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.
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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 on 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**

The DESCRIPTION file: This package was not yet installed at build time.

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

**Author(s)**

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

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**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**

```r
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

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**Description**

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

**Usage**

```r
bacgroundCorrect(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 bitvise 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 correction for non positive data.
    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 transformation.
    blimatesting = backgroundCorrect(blimatesting, normalizationMod=c, channelBackgroundFilter="bgf")
    blimatesting = nonPositiveCorrect(blimatesting, normalizationMod=c, channelCorrect="GrnF", channelBackgroundFilter="bgf")
}
else
{
    print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::install('blimaTestingData').")
}

backgroundCorrectSingleArray

Data background correction.

Description

Background correction procedure selecting beads with background Intensity I_b |mean - I_b | > k*SD(Ibs) 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).
backgroundChannelSubtract

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

```r
if(require("blimaTestingData") && interactive())
{
  # To perform background correction on blimetesting object for two groups. Background correction is followed by correction for non positive data.
  data(blimetesting)
  # Prepare logical vectors corresponding to conditions A and E.
  groups1 = "A";
  groups2 = "E";
  sampleNames = list()
  c = list()
  for(i in 1:length(blimetesting))
  {
    p = pData(blimetesting[[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 transformation.
  blimetesting = backgroundCorrect(blimetesting, normalizationMod=c, channelBackgroundFilter="bgf")
  blimetesting = nonPositiveCorrect(blimetesting, normalizationMod=c, channelCorrect="GrnF", channelBackgroundFilter="bgf")
}
else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::install("blimaTestingData")");
}
```

backgroundChannelSubtractSingleArray

**Background channel subtraction**

### Description

INTERNAL FUNCTION Correction for positive values only

### Usage

```r
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.
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.

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.
**checkIntegrityLogical**

**Value**

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

**Author(s)**

Vojtěch Kulvait

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**checkIntegrityOfListOfBeadLevelDataObjects**

**Internal function**

**Description**

Check integrity of the list of beadLevelData objects, internal.

**Usage**

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

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>listb</td>
<td>List of beadLevelData objects.</td>
</tr>
<tr>
<td>action</td>
<td>What type of action is required in case of invalid object structure. Either return text different from TRUE, warn or error.</td>
</tr>
</tbody>
</table>

**Author(s)**

Vojtěch Kulvait

---
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').
"
)
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 matrize.
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 "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", channelAndVector="bgf")
  #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::install('blimaTestingData').")
}

---

doAction

Internal function

Description

Performs action of certain type

Usage

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

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  \textit{T-test for probe level data.}

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 log2TransformPositive.

Author(s)

Vojtěch Kulvait
doProbeTTests

Examples

```r
if(require("blimaTestingData") && require("illuminaHumanv4.db") && interactive()) {
  # To perform background correction, variance stabilization and quantile normalization then test on probe level, bead level and print top 10 results.
  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 transformation.
  blimatesting = backgroundCorrect(blimatesting, normalizationMod = processingMod, channelBackgroundFilter="bgf")
  blimatesting = nonPositiveCorrect(blimatesting, normalizationMod=processingMod, channelCorrect="GrnF", channelBackgroundFilter="bgf")
  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))
  colnames(adrToSymbol) <- c("Array_Address_Id", "Symbol")

  beadTestID = beadTest[, "ProbeID"]
  probeTestID = cbind(beadTestID, "ProbeID")

  beadTestFC = abs(beadTest[, "mean1"]-beadTest[, "mean2"])
  probeTestFC = abs(probeTest[, "mean1"]-probeTest[, "mean2"])

  beadTestP = beadTest[, "adjustedp"]
  probeTestP = cbind(probeTest[, "adjustedp"]

  beadTestMeasure = (1-beadTestP)*beadTestFC
  probeTestMeasure = (1-probeTestP)*probeTestFC

  beadTest = cbind(beadTestID, beadTestMeasure)
  probeTest = cbind(probeTestID, probeTestMeasure)

  colnames(probeTest) <- c("ArrayAddressID", "difexPL")
  colnames(beadTest) <- c("ArrayAddressID", "difexBL")

  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
  beadTop10 = tocmp[sortPL[1:10],]
  probeTop10 = tocmp[sortBL[1:10],]

