated DNA*, under review.

## Examples

```
# load example data
load(system.file("oxBS.MLE.RData", package="ENmix"))
# run oxBS.MLE
temp<-oxBS.MLE(beta.BS,beta.oxBS,N.BS,N.oxBS)
```

---

pcrplot

*Principal component regression plot*

---

## Description

First, principal component analysis will be performed in the standardized input data matrix (standardized for each row/CpG), and then the specified number of top principal components (that explain most data variation) will be used to perform linear regression with each specified variables. Regression P values will be plotted for exploration of methylation data variance structure or identification of possible confounding variables for association analysis.

## Usage

```
pcrplot(beta, cov, npc=50)
```

## Arguments

beta	A methylation beta value matrix with row for probes and column for samples.
cov	A data frame of covariates. Categorical variables should be converted to factors.
npc	The number of top principal components to plot

## Value

A jpeg figure "svdscreepplot.jpg" to show the variations explained by each principal component.  
A jpeg figure "pcr\_diag.jpg" to show association strength between principal components and covariates with cell colors indicating different levels of association P values.

## Author(s)

Zongli Xu

## References

Zongli Xu, Liang Niu, Leping Li and Jack A. Taylor, *ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip*. Nucleic Acids Research 2015

## Examples

```
if(FALSE){
  if (require(minfiData)) {
    mdat <- preprocessRaw(RGsetEx)
    beta=getBeta(mdat, "Illumina")
    group=pData(mdat)$Sample_Group
    slide=factor(pData(mdat)$Slide)
    cov=data.frame(group,slide)
    pcrplot(beta,cov,npc=6)
  }
}
```

---

plotCtrl	<i>Plot internal controls of 450K or MethylationEPIC BeadChip.</i>
----------	--

---

### Description

Intensity data are plotted for all internal control probe types on the Illumina Infinium HumanMethylation450 or MethylationEPIC BeadChip. These figures can be used to check data quality and experimental procedures.

### Usage

```
plotCtrl(rgSet, IDorder=NULL)
```

### Arguments

rgSet	An object of class RGChannelSet.
IDorder	A list of sample ids in the order user specified. The list can be a subset of the samples in input dataset. If an id list is provided, all plots will be produced in the order of the list. The default is NULL.

### Value

A set of jpeg figures.

### Author(s)

Zongli Xu

### References

Zongli Xu, Liang Niu, Leping Li and Jack A. Taylor, *ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip*. Nucleic Acids Research 2015.

### Examples

```
if(FALSE){  
  if (require(minfiData)) {  
    pinfo=pData(RGsetEx)  
    IDorder=rownames(pinfo)[order(pinfo$Slide,pinfo$Array)]  
    plotCtrl(RGsetEx, IDorder)  
  }  
}
```

---

preprocessENmix	<i>The ENmix background correction for HumanMethylation 450 and MethylationEPIC BeadChip</i>
-----------------	--

---

### Description

ENmix models methylation signal intensities with a flexible exponential-normal mixture distribution, and models background noise with a truncated normal distribution. ENmix will split BeadChip intensity data into 6 parts and separately model methylated and unmethylated intensities, 2 different color channels and 2 different probe designs.

### Usage

```
preprocessENmix(rgSet, bgParaEst = "oob", dyeCorr="RELIC", QCinfo=NULL, exQCsample=TRUE,
                exQCcpg=TRUE, exSample=NULL, exCpG=NULL, nCores = 2)
```

### Arguments

rgSet	An object of class RGChannelSetExtended, RGChannelSet or MethylSet.
bgParaEst	Optional method to estimate background normal distribution parameters. This must be one of the strings: "oob", "est", or "neg".
dyeCorr	Dye bias correction, "mean": correction based on averaged red/green ratio; or "RELIC": correction with RELIC method; or "none": no dye bias correction. The default is RELIC
QCinfo	If QCinfo object from function QCinfo() is provided, low quality samples (if exQCsample=TRUE) and CpGs (if exQCcpg=TRUE) will be excluded before background correction.
exQCsample	If TRUE, low quality samples listed in QCinfo will be excluded.
exQCcpg	If TRUE, low quality CpGs listed in QCinfo will be excluded.
exSample	User specified sample list to be excluded before background correction
exCpG	User specified probe list to be excluded before background correction
nCores	Number of cores will be used for computation

### Details

By default, ENmix will use out-of-band Infinium I intensities ("oob") to estimate normal distribution parameters to model background noise. Option "est" will use combined methylated and unmethylated intensities to estimate background distribution parameters separately for each color channel and each probe type. Option "neg" will use 600 chip internal controls probes to estimate background distribution parameters. If rgSet is a MethylSet, then only option "est" can be selected.

