Package 'cn.farms'

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Title cn.FARMS - factor analysis for copy number estimation

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Type Package

License LGPL (>= 2.0)

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Description This package implements the cn.FARMS algorithm for copy number variation (CNV) analysis. cn.FARMS allows to analyze the most common Affymetrix (250K-SNP6.0) array types, supports high-performance computing using snow and ff.

URL http://www.bioinf.jku.at/software/cnfarms/cnfarms.html

Depends R (>= 3.0), Biobase, methods, ff, oligoClasses, snow

Imports DBI, affxparser, oligo, DNAcopy, preprocessCore, lattice

Suggests pd.mapping250k.sty, pd.mapping250k.nsp, pd.genomewidesnp.5, pd.genomewidesnp.6

Collate 'callSummarize.R' 'combineData.R' 'correctPkgname.R' 'cnFarms.R' 'createAnnotation.R' 'createMatrix.R' 'determineBaselineArray.R' 'distributionDistance.R' 'dnaCopySf.R' 'doCnFarms.R' 'fragLengthCorr.R' 'normAdd.R' 'normalizeAverage.R' 'normalizeCels.R' 'normalizeNpData.R' 'normalizeQuantiles.R' 'normalizeSor.R' 'plotDendrogram.R' 'plotDensity.R' 'plotEvalIc.R' 'plotSmoothScatter.R' 'plotsRegions.R' 'plotViolines.R' 'sparseFarmsC.R' 'summarizationMl.R' 'summarizationSl.R' 'summarizeFarmsGaussian.R' 'summarizeFarmsLaplaceExact.R' 'summarizeFarmsLaplaceVar.R' 'summarizeFarmsMethods.R' 'summarizeStatistics.R' 'windowFunctions.R' 'windowMethods.R' 'normalizeProbeSequence.R' 'snowfallExt.R' 'summarizeFarmsLaplaceExact2.R' 'summarizeFarmsLaplaceExact3.R' 'normalizeNone.R' 'utils-lds.R' 'zzz.R' 'sFclusterFunctions.R' 'sFinit.R' 'sFsnowfall-internal.R' 'sFsnowWrappers.R' 'sFsocketRequest.R' 'vanillaIce.R'

biocViews Microarray, CopyNumberVariation

Roxygen list(wrap = FALSE)

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R topics documented:

callSummarize — *Defines which variables should be written back when calling a cn.farms run*

Description

Defines which variables should be written back when calling a cn.farms run

Usage

```
callSummarize(object, psInfo, summaryMethod, summaryParam, batchList = NULL,
  cores = 1, runtype = "ff", returnValues, saveFile = "summData")
```

Arguments

object	an matrix with normalized intensity values.
psInfo	a data frame stating the physical position.
summaryMethod	the summarization method.
summaryParam	a list with the parameters of the summarization method.
batchList	batchList
cores	cores
runtype	mode how the results are saved. Possible values are ff or bm. If ff is chosen the data will not be saved automatically. With bm the results will be saved permanently.
returnValues	list with return values. For possible values see summaryMethod.
saveFile	name of the file to save.

Value

Results of FARMS run with specified parameters - exact FARMS version

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

cn.farms — *cn.farms*

Description

Wrapper for the cn.farms algorithm

Usage

```
cn.farms(filenames, cores = 1, runtype = "bm")
```

Arguments

filenames	the absolute filepaths of the CEL files.
cores	number of parallel instances.
runtype	either ff or bm.

Value

An instance of ExpressionSet containing the results of the analysis.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
## Not run:
require('hapmapsnp6')
celDir <- system.file('celFiles', package = 'hapmapsnp6')
filenames <- dir(path = celDir, full.names = TRUE)
cn.farms(filenames = filenames)

## End(Not run)
```

---

cnLibrary *This function was taken from snowfall and edited due to some deprecated function calls.*

Description

This function was taken from snowfall and edited due to some deprecated function calls.

Usage

```
cnLibrary(package, pos = 2, lib.loc = NULL, character.only = FALSE,
  warn.conflicts = TRUE, keep.source = getOption("keep.source.pkgs"),
  verbose = getOption("verbose"), version, stopOnError = TRUE)
```

Arguments

package	name of the package. Check 'library' for details.
pos	position in search path to load library.
lib.loc	a character vector describing the location of the R library trees to search through, or 'NULL'. Check 'library' for details.
character.only	a logical indicating package can be assumed to be a character string. Check 'library' for details.
warn.conflicts	warn on conflicts (see "library").
keep.source	DEPRECATED (see "library").
verbose	enable verbose messages.
version	version of library to load (see "library").
stopOnError	logical.

Value

for more information see "library".

Author(s)

xxx

`combineData` *Combine two ExpressionSet objects*

Description

Suitable for SNP or non-polymorphic data which were already processed with single locus FARMS

Usage