  print(beadTop10)
}
```
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

doSTests(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 log2TransformPositive.

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, bead
  #Prepare logical vectors corresponding to conditions A(groups1Mod), E(groups2Mod) and both(processingMod). 
  #groups1 = "A";
  #groups2 = "E";

  print(probeTop10)
} else 
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::install('"
  print(blimaTestingData)
  print(illuminaHumanv4.db)
  print("blimaTestingData')) and illuminaHumanv4.db by running BiocManager::install('"
  print(illuminaHumanv4.db))
  print("").
}
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$Name
}
#Background correction and quantile normalization followed by testing including log2TransformPositive transformation.
blimatesting = backgroundCorrect(blimatesting, normalizationMod = processingMod, channelBackgroundFilter="bgf")
blimatesting = nonPositiveCorrect(blimatesting, normalizationMod=processingMod, channelCorrect="GrnF", channelBackgroundFilter="bgf")
blimatesting = varianceBeadStabilise(blimatesting, normalizationMod = processingMod, quality="GrnF", channelInclude="bgf", channelOutput="vst")
blimatesting = quantileNormalize(blimatesting, normalizationMod = processingMod, channelNormalize="vst", channelOutput="qua", channelInclude="bgf")
beadTest = doTTests(blimatesting, groups1Mod, groups2Mod, "qua", "bgf")
probeTest = doProbeTTests(blimatesting, groups1Mod, groups2Mod, "qua", "bgf")
adrToSymbol <- merge(toTable(illuminaHumanv4ARRAYADDRESS), toTable(illuminaHumanv4SYMBOLREANNOTATED))
adrToSymbol <- adrToSymbol[,c("ArrayAddress", "SymbolReannotated") ]
colnames(adrToSymbol) <- c("Array_Address_Id", "Symbol")
probeTestID = probeTest[,"ProbeID"]
beadTestID = beadTest[,"ProbeID"]
probeTestFC = abs(probeTest[,"mean1"]-probeTest[,"mean2"])
beadTestFC = abs(beadTest[,"mean1"]-beadTest[,"mean2"])
probeTestP = probeTest[,"adjustedp"]
beadTestP = beadTest[,"adjustedp"]
probeTestMeasure = (1-probeTestP)*probeTestFC
beadTestMeasure = (1-beadTestP)*beadTestFC
probeTest = cbind(probeTestID, probeTestMeasure)
beadTest = cbind(beadTestID, beadTestMeasure)
beadToSymbol <- c("ArrayAddressID", "difexBL")
probeToSymbol <- c("ArrayAddressID", "difexPL")
tocmp <- merge(tocmp, beadToSymbol, by.x="ArrayAddressID", by.y="Array_Address_Id")
tocmp = tocmp[,c("ArrayAddress", "Symbol", "difexPL", "difexBL")]
sortPL = sort(-tocmp[,"difexPL"], index.return=TRUE)$ix
sortBL = sort(-tocmp[,"difexBL"], index.return=TRUE)$ix
beadTop10 = tocmp[sortBL[1:10],]
probeTop10 = tocmp[sortPL[1:10],]
print(beadTop10)
print(probeTop10)
}else
{
    print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::install(
    ["blimaTestingData",[c("ArrayAddress", "SymbolReannotated") ]
    colnames(adrToSymbol) <- c("Array_Address_Id", "Symbol")
    probeTestID = probeTest[,"ProbeID"]
    beadTestID = beadTest[,"ProbeID"]
    probeTestFC = abs(probeTest[,"mean1"]-probeTest[,"mean2"])
    beadTestFC = abs(beadTest[,"mean1"]-beadTest[,"mean2"])
    probeTestP = probeTest[,"adjustedp"]
    beadTestP = beadTest[,"adjustedp"]
    probeTestMeasure = (1-probeTestP)*probeTestFC
    beadTestMeasure = (1-beadTestP)*beadTestFC
    probeTest = cbind(probeTestID, probeTestMeasure)
    beadTest = cbind(beadTestID, beadTestMeasure)
    beadToSymbol <- c("ArrayAddressID", "difexBL")
    probeToSymbol <- c("ArrayAddressID", "difexPL")
    tocmp <- merge(tocmp, beadToSymbol, by.x="ArrayAddressID", by.y="Array_Address_Id")
    tocmp = tocmp[,c("ArrayAddress", "Symbol", "difexPL", "difexBL")]
    sortPL = sort(-tocmp[,"difexPL"], index.return=TRUE)$ix
    sortBL = sort(-tocmp[,"difexBL"], index.return=TRUE)$ix
    beadTop10 = tocmp[sortBL[1:10],]
    probeTop10 = tocmp[sortPL[1:10],]
    print(beadTop10)
    print(probeTop10)
}
filterBg

---

**Bg correct vector**

**Description**

Background correction procedure selecting beads with background Intensity $I_b \mid \text{mean} - I_b \mid > k\times SD(I_{bs})$ 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 bead level testing.**

**Description**

Internal function supporting probe and bead 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

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

Description
Internal function to support chipArrayStatistics

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

vector Sorted vector to interpolate.
newSize Size of the vector to produce.

Author(s)

Vojtěch Kulvait

interpolateSortedVectorRcpp

interpolateSortedVectorRcpp

Usage

interpolateSortedVectorRcpp_(vector, newSize)

Arguments

vector
newSize

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 $\geq 1$ 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 performed in this scheme. Top 10 probes is then printed according to certain measure.
  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$Name
  }
  #Background correction and quantile normalization followed by testing including log2TransformPositive transformation.
  blimatesting = backgroundCorrect(blimatesting, normalizationMod=c, channelBackgroundFilter="bgf")
  blimatesting = nonPositiveCorrect(blimatesting, normalizationMod=c, channelCorrect="GrnF", channelBackgroundFilter="bgf")
  blimatesting = quantileNormalize(blimatesting, normalizationMod=c, channelNormalize="GrnF", channelOutput="qua")
}
meanDistribution <- function(b, normalizationMod = NULL, distributionChannel = "Grn", channelInclude = NULL, prvku) {
  if (is.null(normalizationMod)) {
    normalizationMod <- rep(TRUE, length(b))
  }
  if (is.null(channelInclude)) {
    channelInclude <- rep(1, length(b))
  }
  # Process arrays in the object beadLevelData from package beadarray
  sortBL = sort(-beadTest[, "difexBL"], index.return=TRUE)$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") and illuminaHumanv4.db by running BiocManager::install("illuminaHumanv4.db").")
}

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

