

Package ‘blima’

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Description Package blima includes several algorithms for the preprocessing of Illumina microarray data. It focuses to the bead level analysis and provides novel approach to the quantile normalization of the vectors of unequal lengths. It provides variety of the methods for background correction including background subtraction, RMA like convolution and background outlier removal. It also implements variance stabilizing transformation on the bead level. There are also implemented methods for data summarization. It also provides the methods for performing T-tests on the detector (bead) level and on the probe level for differential expression testing.

License GPL-3

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blima-package *Package for the preprocessing and analysis of the Illumina microarrays on the detector (bead) level.*

Description

Package *blima* includes several algorithms for the preprocessing of Illumina microarray data. It focuses to the bead level analysis and provides novel approach to the quantile normalization of the vectors of unequal lengths. It provides variety of the methods for background correction including background subtraction, RMA like convolution and background outlier removal. It also implements variance stabilizing transformation on the bead level. There are also implemented methods for data summarization. It provides the methods for performing T-tests on the detector (bead) level and on the probe level for differential expression testing.

Details

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Index: This package was not yet installed at build time.

Author(s)

Vojtěch Kulvait Maintainer: Vojtěch Kulvait <kulvait@gmail.com>

aggregateAndPreprocess
Aggregate data

Description

This function is not intended to direct use. It helps perform work of `doProbeTTests` function. For each probe it prints mean and sd of an quality.

Usage

```
aggregateAndPreprocess(x, quality = "qua", transformation = NULL)
```

Arguments

x	Two column matrix to aggregate with columns "ProbeID" and quality.
quality	Quality to analyze, default is "qua".
transformation	Function of input data transformation, default is NULL. Any function which for input value returns transformed value may be supplied. T-test then will be evaluated on transformed data, consider use log2TranformPositive.

Value

Some return value

Author(s)

Vojtěch Kulvait

backgroundCorrect *Data background correction.*

Description

Background correction procedure selecting beads with background Intensity I_b $| \text{lmean} - I_b | > k * \text{SD}(I_{bs})$ for exclusion.

Usage

```
backgroundCorrect(b, normalizationMod = NULL, channelBackground = "GrnB",
  k = 3, channelBackgroundFilter = "bgf", channelAndVector = NULL)
```

Arguments

b	List of beadLevelData objects (or single object).
normalizationMod	NULL for normalization of all input b. Otherwise specifies logical vector of the length equals to the number of arrays in b or list of such vectors if b is a list of beadLevelData classes.
channelBackground	Name of channel to normalize.
k	Parameter of method stringency (default is 3).
channelBackgroundFilter	Filtered beads will have weight 0 and non filtered weight 1.
channelAndVector	Represents vector to bitwise multiple to the channelBackgroundFilter vector.

Author(s)

Vojtěch Kulvait

Examples

```

if(require("blimaTestingData") && interactive())
{
  #To perform background correction on blimatesting object for two groups. Background correction is followed by cor
  data(blimatesting)
  #Prepare logical vectors corresponding to conditions A and E.
  groups1 = "A";
  groups2 = "E";
  sampleNames = list()
  c = list()
  for(i in 1:length(blimatesting))
  {
    p = pData(blimatesting[[i]]@experimentData$phenoData)
    c[[i]] = p$Group %in% c(groups1, groups2);
    sampleNames[[i]] = p$Name
  }
  #Background correction and quantile normalization followed by testing including log2TransformPositive transform
  blimatesting = backgroundCorrect(blimatesting, normalizationMod=c, channelBackgroundFilter="bgf")
  blimatesting = nonPositiveCorrect(blimatesting, normalizationMod=c, channelCorrect="GrnF", channelBackgroundF
}else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::in
}

```

backgroundCorrectSingleArray

Data background correction.

Description

Background correction procedure selecting beads with background Intensity I_b $| \text{lmean} - I_b | > k * \text{SD}(I_{bs})$ for exclusion, internal.

Usage

```
backgroundCorrectSingleArray(b, normalizationMod = NULL, channelBackground = "GrnB",
  k = 3, channelBackgroundFilter = "bgf", channelAndVector = NULL)
```

Arguments

b List of beadLevelData objects (or single object).

normalizationMod NULL for normalization of all input b. Otherwise specifies logical vector of the length equals to the number of arrays in b or list of such vectors if b is a list of beadLevelData classes.

channelBackground Name of channel to normalize.

k Parameter of method stringency (default is 3).

channelBackgroundFilter

Filtered beads will have weight 0 and non filtered weight 1.

channelAndVector

Represents vector to bitwise multiple to the channelBackgroundFilter vector.

Author(s)

Vojtěch Kulvait

backgroundChannelSubtract

Background channel subtraction

Description

Function to subtract one channel from another producing new channel. Standard graphic subtraction.

Usage

```
backgroundChannelSubtract(b, normalizationMod = NULL, channelSubtractFrom = "GrnF",
  channelSubtractWhat = "GrnB", channelResult = "Grn")
```

Arguments

b List of beadLevelData objects (or single object).

normalizationMod

NULL for performing on all input b. Otherwise specifies logical vector of the length equals to the number of arrays in b or list of such vectors if b is a list of beadLevelData classes.

channelSubtractFrom

Name of channel to subtract from.

channelSubtractWhat

Name of channel to subtract.

channelResult

Result channel, if this channel exists it will be overwritten.

Author(s)

Vojtěch Kulvait

Examples

```

if(require("blimaTestingData") && interactive())
{
  #To perform background correction on blimatesting object for two groups. Background correction is followed by cor
  data(blimatesting)
  #Prepare logical vectors corresponding to conditions A and E.
  groups1 = "A";
  groups2 = "E";
  sampleNames = list()
  c = list()
  for(i in 1:length(blimatesting))
  {
    p = pData(blimatesting[[i]]@experimentData$phenoData)
    c[[i]] = p$Group %in% c(groups1, groups2);
    sampleNames[[i]] = p$Name
  }
  #Background correction and quantile normalization followed by testing including log2TransformPositive transform
  blimatesting = backgroundCorrect(blimatesting, normalizationMod=c, channelBackgroundFilter="bgf")
  blimatesting = nonPositiveCorrect(blimatesting, normalizationMod=c, channelCorrect="GrnF", channelBackground
}else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::i
}

```

backgroundChannelSubtractSingleArray

Background channel subtraction

Description

INTERNAL FUNCTION Correction for positive values only

Usage

```

backgroundChannelSubtractSingleArray(b, normalizationMod = NULL,
  channelSubtractFrom = "GrnF", channelSubtractWhat = "GrnB",
  channelResult = "Grn")

```

Arguments

b List of beadLevelData objects (or single object).

normalizationMod NULL for normalization of all input b. Otherwise specifies logical vector of the length equals to the number of arrays in b or list of such vectors if b is a list of beadLevelData classes.

channelSubtractFrom Name of channel to subtract from.

channelSubtractWhat Name of channel to subtract.

channelResult Result channel, if this channel exists it will be overwritten.