```
combineData(object01, object02, obj01Var = "intensity",
  obj02Var = "intensity", runtype = "ff", saveFile = "combData")
```

Arguments

`object01`	An instance of `ExpressionSet` either with SNP or non-polymorphic data
`object02`	An instance of `ExpressionSet` either with SNP or non-polymorphic data
`obj01Var`	States the variable which should be combined from the assayData slot. Default is intensity.
`obj02Var`	States the variable which should be combined from the assayData slot. Default is intensity.
`runtype`	Mode how the results are saved. Possible values are ff or bm. If ff is chosen the data will not be saved automatically. With bm the results will be saved permanently.
`saveFile`	Name of the file to save.

Value

An instance of `ExpressionSet`.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
load(system.file("exampleData/normData.RData", package = "cn.farms"))
notes(experimentData(normData))$annotDir <-
        system.file("exampleData/annotation/pd.genomewidesnp.6/1.1.0",
                package = "cn.farms")
summaryMethod <- "Variational"
summaryParam <- list()
summaryParam$cyc <- c(10)
slData <- slSummarization(normData,
        summaryMethod = summaryMethod,
```

```
        summaryParam = summaryParam)
assayData(slData)$L_z[1:10, ]
combData <- combineData(slData, slData)
combData
```

---

createAnnotation *Creation of annotation files*

Description

Annotation files for cn.farms are created

Usage

```
createAnnotation(filenames = NULL, annotation = NULL, annotDir = NULL,
  checks = TRUE)
```

Arguments

filenames	An absolute path of the CEL files to process.
annotation	Optional parameter stating the annotation from a pd-mapping.
annotDir	Optional parameter stating where the annotation should go.
checks	States if sanity checks should be done.

Value

NULL

Note

The annotation files used for cn.farms will be placed in the current work directory under annotations.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
## Not run:
library("hapmapsnp6")
celDir <- system.file("celFiles", package = "hapmapsnp6")
filenames <- dir(path = celDir, full.names = TRUE)
createAnnotation(filenames = filenames)

## End(Not run)
```

createMatrix *Creates the needed matrix*

Description

Creates the needed matrix

Usage

```
createMatrix(runtype, nrow, ncol, type = "double", bmName = "NA")
```

Arguments

runtype	Mode how the results are saved. Possible values are ff or bm. If ff is chosen the data will not be saved automatically. With bm the results will be saved permanently.
nrow	nrow
ncol	ncol
type	type
bmName	Identifier for ff name

Value

a matrix

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

distributionDistance *Computes the distribution distance*

Description

Be aware that this function is implemented quite slow.

Usage

```
distributionDistance(intensityData, method = c("JSDiv", "KLDiv", "KLInf"),
  useSubset = T, subsetFraction = 0.25, useQuantileReference = FALSE)
```

Arguments

intensityData	A matrix or an AffyBatch object.
method	The method you want to use.
useSubset	Logical. States if only a subset should be used.
subsetFraction	The fraction of the subset.
useQuantileReference	Logical for a quantile reference.

Value

Computes the distribution distance

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
load(system.file("exampleData/normData.RData", package = "cn.farms"))
x <- assayData(normData)$intensity[, 1:3]
y <- distributionDistance(x)
attr(y, "Labels") <- substr(sampleNames(normData), 1, 7)
plotDendrogram(y)
```

---

dnaCopySf *Runs DNAcopy in parallel mode*

Description

This function even works very well with ff matrices,

Usage

```
dnaCopySf(x, chrom, maploc, cores = 1, smoothing, ...)
```

Arguments

x	A matrix with data of the copy number experiments
chrom	The chromosomes (or other group identifier) from which the markers came
maploc	The locations of marker on the genome
cores	Number of cores to use
smoothing	States if smoothing of the data should be done
...	Further parameter for the function segment of DNAcopy

