Package ‘blima’

December 21, 2016

Type Package

Title Package for the preprocessing and analysis of the Illumina microarrays on the detector (bead) level.

Version 1.8.0

Date 2015-04-01

Author Vojtech Kulvait

Maintainer Vojtech Kulvait <kulvait@gmail.com>

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

LazyLoad yes

Depends R(>= 3.0.0)

Imports beadarray(>= 2.0.0), Biobase(>= 2.0.0), BiocGenerics, grDevices, stats, graphics

Suggests xtable, blimaTestingData, BiocStyle, illuminaHumanv4.db, lumi

URL https://bitbucket.org/kulvait/blima

biocViews Microarray, Preprocessing, Normalization

NeedsCompilation no

R topics documented:

blima-package .......................................................... 2
aggregateAndPreprocess ............................................ 3
backgroundCorrect .................................................. 4
backgroundCorrectSingleArray ................................... 5
backgroundChannelSubtract ........................................ 5
backgroundChannelSubtractSingleArray ......................... 6
channelExistsIntegrityWithLogicalVectorList .................. 7
checkIntegrity ....................................................... 8
checkIntegrityLogical .............................................. 8
Package for the preprocessing and analysis of the Illumina microarrays on the detector (bead) level.

Package blima includes several algorithms for the preprocessing of Illumina microarray data. It focuses on the bead level analysis and provides a novel approach to the quantile normalization of vectors of unequal lengths. It provides a variety of 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.
aggregateAndPreprocess

Details

Package: blima
Type: Package
Title: Package for the preprocessing and analysis of the Illumina microarrays on the detector (bead) level.
Version: 1.1.03
Date: 2015-04-01
Author: Vojtech Kulvait
Maintainer: Vojtech Kulvait <kulvait@gmail.com>
License: GPL-3
LazyLoad: yes
Depends: R(>= 3.0.0)
Imports: beadarray(>= 2.0.0), Biobase(>= 2.0.0), BiocGenerics, grDevices, stats, graphics
Suggests: xtable, blimaTestingData, BiocStyle, illuminaHumanv4.db, lumi
URL: https://bitbucket.org/kulvait/blima
biocViews: Microarray, Preprocessing, Normalization

Author(s)

Vojtech Kulvait

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 agregate with columns "ProbeID" and quality.
quality Quality to analyze, default is "qua".
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)

Vojtech Kulvait
Data background correction

**Description**

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

**Usage**

```r
correctBackground(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)**

Vojtech Kulvait

**Examples**

```r
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")
}
```
bacgroundCorrectSingleArray

Data background correction.

Description

Background correction procedure selecting beads with background Intensity $I_b \mid \text{mean} - I_b \mid > k*\text{SD}(I Bs)$ for exclusion, internal.

Usage

bacgroundCorrectSingleArray(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)

Vojtech Kulvait

backgroundChannelSubtract

Background channel subtraction

Description

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

**Usage**

```r
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)**

Vojtech Kulvait

**Examples**

```r
if(require("blimaTestingData") && interactive())
{
  #To perform background correction on blimatesting object for two groups. Background correction is followed by correction for non positive data. Array spots out of selected groups will not be processed.
  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 = bacgroundCorrect(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 biocLite(")
  }

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)

Vojtech 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)

Vojtech Kulvait
checkIntegrity

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)
Vojtech Kulvait

checkIntegrityLogical

Description
Check integrity of the list of logical objects, internal.

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

Arguments
- **xx**: List of logical objects compatible with a list b.
- **b**: 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)
Vojtech 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)
Vojtech 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)
Vojtech 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 excludedOnSDMultiple multiple of standard deviations from the background value.

**Usage**