Author(s)

Vojtěch Kulvait

channelExistsIntegrityWithLogicalVectorList
Internal function

Description

Test existence of channel slot based on vector list

Usage

```
channelExistsIntegrityWithLogicalVectorList(b, spotsToCheck = NULL,
      slotToCheck, action = c("returnText", "warn", "error"))
```

Arguments

b	List of beadLevelData objects.
spotsToCheck	NULL for check all spots from b. Otherwise specifies logical vector of the length equals to the number of arrays in b with TRUE for checking.
slotToCheck	Slot name to check
action	What type of action is required in case of invalid object structure. Either return text different from TRUE, warn or error.

Author(s)

Vojtěch Kulvait

checkIntegrity *Internal function*

Description

Check integrity of the list of beadLevelData objects or single beadLevelData object returns waslist.

Usage

```
checkIntegrity(b, action = c("warn", "error"))
```

Arguments

b	List of beadLevelData objects or single.
action	What type of action is required in case of invalid object structure. Either return text different from TRUE, warn or error.

Value

Returns value if the object was list or not before calling this function.

Author(s)

Vojtěch Kulvait

`checkIntegrityLogical` *Internal function*

Description

Check integrity of the list of logical objects, internal.

Usage

```
checkIntegrityLogical(xx, b, action = c("returnText", "warn",  
  "error"))
```

Arguments

<code>xx</code>	List of logical objects compatible with a list <code>b</code> .
<code>b</code>	List of <code>beadLevelData</code> objects.
<code>action</code>	What type of action is required in case of invalid object structure. Either return text different from <code>TRUE</code> , <code>warn</code> or <code>error</code> .

Author(s)

Vojtěch Kulvait

`checkIntegrityOfListOfBeadLevelDataObjects`
Internal function

Description

Check integrity of the list of `beadLevelData` objects, internal.

Usage

```
checkIntegrityOfListOfBeadLevelDataObjects(listb, action = c("returnText",  
  "warn", "error"))
```

Arguments

listb	List of beadLevelData objects.
action	What type of action is required in case of invalid object structure. Either return text different from TRUE, warn or error.

Author(s)

Vojtěch Kulvait

checkIntegrityOfSingleBeadLevelDataObject
Internal function

Description

Check integrity of single beadLevelData object, internal.

Usage

```
checkIntegrityOfSingleBeadLevelDataObject(b, action = c("returnText",
  "warn", "error"))
```

Arguments

b	beadLevelData object.
action	What type of action is required in case of invalid object structure. Either return text different from TRUE, warn or error.

Author(s)

Vojtěch Kulvait

chipArrayStatistics *Statistics of beadLevelData*

Description

This function returns table with statistics of single beadLevelData object indexed by order of spots. It prints number of beads on each array spot mean foreground intensity and optionally mean background intensity, mean number of beads in probe set and unbiased estimate of standard deviations of these parameters. Optionally you can also obtain percentage of removed beads within excludeOnSDMultiple multiple of standard deviations from the background value.

Usage

```
chipArrayStatistics(b, includeBeadStatistic = TRUE, channelForeground = "GrnF",
  channelBackground = "GrnB", includeBackground = TRUE, excludedOnSDMultiple = NA)
```

Arguments

b Single beadLevelData object.

includeBeadStatistic Include number of beads per probe in output.

channelForeground Name of channel of foreground.

channelBackground Name of channel of background.

includeBackground Whether to output background data.

excludedOnSDMultiple If positive number, print how much percents of the background lies more than excludedOnSDMultiple multipliers of standard deviation estimate away from background mean.

Author(s)

Vojtěch Kulvait

Examples

```
if(require("blimaTestingData") && interactive())
{
  #To print basic statistic data about blimatesting[[1]] object.
  data(blimatesting)
  array1stats = chipArrayStatistics(blimatesting[[1]], includeBeadStatistic=TRUE,
    excludedOnSDMultiple=3)
  array1pheno = pData(blimatesting[[1]]@experimentData$phenoData)
  array1stats = data.frame(array1pheno$Name, array1stats)
  colnames(array1stats)[1] <- "Array";
  print(array1stats);
}else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::install('blimaTestingData')")
}
```

createSummarizedMatrix

Summarized value matrix.

Description

This function creates summarized matrix of values of certain type.

Usage

```
createSummarizedMatrix(b, spotsToProcess = NULL, quality = "qua",
  channelInclude = "bgf", annotationTag = NULL)
```

Arguments

b List of beadLevelData objects (or single object).

spotsToProcess NULL for processing all spots in **b**. Otherwise specifies logical vector of the length equals to the number of arrays in **b**.

quality Quality to matelize.

channelInclude This field allows user to set channel with weights which have to be from 0,1. All zero weighted items are excluded from summarization. You can turn this off by setting this NULL. This option may be used together with backgroundCorrect method or/and with beadarray QC (defaults to "bgf").

annotationTag Tag from annotation file which to use in resulting matrix as colname.

Author(s)

Vojtěch Kulvait

Examples

```
if(require("blimaTestingData") && require("illuminaHumanv4.db") && interactive())
{
  #Create summarization of nonnormalized data from GrnF column.
  data(blimatesting)
  blimatesting = backgroundCorrect(blimatesting, channelBackgroundFilter="bgf")
  blimatesting = nonPositiveCorrect(blimatesting, channelCorrect="GrnF", channelBackgroundFilter="bgf", channel
  #Prepare logical vectors corresponding to conditions A(groups1Mod), E(groups2Mod) and both(processingMod).
  nonnormalized = createSummarizedMatrix(blimatesting, quality="GrnF", channelInclude="bgf",
    annotationTag="Name")
  head(nonnormalized)
}else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::in
}
```

doAction

Internal function

Description

Performs action of certain type

Usage

```
doAction(message, action = c("returnText", "warn", "error"))
```

Arguments

message	Text message.
action	What type of action is required in case of invalid object structure. Either return text different from TRUE, warn or error.