```r
if(require("blimaTestingData") && interactive()){
  #To perform background correction on blimatesting object for two groups. Background correction is followed by quantile normalization.
  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 transformation.
  blimatesting = backgroundCorrect(blimatesting, normalizationMod=c, channelBackgroundFilter="bgf")
  blimatesting = nonPositiveCorrect(blimatesting, normalizationMod=c, channelCorrect="GrnF", channelBackgroundFilter="bgf")
}
else{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::install("");
}
```

---

**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 bitvise 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 correction.*

**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)
```
plotBackgroundImageBeforeCorrection

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

```r
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').");
}
```

Description

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

Usage

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

Arguments

b
Single beadLevelData object.

index
Index of spot to generate.

channelForeground
Name of channel of foreground.

cchannelBackground
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 backgroundCorrect 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.
   #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 transformation.
   blimatesting = backgroundCorrect(blimatesting, normalizationMod = processingMod, channelBackgroundFilter="bgf")
   blimatesting = nonPositiveCorrect(blimatesting, normalizationMod = processingMod, channelCorrect="GrnF", channelBackgroundFilter="bgf")
   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::install('blimaTestingData').")
}
**readToVector**

*Support doTTests function.*

**Description**

Internal function supporting doTTests function.

**Usage**

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

**Arguments**

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

**Author(s)**

Vojtěch Kulvait

---

**selectedChannelTransform**

*Channel transformation*

**Description**

Function to transform channel data.

**Usage**

```r
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 log2TransformPositive.

Author(s)
Vojtěch Kulvait

Examples

if(require("blimaTestingData") && interactive())
{
  #To perform background correction on blimatesting object for two groups. Background correction is followed by correction for non positive data.
  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 transformation.
  blimatesting = backgroundCorrect(blimatesting, normalizationMod=c, channelBackgroundFilter="bgf")
  blimatesting = nonPositiveCorrect(blimatesting, normalizationMod=c, channelCorrect="GrnF", channelBackgroundFilter="bgf")
} else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running BiocManager::install('blimaTestingData').")
}

selectedChannelTransformSingleArray

Channel transformation

Description
Function to transform channel data.

Usage

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

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 log2TransformPositive.

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.
singleCheckIntegrityLogicalVector

Author(s)
Vojtěch Kulvait

---

doubleChannelExistsIntegrityWithLogicalVector

Internal function

Description
Test existence of channel slot based on logical list

Usage
doubleChannelExistsIntegrityWithLogicalVector(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

---

doubleCheckIntegrityLogicalVector

Internal function

Description
Check integrity of the logical object, internal.

Usage
doubleCheckIntegrityLogicalVector(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**

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 backgroundCorrect 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 transformation.
blimatesting = backgroundCorrect(blimatesting, normalizationMod = processingMod, channelBackgroundFilter="bgf")
blimatesting = nonPositiveCorrect(blimatesting, normalizationMod = processingMod, channelCorrect="GrnF", channelBackgroundFilter="bgf")
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::install('blimaTestingData').")
}

vBeadStabiliseSingleArray

Bead level VST.

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

```r
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

```r
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
**writeBackgroundImages**

**Reference**


```
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 corelation.
- **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

```r
if(require("blimaTestingData") && interactive())
{
    # Write background images before and after correction for background into /tmp directory. This function creates two
    # 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")");
}
```

---

**xieBacgroundCorrect**  
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**

```r
xieBacgroundCorrect(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 backgroundCorrect method or/and with beadarray QC (defaults to NULL).

**Author(s)**

Vojtěch Kulvait
Examples

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

---

**xieBacgroundCorrectSingleArray**

*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**

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

**Arguments**

- `b` Single beadLevelData 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 backgroundCorrect method or/and with beadarray QC (defaults to NULL).
Author(s)

Vojtěch Kulvait
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