```r
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)**

Vojtech Kulvait

**Examples**

```r
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 biocLite("}
}
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 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 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)

Vojtech 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 biocLite("
)
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)
Vojtech Kulvait

doProbeTTests

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 eval-
uated on transformed data, consider use log2TranformPositive.
doProbeTTests

Author(s)
Vojtech Kulvait

Examples

if(require("blimaTestingData") && require("illuminaHumanv4.db") && interactive())
{
  #To perform background correction, variance stabilization and quantile normalization then test on probe level
  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 tranformation
  blimaTesting = bacgroundCorrect(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", "SymbolReannotated")
  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")
  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)
}
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
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 backroundCorrect 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 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)
Vojtech Kulvait

Examples
if(require("blimaTestingData") & require("illuminaHumanv4.db") & interactive())
{
  #To perform background correction, variance stabilization and quantile normalization then test on probe level
  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))
adrToSymbol <- adrToSymbol[,c("ArrayAddress", "SymbolReannotated")]
colnames(adrToSymbol) <- c("Array_Address_Id", "Symbol")
probeTestID = probeTest[,"ProbeID"]
beadTestID = beadTest[,"ProbeID"]
probeTestFC = abs(probeTest[,"mean1"]-probeTest[,"mean2"]) - 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 = tocmp[, c("ArrayAddressID", "Symbol", "difexBL")]

sortPL = sort(-tocmp[,"difexPL"], index.return=TRUE)$ix
sortBL = sort(-tocmp[,"difexBL"], index.return=TRUE)$ix
beadTop10 = tocmp[sorBL[1:10],]
probeTop10 = tocmp[sorPL[1:10],]
print(beadTop10)
print(probeTop10)
}
else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running biocLite("
})

---

**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)

Vojtech Kulvait

description

Support probe and bead level testing.

Usage
g getNextVector(what, from, length)

Arguments

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

Author(s)

Vojtech 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)

Vojtech Kulvait
**insertColumn**

*Internal function to support chipArrayStatistics*

**Description**

Internal

**Usage**

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

**Arguments**

- `matrix`: Object to insert column to
- `column`: Column to insert
- `name`: Name of column to assign.

**Author(s)**

Vojtech 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**

```r
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)**

Vojtech Kulvait
Examples

```r
if(require("blimaTestingData") && require("illuminaHumanv4.db") && interactive()) {

#To perform background correction, quantile normalization and then bead level t-test on log data run. Vst in 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$Name
}
#Background correction and quantile normalization followed by testing including log2TransformPositive transformation.
blimatesting = backgroundCorrect(blimatesting, normalizationMod = c, channelBackgroundFilter = "bgf")
blimatesting = nonPositiveCorrect(blimatesting, normalizationMod = c, channelCorrect = "GrnF", channelBackgroundFilter = "bgf")
blimatesting = quantileNormalize(blimatesting, normalizationMod = c, channelNormalize = "GrnF", channelOutput = "qua", channelInclude = "bgf")
beadTest <- doTTests(blimatesting, groups1Mod, groups2Mod, transformation = log2TransformPositive, quality = "qua", channelInclude = "bgf")
symbol2address <- merge(toTable(illuminaHumanv4ARRAYADDRESS), toTable(illuminaHumanv4SYMBOLREANNOTATED))
colnames(symbol2address) <- c("Symbol", "ArrayAddressID")
symbol2address <- symbol2address[,c("SymbolReannotated", "ArrayAddress")]
symbol2address <- sym2address[,c("Symbol", "ArrayAddressID")]
beadTestID = beadTest[,c("ProbeID", "Symbol")]
beadTestFC = abs(beadTest[,"mean1"]-beadTest[,"mean2"])
beadTestP = beadTest[,"adjustedp"]
beadTestMeasure = (1-beadTestP)*beadTestFC
beadTest <- cbind(beadTestID, beadTestMeasure)
sortBL = sort(-beadTest[,"difexBL"], index.return=TRUE)$ix
beadTop10 = beadTest[sortBL[1:10],]
print(beadTop10)
}
else
{
  print("To run this example, please install blimaTestingData package from bioconductor by running biocLite("")
}
```

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**

```r
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)**

Vojtech 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**