Author(s)

Vojtěch Kulvait

doProbeTTests	<i>T-test for probe level data.</i>
---------------	-------------------------------------

Description

This function does aggregated probe level t-tests on the data provided by the object beadLevelData from package beadarray.

Usage

```
doProbeTTests(b, c1, c2, quality = "qua", channelInclude = "bgf",
              correction = "BY", transformation = NULL)
```

Arguments

b	List of beadLevelData objects (or single object).
c1	List of logical vectors of data to assign to the first group (or single vector).
c2	List of logical vectors of data to assign to the second group (or single vector).
quality	Quality to analyze, default is "qua".
channelInclude	This field allows user to set channel with weights which have to be 0,1. All zero weighted items are excluded from t-test. You can turn this off by setting this NULL. This option may be used together with backgroundCorrect method or/and with beadarray QC (defaults to "bgf").
correction	Multiple testing adjustment method as defined by p.adjust function, default is "BY".
transformation	Function of input data trasformation, default is NULL. Any function which for input value returns transformed value may be supplied. T-test then will be evaluated on transformed data, consider use log2TranformPositive.

Author(s)

Vojtěch Kulvait

Examples

```

if(require("blimaTestingData") && require("illuminaHumanv4.db") && interactive())
{
  #To perform background correction, variance stabilization and quantile normalization then test on probe level, b
  data(blimatesting)
  #Prepare logical vectors corresponding to conditions A(groups1Mod), E(groups2Mod) and both(processingMod).
  groups1 = "A";
  groups2 = "E";
  sampleNames = list()
  groups1Mod = list()
  groups2Mod = list()
  processingMod = list()
  for(i in 1:length(blimatesting))
  {
    p = pData(blimatesting[[i]]@experimentData$phenoData)
    groups1Mod[[i]] = p$Group %in% groups1;
    groups2Mod[[i]] = p$Group %in% groups2;
    processingMod[[i]] = p$Group %in% c(groups1, groups2);
    sampleNames[[i]] = p$Name
  }
  #Background correction and quantile normalization followed by testing including log2TransformPositive transform
  blimatesting = backgroundCorrect(blimatesting, normalizationMod=processingMod, channelBackgroundFilter="bgf")
  blimatesting = nonPositiveCorrect(blimatesting, normalizationMod=processingMod, channelCorrect="GrnF", channel
  blimatesting = varianceBeadStabilise(blimatesting, normalizationMod = processingMod,
    quality="GrnF", channelInclude="bgf", channelOutput="vst")
  blimatesting = quantileNormalize(blimatesting, normalizationMod = processingMod,
    channelNormalize="vst", channelOutput="qua", channelInclude="bgf")
  beadTest = doTTests(blimatesting, groups1Mod, groups2Mod, "qua", "bgf")
  probeTest = doProbeTTests(blimatesting, groups1Mod, groups2Mod, "qua", "bgf")
  adrToSymbol <- merge(toTable(illuminaHumanv4ARRAYADDRESS), toTable(illuminaHumanv4SYMBOLREANNOTATED))
  adrToSymbol <- adrToSymbol[,c("ArrayAddress", "SymbolReannotated") ]
  colnames(adrToSymbol) <- c("Array_Address_Id", "Symbol")
  probeTestID = probeTest[, "ProbeID"]
  beadTestID = beadTest[, "ProbeID"]
  probeTestFC = abs(probeTest[, "mean1"] - probeTest[, "mean2"])
  beadTestFC = abs(beadTest[, "mean1"] - beadTest[, "mean2"])
  probeTestP = probeTest[, "adjustedp"]
  beadTestP = beadTest[, "adjustedp"]
  probeTestMeasure = (1 - probeTestP) * probeTestFC
  beadTestMeasure = (1 - beadTestP) * beadTestFC
  probeTest = cbind(probeTestID, probeTestMeasure)
  beadTest = cbind(beadTestID, beadTestMeasure)
  colnames(probeTest) <- c("ArrayAddressID", "difexPL")
  colnames(beadTest) <- c("ArrayAddressID", "difexBL")
  tocmp <- merge(probeTest, beadTest)
  tocmp = merge(tocmp, adrToSymbol, by.x="ArrayAddressID", by.y="Array_Address_Id")
  tocmp = tocmp[, c("ArrayAddressID", "Symbol", "difexPL", "difexBL")]
  sortPL = sort(-tocmp[, "difexPL"], index.return=TRUE)$ix
  sortBL = sort(-tocmp[, "difexBL"], index.return=TRUE)$ix
  beadTop10 = tocmp[sortBL[1:10], ]
  probeTop10 = tocmp[sortPL[1:10], ]
  print(beadTop10)
}

```

```

    print(probeTop10)
  }else
  {
    print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::i
  }

```

doTTests

*T-test for bead (detector) level data.***Description**

This function does t-tests on the data provided by the object `beadLevelData` from package `beadarray`.

Usage

```
doTTests(b, c1, c2, quality = "qua", channelInclude = "bgf",
         correction = "BY", transformation = NULL)
```

Arguments

<code>b</code>	List of <code>beadLevelData</code> objects (or single object).
<code>c1</code>	List of logical vectors of data to assign to the first group (or single vector).
<code>c2</code>	List of logical vectors of data to assign to the second group (or single vector).
<code>quality</code>	Quality to analyze, default is "qua".
<code>channelInclude</code>	This field allows user to set channel with weights which have to be 0,1. All zero weighted items are excluded from t-test. You can turn this off by setting this NULL. This option may be used together with <code>backgroundCorrect</code> method or/and with <code>beadarray QC</code> (defaults to "bgf").
<code>correction</code>	Multiple testing adjustment method as defined by <code>p.adjust</code> function, default is "BY".
<code>transformation</code>	Function of input data transformation, default is NULL. Any function which for input value returns transformed value may be supplied. T-test then will be evaluated on transformed data, consider use <code>log2TransformPositive</code> .