Value

An instance of ExpressionSet containing the segments.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
load(system.file("exampleData/mlData.RData", package = "cn.farms"))
mlData <- mlData[, 1:3]
colnames(assayData(mlData)$L_z) <- sampleNames(mlData)
segments <- dnaCopySf(
        x         = assayData(mlData)$L_z,
        chrom     = fData(mlData)$chrom,
        maploc    = fData(mlData)$start,
        cores     = 1,
        smoothing = FALSE)
fData(segments)
```

---

doCnFarmsSingle *Does the whole cn.farms process in one call*

Description

Works for all kind of Affymetrix SNP arrays

Usage

```
doCnFarmsSingle(celfiles, samplenames, normalization)
```

Arguments

celfiles	The celfiles which you want to process with the whole path. Either a vector or a matrix with two columns for combined analysis e.g. 500K Array.
samplenames	An optional vector with the same dimension as the number of cel files
normalization	The normalization method you want to use.

Value

The ready cn.FARMS results.

Author(s)

Andreas Mitterecker

---

flcSnp6Std *Does a fragment length correction on intensities*

Description

Does a fragment length correction on intensities

Usage

```
flcSnp6Std(y, fragmentLengths, targetFcn = NULL, subsetToFit = NULL,
  runtype = "ff", cores = 1, saveFile = "flc", ...)
```

Arguments

y	y
fragmentLengths	fragmentLengths
targetFcn	targetFcn
subsetToFit	subsetToFit
runtype	runtype
cores	cores
saveFile	Name of the file to save.
...	...

Value

data frame

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

---

flcStd *Does a fragment length correction on intensities*

Description

Does a fragment length correction on intensities

Usage

```
flcStd(y, fragmentLengths, targetFcn = NULL, subsetToFit = NULL,
  runtype = "ff", cores = 1, saveFile = "flc", ...)
```

Arguments

y	y
fragmentLengths	fragmentLengths
targetFcn	targetFcn
subsetToFit	subsetToFit
runtype	Mode how the results are saved. Possible values are ff or bm. If ff is chosen the data will not be saved automatically. With bm the results will be saved permanently.
cores	cores
saveFile	Name of the file to save.
...	...

Value

data frame

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

`fragLengCorr` *Does a fragment length correction*

Description

Does a fragment length correction

Usage

```
fragLengCorr(object, runtype = "ff", saveFile = "slDataFlc", ...)
```

Arguments

`object`	An instance of `ExpressionSet`
`runtype`	Mode how the results are saved. Possible values are ff or bm.
`...`	Further parameters passed to the correction method.
`saveFile`	Name of the file to save.

Value

An instance of `ExpressionSet`.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
load(system.file("exampleData/slData.RData", package = "cn.farms"))
slDataFlc <- fragLengCorr(slData)
```

`getFragmentSet` *Finds SNPs which belong to one fragment*

Description

Finds SNPs which belong to one fragment

Usage

```
getFragmentSet(fragLength)
```

Arguments

`fragLength`	fragLength

Value

windows for fragments

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

---

getSingleProbeSetSize *Combines data for probeset summarization*

Description

Combines data for probeset summarization

Usage

```
getSingleProbeSetSize(fsetid)
```

Arguments

fsetid	fsetid

Value

a Indices whhich are used for probeset summarization

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

---

mlSummarization *Method for computation of the multi-loci summarization*

Description

Method for computation of the multi-loci summarization

Usage

```
mlSummarization(object, windowMethod, windowParam, summaryMethod, summaryParam,
  callParam = list(runtype = "ff"), returnValues, saveFile = "mlData")
```

Arguments

object	an instance of ExpressionSet
windowMethod	Method for combination of neighbouring SNPs. Possible values are Std and Bps.
windowParam	further parameters as the window size
summaryMethod	allowed versions for the summarization step are: Gaussian, Variational, Exact. Default is Variational.
summaryParam	The parameters for the summaryMethod. Further information can be obtained via the according functions: cn.farms, cn.farms or cn.farms
callParam	Additional parameters for runtype (ff or bm) as well as cores for parallelization.
returnValues	List with return values.
saveFile	Name of the file to save. For possible values see summaryMethod.