```r
nonParametricEstimator(toCorrectAll, toCorrectNeg)
```

**Arguments**

- `toCorrectAll`
- `toCorrectNeg`

**Author(s)**

Vojtech 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)
Vojtech Kulvait

Examples
if(require("blimaTestingData") && interactive())
{
  #To perform background correction on blimatesting object for two groups. Background correction is followed
  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 biocLite()")
}
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)
Vojtech 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**:
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)

Vojtech 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**

*Plot background image before correction*

**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)**

Vojtech 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 biocLite("
}
```

**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)
```

**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.
quantileNormalize

Author(s)
Vojtech Kulvait

Examples

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

quantileNormalize Bead level quantile normalization.

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

Usage

```r
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)
Vojtech Kulvait
Examples

```r
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 biocLite().")
}
```

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)

Vojtech Kulvait
selectedChannelTransform

Channel transformation

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 log2TransformPositive.

Author(s)

Vojtech Kulvait

Examples

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

### selectedChannelTransformSingleArray

**Channel transformation**

**Description**

Function to transform channel data.

**Usage**

```r
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)**

Vojtech 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**

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

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 asigned 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**: 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)

Vojtech Kulvait

Description

Test existence of channel slot based on logical list

Usage

```r
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)

Vojtech 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)**
Vojtech 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`: channelInclude

**Author(s)**
Vojtech 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)
Vojtech 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 (default to "bgf").
channelOutput Output from VST.
Examples

```r
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, 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 biocLite(
})
```

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".

Bead level VST.
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)

Vojtech 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 Vojtech Kulvait

**References**

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 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)

Vojtech Kulvait

Examples

if(require("blimaTestingData") && interactive())
{
  #Write background images before and after correction for background into /tmp directory. This function creates data(blimaTesting)
p = pData(blimaTesting[[2]]@experimentData$phenoData)
spotsToGenerate = p$Group %in% "D"
writeBackgroundImages(blimaTesting[[2]], imageType="jpg", spotsToGenerate=spotsToGenerate, includePearson=FALSE, outputDir="/tmp")
}

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

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)

Vojtech Kulvait

Examples

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) = backgroundCorrect(blimatesting, channelBackgroundFilter="bgf")
  blimatesting = nonPositiveCorrect(blimatesting, channelCorrect="GrnF", channelBackgroundFilter="bgf", channelInclude=NULL)
  blimatesting = xieBacgroundCorrect(blimatesting, negativeArrayAddresses=negAdr, channelCorrect="GrnF", channelInclude="bgf")
  #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 biocLite(
  
)}
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

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)

Vojtech Kulvait
Index

*Topic package
  blima-package, 2
aggregateAndPreprocess, 3
backgroundCorrect, 4
backgroundCorrectSingleArray, 5
backgroundChannelSubtract, 5
backgroundChannelSubtractSingleArray, 6
blima (blima-package), 2
blima-package, 2
channelExistsIntegrityWithLogicalVectorList, 7
checkIntegrity, 8
checkIntegrityLogical, 8
checkIntegrityOfListOfBeadLevelDataObjects, 9
checkIntegrityOfSingleBeadLevelDataObject, 9
chipArrayStatistics, 10
createSummarizedMatrix, 11
doAction, 12
doProbeTTests, 12
doTTests, 14
filterBg, 15
getNextVector, 16
initMeanDistribution, 16
insertColumn, 17
log2TransformPositive, 17
meanDistribution, 18
nonParametricEstimator, 19
nonPositiveCorrect, 20
nonPositiveCorrectSingleArray, 21
numberOfDistributionElements, 21
performXieCorrection, 22
plotBackgroundImageAfterCorrection, 22
quantileNormalize, 24
readToVector, 25
selectedChannelTransform, 26
selectedChannelTransformSingleArray, 27
singleArrayNormalize, 27
singleChannelExistsIntegrityWithLogicalVector, 28
singleCheckIntegrityLogicalVector, 29
singleNumberOfDistributionElements, 29
updateMeanDistribution, 30
varianceBeadStabilise, 30
varianceBeadStabiliseSingleArray, 31
vstFromLumi, 32
writeBackgroundImages, 33
xieBackgroundCorrect, 34
xieBackgroundCorrectSingleArray, 35