Author(s)

Vojtěch Kulvait

Examples

```

if(require("blimaTestingData") && require("illuminaHumanv4.db") && interactive())
{
  #To perform background correction, variance stabilization and quantile normalization then test on probe level, b
  data(blimatesting)
  #Prepare logical vectors corresponding to conditions A(groups1Mod), E(groups2Mod) and both(processingMod).
  groups1 = "A";
  groups2 = "E";

```

```

sampleNames = list()
groups1Mod = list()
groups2Mod = list()
processingMod = list()
for(i in 1:length(blimatesting))
{
  p = pData(blimatesting[[i]]@experimentData$phenoData)
  groups1Mod[[i]] = p$Group %in% groups1;
  groups2Mod[[i]] = p$Group %in% groups2;
  processingMod[[i]] = p$Group %in% c(groups1, groups2);
  sampleNames[[i]] = p$Name
}
#Background correction and quantile normalization followed by testing including log2TransformPositive transform
blimatesting = backgroundCorrect(blimatesting, normalizationMod=processingMod, channelBackgroundFilter="bgf")
blimatesting = nonPositiveCorrect(blimatesting, normalizationMod=processingMod, channelCorrect="GrnF", channel
blimatesting = varianceBeadStabilise(blimatesting, normalizationMod = processingMod,
  quality="GrnF", channelInclude="bgf", channelOutput="vst")
blimatesting = quantileNormalize(blimatesting, normalizationMod = processingMod,
  channelNormalize="vst", channelOutput="qua", channelInclude="bgf")
beadTest = doTTests(blimatesting, groups1Mod, groups2Mod, "qua", "bgf")
probeTest = doProbeTTests(blimatesting, groups1Mod, groups2Mod, "qua", "bgf")
adrToSymbol <- merge(toTable(illuminaHumanv4ARRAYADDRESS), toTable(illuminaHumanv4SYMBOLREANNOTATED))
adrToSymbol <- adrToSymbol[,c("ArrayAddress", "SymbolReannotated") ]
colnames(adrToSymbol) <- c("Array_Address_Id", "Symbol")
probeTestID = probeTest[, "ProbeID"]
beadTestID = beadTest[, "ProbeID"]
probeTestFC = abs(probeTest[, "mean1"]-probeTest[, "mean2"])
beadTestFC = abs(beadTest[, "mean1"]-beadTest[, "mean2"])
probeTestP = probeTest[, "adjustedp"]
beadTestP = beadTest[, "adjustedp"]
probeTestMeasure = (1-probeTestP)*probeTestFC
beadTestMeasure = (1-beadTestP)*beadTestFC
probeTest = cbind(probeTestID, probeTestMeasure)
beadTest = cbind(beadTestID, beadTestMeasure)
colnames(probeTest) <- c("ArrayAddressID", "difexPL")
colnames(beadTest) <- c("ArrayAddressID", "difexBL")
tocmp <- merge(probeTest, beadTest)
tocmp = merge(tocmp, adrToSymbol, by.x="ArrayAddressID", by.y="Array_Address_Id")
tocmp = tocmp[, c("ArrayAddressID", "Symbol", "difexPL", "difexBL")]
sortPL = sort(-tocmp[, "difexPL"], index.return=TRUE)$ix
sortBL = sort(-tocmp[, "difexBL"], index.return=TRUE)$ix
beadTop10 = tocmp[sortBL[1:10],]
probeTop10 = tocmp[sortPL[1:10],]
print(beadTop10)
print(probeTop10)
}else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::in
}

```

filterBg *Bg correct vector*

Description

Background correction procedure selecting beads with background Intensity I_b $|mean - I_b| > k * SD(I_bs)$ for exclusion, internal.

Usage

```
filterBg(x, k = 3)
```

Arguments

x	Vector to correct
k	Parameter of method stringency (default is 3).

Author(s)

Vojtěch Kulvait

getNextVector *Support probe and beadl level testing.*

Description

Internal function supporting probe and beadl level testing.

Usage

```
getNextVector(what, from, length)
```

Arguments

what	Two column sorted matrix with probe values.
from	Index to start on
length	nrow(what)

Author(s)

Vojtěch Kulvait

initMeanDistribution *initMeanDistribution*

Description

This is internal function not intended to direct use which initializes mean distribution.

Usage

```
initMeanDistribution(srt, prvku)
```

Arguments

srt	vector of sorted values
prvku	number of items in meanDistribution

Author(s)

Vojtěch Kulvait

insertColumn *Internal function to support chipArrayStatistics*

Description

Internal

Usage

```
insertColumn(matrix, column, name)
```

Arguments

matrix	Object to insert column to
column	Column to insert
name	Name of column to assign.

Author(s)

Vojtěch Kulvait

`interpolateSortedVector`*Interpolate sorted vector*

Description

Interpolates given sorted vector to the vector of different length. It does not sort input vector thus for unsorted vectors do not guarantee functionality. Internal function.

Usage

```
interpolateSortedVector(vector, newSize)
```

Arguments

<code>vector</code>	Sorted vector to interpolate.
<code>newSize</code>	Size of the vector to produce.

Author(s)

Vojtěch Kulvait

`interpolateSortedVectorRcpp_`*interpolateSortedVectorRcpp*

Usage

```
interpolateSortedVectorRcpp_(vector, newSize)
```

Arguments

<code>vector</code>
<code>newSize</code>

Author(s)

Vojtěch Kulvait

log2TransformPositive *Log2 transform of numbers >1.*

Description

Transformation function are popular in beadarray package. Here this is similar concept. This function allow user to perform log transformation before doing t-tests.

Usage

```
log2TransformPositive(x)
```

Arguments

x Number to transform.

Value

This function returns logarithm of base 2 for numbers ≥ 1 and zero for numbers < 1 .

Author(s)