### Value

An object of class MethylSet

### Author(s)

Zongli Xu and Liang Niu

## References

Zongli Xu, Liang Niu, Leping Li and Jack A. Taylor, ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip. *Nucleic Acids Research* 2015.

Zongli Xu, Sabine A. S. Langie, Patrick De Boever, Jack A. Taylor<sup>1</sup> and Liang Niu, RELIC: a novel dye-bias correction method for Illumina Methylation BeadChip, in review 2016

## See Also

Package minfi for classes [RGChannelSet](#) and [MethylSet](#)

## Examples

```
if(FALSE){
  if (require(minfiData)) {
    mdat=preprocessENmix(RGsetEx,nCores=6)
  }
}
```

---

QCfilter

*Sample or CpG probe filter.*

---

## Description

Filter low quality samples or CpGs, outlier samples or user specified samples or CpGs.

## Usage

```
QCfilter(mdat, qcinfo=NULL, detPthre=0.000001, nbthre=3, samplethre=0.05, CpGthre=0.05,
  bisulthre=NULL, outlier=FALSE, outid=NULL, outCpG=NULL, plot=FALSE)
```

## Arguments

mdat	An object of class <code>MethylSet</code> or beta value matrix.
qcinfo	An object outputed from function <code>QCinfo</code>
detPthre	Detection P value threshold to identify low quality data point
nbthre	Number of bead threshold to identify low quality data point
samplethre	Threshold to identify low quality samples, the percentage of low quality methylation data points across probes for each sample
CpGthre	Threshold to identify low quality probes, percentage of low quality methylation data points across samples for each probe
bisulthre	Threshold of bisulfite intensity for identification of low quality samples. By default, Mean - 3 x SD of sample bisulfite control intensities will be used as the threshold.
outlier	If TRUE, outlier samples will be excluded.
outid	A list of user specified samples to be excluded.
outCpG	A list of user specified CpGs to be excluded.
plot	TRUE or FALSE, whether to produce quality checking plots.

**Value**

An same type object as input object after excluding low quality samples and CpGs

Figure "qc\_sample.jpg": scatter plot for Percent of low quality data per sample and Average bisulfite conversion intensity

Figure "qc\_CpG.jpg": histogram for Percent of low quality data per CpG.

Figure "freqpolygon\_beta\_beforeQC.jpg": distribution plot before filtering.

Figure "freqpolygon\_beta\_afterQC.jpg": distribution plot after filtering.

**Author(s)**

Zongli Xu

**References**

Zongli Xu, Liang Niu, Leping Li and Jack A. Taylor, *ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip*. Nucleic Acids Research 2015.

**Examples**

```
if(FALSE){
  if (require(minfiData)) {
    sheet <- read.metharray.sheet(file.path(find.package("minfiData"), "extdata"), pattern = "csv$")
    rgSet <- read.metharray.exp(targets = sheet, extended = TRUE)
    qcscore<-QCinfo(rgSet)
    rgSet=QCfilter(rgSet, qcinfo=qcscore, outlier=TRUE)
  }}

```

---

QCinfo

*QC information.*

---

**Description**

Extract informations for data quanlity controls: detection P values, number of beads and averaged bisulfite conversion intensity. The function can also identify low quality samples and probes, as well as outlier samples based on total intensity or beta value distribution.

**Usage**

```
QCinfo(rgSet, detPthre=0.000001, nbthre=3, samplethre=0.05, CpGthre=0.05,
       bisulthre=NULL, outlier=TRUE, distplot=TRUE)
```

**Arguments**

rgSet	An object of class RGChannelSetExtended.
detPthre	Detection P value threshold to identify low quality data point
nbthre	Number of bead threshold to identify low quality data point
samplethre	Threshold to identify low quality samples, the percentage of low quality methylation data points across probes for each sample
CpGthre	Threshold to identify low quality probes, percentage of low quality methylation data points across samples for each probe

bisulthre	Threshold of bisulfite intensity for identification of low quality samples. By default, Mean - 3 x SD of sample bisulfite control intensities will be used as the threshold.
outlier	If TRUE, outlier samples in total intensity or beta value distribution will be identified and classified as bad samples.
distplot	TRUE or FALSE, whether to produce beta value distribution plots before and after QC.