Value

Multi-loci summarized data of an instance of ExpressionSet

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
load(system.file("exampleData/slData.RData", package = "cn.farms"))
windowMethod <- "std"
windowParam <- list()
windowParam$windowSize <- 5
windowParam$overlap <- TRUE
summaryMethod <- "Variational"
summaryParam <- list()
summaryParam$cyc <- c(20)
mlData <- mlSummarization(slData, windowMethod, windowParam,
        summaryMethod, summaryParam)
assayData(mlData)
```

---

normAdd *Extracts info from the package name*

Description

Extracts info from the package name

Usage

```
normAdd(pkgname)
```

Arguments

pkgname	The package name according to the bioconductor annotation names.

Value

Additional info for save files.

Author(s)

Andreas Mitterecker

`normalizeAverage` *Scales the range of the non-polymorphic data to the range of a given array.*

Description

Scales the range of the non-polymorphic data to the range of a given array.

Usage

```
normalizeAverage(x, baselineArray, avg = median, targetAvg = 2200, ...)
```

Arguments

`x`	Data matrix
`baselineArray`	Choose the baseline channel array.
`avg`	The function for averaging.
`targetAvg`	Value to which the array should be averaged.
`...`	Further optional parameters.

Value

Normalized non-polymorphic data.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
x <- matrix(rnorm(100, 11), 20, 5)
normalizeAverage(x, x[, 1])
```

normalizeCels *Wrapper for the normalization functions*

Description

This functions provides different normalization methods for microarray data. At the moment only SOR and quantile normalization are implemented.

Usage

```
normalizeCels(filenames, method = c("SOR", "quantiles", "none"), cores = 1,
  alleles = FALSE, runtype = "bm", annotDir = NULL,
  saveFile = "normData", ...)
```

Arguments

filenames	The absolute path of the CEL files as a list.
method	The normalization method. Possible methods so far: SOR, quantiles
cores	Number of cores for used for parallelization.
alleles	States if information for allele A and B should be given back.
runtype	Mode how the results are saved. Possible values are ff or bm. If ff is chosen the data will not be saved automatically. With bm the results will be saved permanently.
annotDir	An optional annotation directory.
saveFile	Name of the file to save.
...	Further parameters for the normalization method.

Value

An ExpressionSet object with the normalized data.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
## Not run:
library("hapmapsnp6")
celDir <- system.file("celFiles", package = "hapmapsnp6")
filenames <- dir(path = celDir, full.names = TRUE)
createAnnotation(filenames = filenames)
normData <- normalizeCels(filenames, method = "SOR")

## End(Not run)
```

normalizeNone *Runs the SOR normalization on microarray data*

Description

Runs the SOR normalization on microarray data

Usage

```
normalizeNone(filenames, cores = 1, annotDir = NULL, alleles = FALSE,
  runtype = "ff", cyc = 5, pkgname = NULL, saveFile = "Sor")
```

Arguments

filenames	an absolute path of the CEL files
cores	cores
annotDir	annotDir
alleles	alleles
cyc	states the number of cycles for the EM algorithm.
runtype	Mode how the results are saved. Possible values are ff or bm. If ff is chosen the data will not be saved automatically. With bm the results will be saved permanently.
pkgname	Optional parameter for the CEL mapping.
saveFile	Name of the file to save.

Value

An instance of ExpressionSet

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

normalizeNpData *Processes the non-polymorphic data*

Description

Normalization for non-polymorphic data for Affymetrix SNP5 and SNP6

Usage

```
normalizeNpData(filenames, cores = 1, annotDir = NULL, runtype = "ff",
  saveFile = "npData", method = c("baseline", "quantiles", "none"))
```

Arguments

filenames	the absolute path of the CEL files as a list
cores	number of cores for used for parallelization
annotDir	Optional annotation directory.
runtype	Mode how the results are saved. Possible values are ff or bm. If ff is chosen the data will not be saved automatically. With bm the results will be saved permanently.
saveFile	Name of the file to save.
method	The method for the normalization.

Value

An instance of ExpressionSet containing the non-polymorphic data of the microarray.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
## Not run:
library("hapmapsnp6")
celDir <- system.file("celFiles", package = "hapmapsnp6")
filenames <- dir(path = celDir, full.names = TRUE)
createAnnotation(filenames = filenames)
npData <- normalizeNpData(filenames)

## End(Not run)
```

---

normalizeQuantiles *Normalization Quantiles*

Description

Normalization Quantiles

Usage

```
normalizeQuantiles(filenames, cores = 1, batch = NULL, annotDir = NULL,
  runtype = "ff", pkgname = NULL, saveFile = "normDataQuant")
```

Arguments

filenames	filenames
cores	cores
batch	batch
annotDir	annotDir
runtype	Mode how the results are saved. Possible values are ff or bm. If ff is chosen the data will not be saved automatically. With bm the results will be saved permanently.
pkgname	Optional parameter for the CEL mapping.
saveFile	Name of the file to save.