Vojtěch Kulvait

Examples

```
if(require("blimaTestingData") && require("illuminaHumanv4.db") && interactive())
{
  #To perform background correction, quantile normalization and then bead level t-test on log data run. Vst is not p
  data(blimatesting)
  #Prepare logical vectors corresponding to conditions A(groups1Mod), E(groups2Mod) and both(c).
  groups1 = "A";
  groups2 = "E";
  sampleNames = list()
  groups1Mod = list()
  groups2Mod = list()
  c = list()
  for(i in 1:length(blimatesting))
  {
    p = pData(blimatesting[[i]]@experimentData$phenoData)
    groups1Mod[[i]] = p$Group %in% groups1;
    groups2Mod[[i]] = p$Group %in% groups2;
    c[[i]] = p$Group %in% c(groups1, groups2);
    sampleNames[[i]] = p$Name
  }
  #Background correction and quantile normalization followed by testing including log2TransformPositive transform
  blimatesting = bacgroundCorrect(blimatesting, normalizationMod=c, channelBackgroundFilter="bgf")
  blimatesting = nonPositiveCorrect(blimatesting, normalizationMod=c, channelCorrect="GrnF", channelBackgroundF
  blimatesting = quantileNormalize(blimatesting, normalizationMod=c, channelNormalize="GrnF", channelOutput="qu
```

```

    beadTest <- doTTests(blimatesting, groups1Mod, groups2Mod,
      transformation=log2TransformPositive, quality="qua", channelInclude="bgf")
    symbol2address <- merge(toTable(illuminaHumanv4ARRAYADDRESS), toTable(illuminaHumanv4SYMBOLREANNOTATED))
    symbol2address <- symbol2address[,c("SymbolReannotated", "ArrayAddress") ]
    colnames(symbol2address) <- c("Symbol", "ArrayAddressID")
    beadTest = merge(beadTest, symbol2address, by.x="ProbeID", by.y="ArrayAddressID")
    beadTestID = beadTest[,c("ProbeID", "Symbol")]
    beadTestFC = abs(beadTest[, "mean1"]-beadTest[, "mean2"])
    beadTestP = beadTest[, "adjustedp"]
    beadTestMeasure = (1-beadTestP)*beadTestFC
    beadTest = cbind(beadTestID, beadTestMeasure)
    colnames(beadTest) <- c("ArrayAddressID", "Symbol", "difexBL")
    sortBL = sort(-beadTest[, "difexBL"], index.return=TRUE)$ix
    beadTop10 = beadTest[sortBL[1:10],]
    print(beadTop10)
  }else
  {
    print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::install('blimaTestingData')")
  }
}

```

meanDistribution

Produce sorted double vector with mean distribution.

Description

This function processes arrays in the object `beadLevelData` from package `beadarray` and returns sorted double vector. The vector has length `prvku`. And the distribution of this vector is a "mean" of all distributions of `distributionChannel` quantity in arrays. In case that probe numbers are different from `prvku` it does some averaging.

Usage

```
meanDistribution(b, normalizationMod = NULL, distributionChannel = "Grn",
  channelInclude = NULL, prvku)
```

Arguments

b Object `beadLevelData` from package `beadarray` or list of these objects

normalizationMod NULL for normalization of all input `b`. Otherwise specifies logical vector of the length equals to the number of arrays in `b` or list of such vectors if `b` is a list of `beadLevelData` classes (defaults to NULL).

distributionChannel Channel to do mean distribution from (defaults to "Grn").

channelInclude This field allows user to set channel with weights which have to be in 0,1. All zero weighted items are excluded from quantile normalization and the value assigned to such probes is a close to value which would be assigned to them if not being excluded. You can turn this off by setting this NULL. This option

may be used together with backgroundCorrect method or/and with beadarray QC (defaults to NULL).

prvku Number of items in a resulting double vector. Prvku must not be more than minimal number of included items in any distributionChannel.

Author(s)

Vojtěch Kulvait

nonParametricEstimator

INTERNAL FUNCTION Xie background correct.

Description

INTERNAL This function is not intended for direct use. Background correction according to non parametric estimator in Xie, Yang, Xinlei Wang, and Michael Story. "Statistical Methods of Background Correction for Illumina BeadArray Data." *Bioinformatics* 25, no. 6 (March 15, 2009): 751-57. doi:10.1093/bioinformatics/btp040. The method is applied on the bead level.

Usage

nonParametricEstimator(toCorrectAll, toCorrectNeg)

Arguments

toCorrectAll

toCorrectNeg

Author(s)

Vojtěch Kulvait

nonPositiveCorrect

Correct non positive

Description

Correction for positive values only

Usage

nonPositiveCorrect(b, normalizationMod = NULL, channelCorrect = "GrnF",
channelBackgroundFilter = "bgf", channelAndVector = NULL)

Arguments

b List of beadLevelData objects (or single object).

normalizationMod NULL for normalization of all input b. Otherwise specifies logical vector of the length equals to the number of arrays in b or list of such vectors if b is a list of beadLevelData classes.

channelCorrect Name of channel to correct.

channelBackgroundFilter Filtered beads will have weight 0 and non filtered weight 1.

channelAndVector Represents vector to bitwise multiple to the channelBackgroundFilter vector.

Author(s)

Vojtěch Kulvait

Examples

```

if(require("blimaTestingData") && interactive())
{
  #To perform background correction on blimatesting object for two groups. Background correction is followed by cor
  data(blimatesting)
  #Prepare logical vectors corresponding to conditions A and E.
  groups1 = "A";
  groups2 = "E";
  sampleNames = list()
  c = list()
  for(i in 1:length(blimatesting))
  {
    p = pData(blimatesting[[i]]@experimentData$phenoData)
    c[[i]] = p$Group %in% c(groups1, groups2);
    sampleNames[[i]] = p$Name
  }
  #Background correction and quantile normalization followed by testing including log2TransformPositive transform
  blimatesting = backgroundCorrect(blimatesting, normalizationMod=c, channelBackgroundFilter="bgf")
  blimatesting = nonPositiveCorrect(blimatesting, normalizationMod=c, channelCorrect="GrnF", channelBackgroundF
}else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::in
}

```

nonPositiveCorrectSingleArray

Correct non positive

Description

INTERNAL FUNCTION Correction for positive values only

Usage

```
nonPositiveCorrectSingleArray(b, normalizationMod = NULL, channelCorrect = "GrnF",
channelBackgroundFilter = "bgf", channelAndVector = NULL)
```

Arguments

b List of beadLevelData objects (or single object).

normalizationMod NULL for normalization of all input b. Otherwise specifies logical vector of the length equals to the number of arrays in b or list of such vectors if b is a list of beadLevelData classes.

channelCorrect Name of channel to correct.

channelBackgroundFilter Filtered beads will have weight 0 and non filtered weight 1.

channelAndVector Represents vector to bitwise multiple to the channelBackgroundFilter vector.

Author(s)

Vojtěch Kulvait

numberOfDistributionElements

Internal

Description

Internal function

Usage

```
numberOfDistributionElements(b, normalizationMod = NULL, channelInclude = NULL)
```

Arguments

b Object beadLevelData from package beadarray or list of these objects

normalizationMod NULL for normalization of all input b. Otherwise specifies logical vector of the length equals to the number of arrays in b or list of such vectors if b is a list of beadLevelData classes.

channelInclude

Author(s)

Vojtěch Kulvait

performXieCorrection *INTERNAL FUNCTION Xie background correct.*

Description

INTERNAL This function is not intended for direct use. Background correction according to non parametric estimator in Xie, Yang, Xinlei Wang, and Michael Story. "Statistical Methods of Background Correction for Illumina BeadArray Data." *Bioinformatics* 25, no. 6 (March 15, 2009): 751-57. doi:10.1093/bioinformatics/btp040. ###The method is applied on the bead level.