### Value

detP: a matrix of detection P values

nbead: a matrix for number of beads

bisul: a vector of averaged intensities for bisulfite conversion controls

badsample: a list of low quality or outlier samples

badCpG: a list of low quality CpGs

outlier\_sample: a list of outlier samples

Figure "qc\_sample.jpg": scatter plot for Percent of low quality data per sample and Average bisulfite conversion intensity

Figure "qc\_CpG.jpg": histogram for Percent of low quality data per CpG.

Figure "freqpolygon\_beta\_beforeQC.jpg": distribution plot before filtering.

Figure "freqpolygon\_beta\_afterQC.jpg": distribution plot after filtering.

### Author(s)

Zongli Xu

### References

Zongli Xu, Liang Niu, Leping Li and Jack A. Taylor, *ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip*. Nucleic Acids Research 2015.

### Examples

```
if(FALSE){
  if (require(minfiData)) {
    sheet <- read.metharray.sheet(file.path(find.package("minfiData"), "extdata"), pattern = "csv$")
    rgSet <- read.metharray.exp(targets = sheet, extended = TRUE)
    qcscore<-QCinfo(rgSet)
  }}
}
```



---

rcp *Regression on Correlated Probes(RCP)*

---

### Description

Probe design type bias correction using Regression on Correlated Probes (RCP) method

### Usage

```
rcp(mdat, dist=25, quantile.grid=seq(0.001,0.999,by=0.001), qcscore = NULL, nbthre=3, detPthre=0.000001)
```

### Arguments

mdat	An object of class MethylSet.
dist	Maximum distance in base pair between type I and type II probe pairs for regression calibration
quantile.grid	Quantile grid used in linear regression
qcscore	If the data quality information (the output from function QCinfo) is provided, low quality data points as defined by detection p value threshold (detPthre=0.000001) or number of bead threshold (nbthre=3) will be set to missing.
detPthre	Detection P value threshold to define low quality data points, detPthre=0.000001 in default.
nbthre	Number of beads threshold to define low quality data points, nbthre=3 in default.

### Details

The function will first identify type I and type II probe pairs within specified distance, and then perform linear regression between the probe types to estimate regression coefficients. With the estimates the function will then calibrates type II data using type I data as references.

### Value

A beta value matrix

### Author(s)

Liang Niu, Zongli Xu

### References

Liang Niu, Zongli Xu and Jack A. Taylor *RCP: a novel probe design bias correction method for Illumina Methylation BeadChip*, *Bioinformatics* 2016

### Examples

```
if(FALSE){
  if (require(minfiData)) {
    mdat=preprocessENmix(RGsetEx,bgParaEst="oob",nCores=6)
    mdatq1=normalize.quantile(mdat,method="quantile1")
    beta=rcp(mdatq1)
  }
}
```

---

relic	<i>RELIC dye bias correction method for Illumina HumanMethylation450 and MethylationEPIC BeadChip</i>
-------	---

---

### Description

REgression on Logarithm of Internal Control probes (RELIC) correct for dye bias on whole array by utilizing the intensity values of paired internal control probes that monitor the two color channels.

### Usage

```
relic (mdat, at_red, cg_grn)
```

### Arguments

mdat	An object of class MethylSet.
at_red	an intensity matrix for Illumina control probes "NORM_A" and "NORM_T"
cg_grn	an intensity matrix for Illumina control probes "NORM_C" and "NORM_G"

### Details

The Illumina MethylationEPIC BeadChip contains 85 pairs of internal normalization control probes (name with prefix NORM\_A, NORM\_T, NORM\_G or NORM\_C), while its predecessor, Illumina HumanMethyl-ation450 BeadChip contains 93 pairs. RELIC first performs a regression on the logarithms of the intensity values of the normalization control probes to derive a quantitative relationship between red and green channels, and then uses the relationship to correct for dye-bias on intensity values for whole array.