Value

The normalized data.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

`normalizeSequenceEffect` *Correction for probe sequence effects*

Description

Correction for probe sequence effects

Usage

```
normalizeSequenceEffect(object, annotDir = NULL, runtype = "ff",
  saveFile = "seqNorm")
```

Arguments

`object`	an instance of `ExpressionSet`
`annotDir`	the directory where the anntotation can be found
`runtype`	mode how the results are saved. Possible values are ff or bm. If ff is chosen the data will not be saved automatically.
`saveFile`	name of the file to save.

Value

Some data

Author(s)

Andreas Mitterecker

`normalizeSor` *Runs the SOR normalization on microarray data*

Description

Runs the SOR normalization on microarray data

Usage

```
normalizeSor(filenames, cores = 1, annotDir = NULL, alleles = FALSE,
  runtype = "ff", cyc = 5, pkgname = NULL, saveFile = "Sor")
```

Arguments

filenames	an absolute path of the CEL files
cores	cores
annotDir	annotDir
alleles	alleles
cyc	states the number of cycles for the EM algorithm.
runtype	Mode how the results are saved. Possible values are ff or bm. If ff is chosen the data will not be saved automatically. With bm the results will be saved permanently.
pkgname	Optional parameter for the CEL mapping.
saveFile	Name of the file to save.

Value

An instance of ExpressionSet

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

---

plotDendrogram *Plots a dendrogram*

Description

Plots a dendrogram

Usage

```
plotDendrogram(DivMetric, colorLabels)
```

Arguments

DivMetric	The input data (see example).
colorLabels	A color label with the dimension of the columns.

Value

A dendrogram.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
load(system.file("exampleData/normData.RData", package = "cn.farms"))
x <- assayData(normData)$intensity[, 1:3]
y <- distributionDistance(x)
attr(y, "Labels") <- substr(sampleNames(normData), 1, 7)
plotDendrogram(y)
```

plotDensity *Function to create a density plot*

Description

Simple density plot. Adapted from the aroma.affymetrix package (www.aroma-project.org)

Usage

```
plotDensity(x, xlim = c(0, 16), ylim, col, lty, lwd, add = FALSE, xlab,
  ylab, log = TRUE, ...)
```

Arguments

x	Matrix with numeric values.
xlim	The limits for the x axis.
ylim	The limits for the y axis.
col	Vector with colors corresponding to the columns of the matrix.
lty	The line type (see graphics).
lwd	The line width, a positive number, defaulting to 1 (see graphics).
add	If FALSE (the default) then a new plot is produced. If TRUE, density lines are added to the open graphics device.
xlab	The labeling of the x axis.
ylab	The labeling of the y axis.
log	Logical values which states if the log2 should be taken from the data.
...	Further arguments of the plot function '

Value

A plot written to the graphics device.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
load(system.file("exampleData/slData.RData", package = "cn.farms"))
plotDensity(assayData(slData)$intensity)
```

plotEvalIc *Creates a plot with known regions and a numeric vector*

Description

Creates a plot with known regions and a numeric vector

Usage

```
plotEvalIc(object, segments, chrom, variable, ylim, ylab = "CN indicator",
  stripCol = "lightgray", regionCol = rgb(130, 0, 139, maxColorValue = 255),
  pointSize = 0.75, pointType = 4, bandwidth = c(0.01, 1000),
  nbin = 100)
```

Arguments

object	an instance of ExpressionSet
segments	A data.frame with known regions.
chrom	the chromosome.
variable	The numeric vector which should be plotted.
ylim	the limits of the y axis.
ylab	the ylab from function par.
stripCol	color of points.
regionCol	color of regions.
pointSize	size of the points.
pointType	type of the points.
bandwidth	for the color of the plot.
nbin	number of bins for the coloring.

Value

Some data

Author(s)

Andreas Mitterecker

Examples

```
load(system.file("exampleData/slData.RData", package = "cn.farms"))
load(system.file("exampleData/testSegments.RData", package = "cn.farms"))
plotEvalIc(slData, fData(testSegments),
     variable = assayData(slData)$L_z[, 1], 23)
```

plotRegions *Plots given regions by segments*

Description

A pdf in the working directory is produced.

Usage

```
plotRegions(object, segments, addInd = NULL, ylim, variable,
  colorVersion = 0, plotLegend = TRUE, pdfname)
```

Arguments

object	An instance of ExpressionSet
segments	An instance of ExpressionSet with the segments to plot
addInd	States how many indices should be plotted besides the region
ylim	The limits for the y axis.
variable	States which variable of the assayData should be plotted.
colorVersion	States different color versions.
plotLegend	If a legend should be plotted or not.
pdfname	The name of the pdf file.