Usage

```
performXieCorrection(value, alpha, mu, sigma)
```

Arguments

value
alpha
mu
sigma

Author(s)

Vojtěch Kulvait

plotBackgroundImageAfterCorrection
Plot background image after correction

Description

This function plots image of background distribution versus to foreground after background subtraction.

Usage

```
plotBackgroundImageAfterCorrection(b, index, channelForeground = "GrnF",  
channelBackground = "GrnB", SDMultiple = 3, includePearson = FALSE)
```

Arguments

b Single beadLevelData object.
index Index of spot to generate.
channelForeground Name of channel of foreground.
channelBackground Name of channel of background.
SDMultiple Correct on this level.
includePearson Include Pearson correlation.

Author(s)

Vojtěch Kulvait

Examples

```
if(require("blimaTestingData") && interactive())
{
  #Write background images after correction. This function prints graph for condition D4. Call dev.off() to close.
  data(blimatesting)
  p = pData(blimatesting[[2]]@experimentData$phenoData)
  index = base::match("D4", p$Name)
  plotBackgroundImageAfterCorrection(blimatesting[[2]], index)
}else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::install('blimaTestingData')")
}
```

plotBackgroundImageBeforeCorrection

Plot background image before correction

Description

This function plots image of background distribution versus to foreground before background subtraction.

Usage

```
plotBackgroundImageBeforeCorrection(b, index, channelForeground = "GrnF",
  channelBackground = "GrnB", includePearson = FALSE)
```

Arguments

`b` Single beadLevelData object.
`index` Index of spot to generate.
`channelForeground` Name of channel of foreground.
`channelBackground` Name of channel of background.
`includePearson` Include Pearson correlation.

Author(s)

Vojtěch Kulvait

Examples

```
if(require("blimaTestingData") && interactive())
{
  #Write background images before correction. This function prints graph for condition D4. Call dev.off() to close.
  data(blimatesting)
  p = pData(blimatesting[[2]]@experimentData$phenoData)
  index = base::match("D4", p$Name)
  plotBackgroundImageBeforeCorrection(blimatesting[[2]], index)
}else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::install('blimaTestingData')")
}
```

quantileNormalize *Bead level quantile normalization.*

Description

This function does quantile normalization of object beadLevelData from package beadarray.

Usage

```
quantileNormalize(b, normalizationMod = NULL, channelNormalize = "Grn",
  channelOutput = "qua", channelInclude = NULL, dst)
```

Arguments

`b` Object beadLevelData from package beadarray or list of these objects
`normalizationMod` NULL for normalization of all input `b`. Otherwise specifies logical vector of the length equals to the number of arrays in `b` or list of such vectors if `b` is a list of beadLevelData classes.

channelNormalize	Name of channel to normalize.
channelOutput	Name of output normalized channel.
channelInclude	This field allows user to set channel with weights which have to be in 0,1. All zero weighted items are excluded from quantile normalization and the value assigned to such probes is a close to value which would be assigned to them if not being excluded. You can turn this off by setting this NULL. This option may be used together with bacgroundCorrect method or/and with beadarray QC (defaults to NULL).
dst	User can specify sorted vector which represents distribution that should be assigned to items.

Author(s)

Vojtěch Kulvait

Examples

```

if(require("blimaTestingData") && interactive())
{
  #To perform background correction, variance stabilization and quantile normalization.
  data(blimatesting)
  #Prepare logical vectors corresponding to conditions A(groups1Mod), E(groups2Mod) and both(c).
  groups1 = "A";
  groups2 = "E";
  sampleNames = list()
  processingMod = list()
  for(i in 1:length(blimatesting))
  {
    p = pData(blimatesting[[i]]@experimentData$phenoData)
    processingMod[[i]] = p$Group %in% c(groups1, groups2);
    sampleNames[[i]] = p$Name
  }
  #Background correction and quantile normalization followed by testing including log2TransformPositive transform
  blimatesting = bacgroundCorrect(blimatesting, normalizationMod = processingMod, channelBackgroundFilter="bgf")
  blimatesting = nonPositiveCorrect(blimatesting, normalizationMod = processingMod, channelCorrect="GrnF", chan
  blimatesting = varianceBeadStabilise(blimatesting, normalizationMod = processingMod,
    quality="GrnF", channelInclude="bgf", channelOutput="vst")
  blimatesting = quantileNormalize(blimatesting, normalizationMod = processingMod,
    channelNormalize="vst", channelOutput="qua", channelInclude="bgf")
}else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::i
}

```

readToVector	<i>Support doTTests function.</i>
--------------	-----------------------------------

Description

Internal function supporting doTTests function.

Usage

```
readToVector(what, from, length, quality)
```

Arguments

what	Item to read.
from	From index.
length	Length of vector.
quality	Column.

Author(s)

Vojtěch Kulvait

selectedChannelTransform	<i>Channel transformation</i>
--------------------------	-------------------------------

Description

Function to transform channel data.

Usage

```
selectedChannelTransform(b, normalizationMod = NULL, channelTransformFrom,  
channelResult, transformation = NULL)
```

Arguments

b	List of beadLevelData objects (or single object).
normalizationMod	NULL for performing on all input b. Otherwise specifies logical vector of the length equals to the number of arrays in b or list of such vectors if b is a list of beadLevelData classes.
channelTransformFrom	Name of channel to transform.

`channelResult` Result channel, if this channel exists it will be overwritten.

`transformation` Function of input data transformation, default is NULL. Any function which for input value returns transformed value may be supplied. T-test then will be evaluated on transformed data, consider use `log2TranformPositive`.

Author(s)

Vojtěch Kulvait

Examples

```

if(require("blimaTestingData") && interactive())
{
  #To perform background correction on blimatesting object for two groups. Background correction is followed by cor
  data(blimatesting)
  #Prepare logical vectors corresponding to conditions A and E.
  groups1 = "A";
  groups2 = "E";
  sampleNames = list()
  c = list()
  for(i in 1:length(blimatesting))
  {
    p = pData(blimatesting[[i]]@experimentData$phenoData)
    c[[i]] = p$Group %in% c(groups1, groups2);
    sampleNames[[i]] = p$Name
  }
  #Background correction and quantile normalization followed by testing including log2TransformPositive transform
  blimatesting = bacgroundCorrect(blimatesting, normalizationMod=c, channelBackgroundFilter="bgf")
  blimatesting = nonPositiveCorrect(blimatesting, normalizationMod=c, channelCorrect="GrnF", channelBackgroundF
}else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::in
}

```

`selectedChannelTransformSingleArray`
Channel transformation

Description

Function to transform channel data.