### Value

An object of class MethylSet

### Author(s)

Zongli Xu and Liang Niu

### References

Zongli Xu, Sabine A. S. Langie, Patrick De Boever, Jack A. Taylor and Liang Niu, RELIC: a novel dye-bias correction method for Illumina Methylation BeadChip, in review 2016

### See Also

Package preprocessENmix

**Examples**

```

if(FALSE){
if (require(minfiData)) {
  #background correction and dye bias correction
  mdat <- preprocessENmix(RGsetEx,bgParaEst="oob",nCores=6,dyeCorr == "RELIC")
  #dye bias correction only
  ctrls <- getProbeInfo(RGsetEx,type="Control")
  ctrls <- ctrls[ctrls$Address %in% featureNames(RGsetEx),]
  ctrl_r <- getRed(RGsetEx)[ctrls$Address,]
  ctrl_g <- getGreen(RGsetEx)[ctrls$Address,]
  CG.controls <- ctrls$Type %in% c("NORM_C", "NORM_G")
  AT.controls <- ctrls$Type %in% c("NORM_A", "NORM_T")
  cg_grn <- ctrl_g[CG.controls,]
  rownames(cg_grn) = ctrls$ExtendedType[CG.controls]
  at_red <- ctrl_r[AT.controls,]
  rownames(at_red) = ctrls$ExtendedType[AT.controls]
  mdat <- preprocessRaw(RGsetEx)
  mdat <- relic(mdat,at_red,cg_grn)
}}

```

rm.outlier

*Filtering out outlier and/or low quality values***Description**

Setting outliers as missing value. Outlier was defined as value smaller than 3 times IQR from the lower quartile or larger than 3 times IQR from the upper quartile. If data quality information were provided, low quality data points will be set to missing first before looking for outliers. If specified, imputation will be performed using k-nearest neighbors method to impute all missing values.

**Usage**

```

rm.outlier(mat,byrow=TRUE,qcscore=NULL,detPthre=0.000001,nbthre=3,
           rmcr=FALSE,rthre=0.05,cthre=0.05,impute=FALSE,
           imputebyrow=TRUE,...)

```

**Arguments**

mat	An numeric matrix
byrow	TRUE: Looking for outliers row by row, or FALSE: column by column.
qcscore	If the data quality information (the output from function QCinfo) were provided, low quality data points as defined by detection p value threshold (detPthre) or number of bead threshold (nbthre) will be set to missing.
detPthre	Detection P value threshold to define low quality data points, detPthre=0.000001 in default.
nbthre	Number of beads threshold define low quality data points, nbthre=3 in default.
rmcr	TRUE: excluded rows and columns with too many missing values as defined by rthre and cthre. FALSE is in default
rthre	Minimum of percentage of missing values for a row to be excluded
cthre	Minimum of percentage of missing values for a column to be excluded

**impute** Whether to impute missing values. If TRUE, k-nearest neighbors methods will be used for imputation. FALSE is in default. Warning: imputed values for multi-modal distributed CpGs may not be correct.  
**imputebyrow** TRUE: impute missing values using similar values in row, or FALSE: in column  
**...** Arguments to be passed to the function impute.knn in R package "impute"

### Value

An numeric matrix of same dimension as the input matrix.

### Author(s)

Zongli Xu

### References

Zongli Xu, Liang Niu, Leping Li and Jack A. Taylor, *ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip*. Nucleic Acids Research 2015.

### Examples

```

if(FALSE){
if (require(minfiData)) {
sheet <- read.metharray.sheet(file.path(find.package("minfiData"),"extdata"), pattern = "csv$")
rgSet <- read.metharray.exp(targets = sheet,extended = TRUE)
qcscore<-QCinfo(rgSet)
mdat <- preprocessRaw(rgSet)
beta=getBeta(mdat, "Illumina")
#filter out outliers
b1=rm.outlier(beta)
#filter out low quality and outlier values
b2=rm.outlier(beta,qcscore=qcscore)
#filter out low quality and outlier values, remove rows and columns with too many missing values
b3=rm.outlier(beta,qcscore=qcscore,rmcr=TRUE)
#filter out low quality and outlier values, remove rows and columns with too many missing values, and then do
b3=rm.outlier(beta,qcscore=qcscore,rmcr=TRUE,impute=TRUE)
}}

```

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