Usage

```

selectedChannelTransformSingleArray(b, normalizationMod = NULL,
  channelTransformFrom, channelResult, transformation)

```

Arguments

b	List of beadLevelData objects (or single object).
normalizationMod	NULL for performing on all input b. Otherwise specifies logical vector of the length equals to the number of arrays in b or list of such vectors if b is a list of beadLevelData classes.
channelTransformFrom	Name of channel to transform.
channelResult	Result channel, if this channel exists it will be overwritten.
transformation	Function of input data trasformation, default is NULL. Any function which for input value returns transformed value may be supplied. T-test then will be evaluated on transformed data, consider use log2TranformPositive.

Author(s)

Vojtěch Kulvait

singleArrayNormalize *Bead level quantile normalization.*

Description

This function does quantile normalization of object beadLevelData from package beadarray. Internal function not intended to direct use. Please use quantileNormalize.

Usage

```
singleArrayNormalize(b, normalizationMod = NULL, channelNormalize = "Grn",
  channelOutput = "qua", channelInclude = NULL, dst)
```

Arguments

b	Object beadLevelData from package beadarray
normalizationMod	NULL for normalization of all input b. Otherwise specifies logical vector of the length equals to the number of arrays in b.
channelNormalize	Name of channel to normalize.
channelOutput	Name of output normalized channel.
channelInclude	This field allows user to set channel with weights which have to be in 0,1. All zero weighted items are excluded from quantile normalization and the value assigned to such probes is a close to value which would be assigned to them if not being excluded. You can turn this off by setting this NULL. This option may be used together with backgroundCorrect method or/and with beadarray QC (defaults to NULL).
dst	This field must be sorted. It is a distribution of values to assign to ports. By default this distribution is computed using meanDistribution function.

Author(s)

Vojtěch Kulvait

singleChannelExistsIntegrityWithLogicalVector
Internal function

Description

Test existence of channel slot based on logical list

Usage

```
singleChannelExistsIntegrityWithLogicalVector(b, spotsToCheck = NULL,  
slotToCheck, action = c("returnText", "warn", "error"))
```

Arguments

b	single beadLevelData object
spotsToCheck	NULL for check all spots from b. Otherwise specifies logical vector of the length equals to the number of arrays in b with TRUE for checking.
slotToCheck	Slot name to check
action	What type of action is required in case of invalid object structure. Either return text different from TRUE, warn or error.

Author(s)

Vojtěch Kulvait

singleCheckIntegrityLogicalVector
Internal function

Description

Check integrity of the logical object, internal.

Usage

```
singleCheckIntegrityLogicalVector(xx, b, action = c("returnText",  
"warn", "error"))
```


Arguments

xx	Logical object compatible with b.
b	Single beadLevelData object.
action	What type of action is required in case of invalid object structure. Either return text different from TRUE, warn or error.

Author(s)

Vojtěch Kulvait

singleNumberOfDistributionElements
Internal

Description

Internal function

Usage

```
singleNumberOfDistributionElements(b, normalizationMod = NULL,  
channelInclude = NULL)
```

Arguments

b	Object beadLevelData from package beadarray
normalizationMod	NULL for normalization of all input b. Otherwise specifies logical vector of the length equals to the number of arrays in b or list of such vectors if b is a list of beadLevelData classes.
channelInclude	

Author(s)

Vojtěch Kulvait

```
updateMeanDistribution
      updateMeanDistribution
```

Description

This is internal function not intended to direct use. Updates mean distribution.

Usage

```
updateMeanDistribution(meanDistribution, srt, arraysUsed)
```

Arguments

meanDistribution

srt vector of sorted values

arraysUsed number of arrays already used to create distribution

Author(s)

Vojtěch Kulvait

```
varianceBeadStabilise Bead level VST.
```

Description

This function does variance stabilising step on bead level.

Usage

```
varianceBeadStabilise(b, normalizationMod = NULL, quality = "qua",
  channelInclude = "bgf", channelOutput = "vst")
```

Arguments

b List of beadLevelData objects (or single object).

normalizationMod

NULL for normalization of all input b. Otherwise specifies logical vector of the length equal to the number of arrays in b or list of such vectors if b is a list of beadLevelData classes.

quality Quality to analyze, default is "qua".

- channelInclude This field allows user to set channel with weights which have to be in 0,1. All zero weighted items are excluded from t-test. You can turn this off by setting this NULL. This option may be used together with bacgroundCorrect method or/and with beadarray QC (defaults to "bgf").
- channelOutput Output from VST.

Author(s)

Vojtěch Kulvait

Examples

```

if(require("blimaTestingData") && interactive())
{
  #To perform background correction, variance stabilization and quantile normalization.
  data(blimatesting)
  #Prepare logical vectors corresponding to conditions A(groups1Mod), E(groups2Mod) and both(c).
  groups1 = "A";
  groups2 = "E";
  sampleNames = list()
  processingMod = list()
  for(i in 1:length(blimatesting))
  {
    p = pData(blimatesting[[i]]@experimentData$phenoData)
    processingMod[[i]] = p$Group %in% c(groups1, groups2);
    sampleNames[[i]] = p$Name
  }
  #Background correction and quantile normalization followed by testing including log2TransformPositive transform
  blimatesting = bacgroundCorrect(blimatesting, normalizationMod = processingMod, channelBackgroundFilter="bgf")
  blimatesting = nonPositiveCorrect(blimatesting, normalizationMod = processingMod, channelCorrect="GrnF", chan
  blimatesting = varianceBeadStabilise(blimatesting, normalizationMod = processingMod,
    quality="GrnF", channelInclude="bgf", channelOutput="vst")
  blimatesting = quantileNormalize(blimatesting, normalizationMod = processingMod,
    channelNormalize="vst", channelOutput="qua", channelInclude="bgf")
}
else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::in
}

```

varianceBeadStabiliseSingleArray

Bead level VST.

Description

This function is not intended to direct use it takes single beadLevelData object and do bead level variance stabilisation.

Usage

```
varianceBeadStabiliseSingleArray(b, normalizationMod = NULL,
  quality = "qua", channelInclude = "bgf", channelOutput = "vst")
```

Arguments

b	Object beadLevelData.
normalizationMod	NULL for normalization of all input b. Otherwise specifies logical vector of the length equals to the number of arrays in b.
quality	Quality to analyze, default is "qua".
channelInclude	This field allows user to set channel with weights which have to be in 0,1. All zero weighted items are excluded from t-test. You can turn this off by setting this NULL. This option may be used together with bacgroundCorrect method or/and with beadarray QC (defaults to "bgf").
channelOutput	Output from VST.

Author(s)

Vojtěch Kulvait

vstFromLumi

Function from LGPL lumi package 2.16.0

Description

This function is derived from copy and paste of lumi::vst function. Since lumi package has extensive imports I decided to hardcode this function to the blima instead of importing lumi package.

Usage

```
vstFromLumi(u, std, nSupport = min(length(u), 500), backgroundStd = NULL,
  lowCutoff = 1/3)
```

Arguments

u	The mean of probe beads
std	The standard deviation of the probe beads
nSupport	Something for c3 guess.
backgroundStd	Estimate the background variance c3. Input should be variance according to article, not SD.
lowCutoff	Something for c3 guess.

Author(s)

authors are Pan Du, Simon Lin, the function was edited by Vojtěch Kulvait

References

<http://www.bioconductor.org/packages/release/bioc/html/lumi.html>

writeBackgroundImages *Write Background Images*

Description

This function writes images with background distribution according to foreground before and after background subtraction.

Usage

```
writeBackgroundImages(b, spotsToGenerate = NULL, imageType = c("jpg",  
  "png", "eps"), channelForeground = "GrnF", channelBackground = "GrnB",  
  SDMultiple = 3, includePearson = FALSE, outputDir = getwd(),  
  width = 505, height = 505)
```

Arguments

b	Single beadLevelData object.
spotsToGenerate	NULL for generate images for all spots from b. Otherwise specifies logical vector of the length equals to the number of arrays in b with TRUE for images to generate.
imageType	Type of images produced, either jpg, png or eps
channelForeground	Name of channel of foreground.
channelBackground	Name of channel of background.
SDMultiple	Correct on this level.
includePearson	Include Pearson correlation.
outputDir	Directory where to output images.
width	Width of image (default 505 fits well for 86mm 150dpi illustration in Bioinformatics journal:)
height	Height of image

Author(s)

Vojtěch Kulvait

Examples

```

if(require("blimaTestingData") && interactive())
{
  #Write background images before and after correction for background into /tmp directory. This function creates tw
  data(blimatesting)
  p = pData(blimatesting[[2]]@experimentData$phenoData)
  spotsToGenerate = p$Group %in% "D";
  writeBackgroundImages(blimatesting[[2]], imageType="jpg", spotsToGenerate=spotsToGenerate, includePearson=FALSE)
}else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::install('blimaTestingData')")
}

```

xieBackgroundCorrect *Xie background correct.*

Description

Background correction according to non parametric estimator in Xie, Yang, Xinlei Wang, and Michael Story. "Statistical Methods of Background Correction for Illumina BeadArray Data." *Bioinformatics* 25, no. 6 (March 15, 2009): 751-57. doi:10.1093/bioinformatics/btp040.###The method is applied on the bead level.

Usage

```

xieBackgroundCorrect(b, normalizationMod = NULL, negativeArrayAddresses,
  channelCorrect, channelResult, channelInclude = NULL)

```

Arguments

b List of beadLevelData objects (or single object).

normalizationMod NULL for processing all spots in b. Otherwise specifies logical vector of the length equals to the number of arrays in b.

negativeArrayAddresses Vector of addresses of negative control probes on array

channelCorrect Slot to perform convolution correction.

channelResult Result channel, if this channel exists it will be overwritten.

channelInclude This field allows user to set channel with weights which have to be from 0,1. All zero weighted items are excluded from summarization. You can turn this off by setting this NULL. This option may be used together with bacgroundCorrect method or/and with beadarray QC (defaults to NULL).

Author(s)

Vojtěch Kulvait

Examples

```

if(require("blimaTestingData") && exists("annotationHumanHT12V4") && interactive())
{
  #Create vector of negative array addresses.
  negAdr = unique(annotationHumanHT12V4$Controls[annotationHumanHT12V4$Controls$Reporter_Group_Name=="negative"])
  #Create summarization of nonnormalized data from GrnF column.
  data(blimatesting)
  blimatesting = backgroundCorrect(blimatesting, channelBackgroundFilter="bgf")
  blimatesting = nonPositiveCorrect(blimatesting, channelCorrect="GrnF", channelBackgroundFilter="bgf", channelInclude=NULL)
  blimatesting = xieBackgroundCorrect(blimatesting, negativeArrayAddresses=negAdr, channelCorrect="GrnF", channelInclude=NULL)
  #Prepare logical vectors corresponding to conditions A(groups1Mod), E(groups2Mod) and both(processingMod).
  xiecorrected = createSummarizedMatrix(blimatesting, quality="GrnFXIE", channelInclude="bgf",
    annotationTag="Name")
  head(xiecorrected)
}else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::install('blimaTestingData')")
}

```

```
xieBackgroundCorrectSingleArray
```

INTERNAL FUNCTION Xie background correct.

Description

INTERNAL This function is not intended for direct use. Background correction according to non parametric estimator in Xie, Yang, Xinlei Wang, and Michael Story. "Statistical Methods of Background Correction for Illumina BeadArray Data." *Bioinformatics* 25, no. 6 (March 15, 2009): 751-57. doi:10.1093/bioinformatics/btp040. The method is applied on the bead level.

Usage

```
xieBackgroundCorrectSingleArray(b, normalizationMod = NULL, negativeArrayAddresses,
  channelCorrect, channelResult, channelInclude = NULL)
```

Arguments

<code>b</code>	Single beadLevelData object.
<code>normalizationMod</code>	NULL for processing all spots in b. Otherwise specifies logical vector of the length equals to the number of arrays in b.
<code>negativeArrayAddresses</code>	Vector of addresses of negative control probes on array
<code>channelCorrect</code>	Slot to perform convolution correction.
<code>channelResult</code>	Result channel, if this channel exists it will be overwritten.
<code>channelInclude</code>	This field allows user to set channel with weights which have to be from 0,1. All zero weighted items are excluded from summarization. You can turn this off by setting this NULL. This option may be used together with backgroundCorrect method or/and with beadarray QC (defaults to NULL).

Author(s)

Vojtěch Kulvait

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