Value

A graph. Normally a pdf in the current work directory.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
load(system.file("exampleData/slData.RData", package = "cn.farms"))
load(system.file("exampleData/testSegments.RData", package = "cn.farms"))
plotRegions(slData, testSegments, addInd = 10, ylim = c(-2, 2),
        variable = "L_z", colorVersion = 1, plotLegend = TRUE,
        pdfname = "slData.pdf")
```

plotSmoothScatter *Creates a smooth scatter plot*

Description

Creates a smooth scatter plot

Usage

```
plotSmoothScatter(object, variable, chrom, start, end, ylim, pdfname, ...)
```

Arguments

object	An instance of ExpressionSet.
variable	States which variable of the assayData should be plotted.
chrom	The chromosome you want to plot.
start	The physical start position.
end	The physical end position.
ylim	The limits for the y axis.
pdfname	The name of the pdf file.
...	Further arguments passed to smoothScatter function.

Value

A graph.

Author(s)

Andreas Mitterecker

Examples

```
load(system.file("exampleData/slData.RData", package = "cn.farms"))
plotSmoothScatter(slData[, 1:3], chrom = "23")
```

plotViolines *Create a violine plot*

Description

This function creates a violine plot on intensity values

Usage

```
plotViolines(object, variable = "intensity", groups, ...)
```

Arguments

object	An instance of ExpressionSet
variable	states which variable of assayData should be plotted.
groups	Vector with the dimension of the samples for coloring.
...	Further arguments passed to the lattice graph.

Value

Creates a violine plot.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
load(system.file("exampleData/normData.RData", package = "cn.farms"))
normData <- normData[, 1:10]
groups <- seq(sampleNames(normData))
plotViolines(normData, variable = "intensity", groups, xlab = "Intensity values")
```

---

slSummarization *Method for computation of the single-locus summarization*

Description

The different probes of the SNPs of the array are summarized to a probeset.

Usage

```
slSummarization(object, summaryMethod = "Exact", summaryParam = list(),
  callParam = list(runtype = "ff", cores = 1), summaryWindow = c("std",
  "fragment"), returnValues, saveFile = "slData")
```

Arguments

object	An instance of ExpressionSet
summaryMethod	allowed versions for the summarization step are: Gaussian,Variational, Exact. Default is Variational.
summaryParam	The parameters for the summaryMethod. Further information can be obtained via the according functions: cn.farms, cn.farms or cn.farms
callParam	Additional parameters for runtype (ff or bm) as well as cores for parallelization.
summaryWindow	Method for combination of the SNPs. Possible values are sl and fragment.
returnValues	List with return values.
saveFile	Name of the file to save.

Value

Single-locus summarized data of an instance of ExpressionSet

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

See Also

summarizeFarmsExact

Examples

```
load(system.file("exampleData/normData.RData", package = "cn.farms"))
notes(experimentData(normData))$annotDir <-
        system.file("exampleData/annotation/pd.genomewidesnp.6/1.1.0",
                package = "cn.farms")
summaryMethod <- "Variational"
summaryParam <- list()
summaryParam$cyc <- c(10)
slData <- slSummarization(normData,
        summaryMethod = summaryMethod,
        summaryParam = summaryParam)
assayData(slData)$L_z[1:10, 1:10]

summaryMethod <- "Gaussian"
summaryParam <- list()
summaryParam$cyc <- c(10)
slData <- slSummarization(normData,
        summaryMethod = summaryMethod,
        summaryParam = summaryParam)
assayData(slData)$L_z[1:10, 1:10]

summaryMethod <- "Exact"
summaryParam <- list()
summaryParam$cyc <- c(10, 20)
slData <- slSummarization(normData,
        summaryMethod = summaryMethod,
        summaryParam = summaryParam)
assayData(slData)$L_z[1:10, 1:10]
```

---

sparseFarmsC *Normalizes the data with SOR*

Description

Normalizes the data with SOR

Usage

```
sparseFarmsC(probes, cyc = 5)
```

Arguments

probes	The intensity matrix.
cyc	Number of cycles.

Value

Normalized Data.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
x <- matrix(rnorm(100, 11), 20, 5)
sparseFarmsC(x, 50)
```

`summarizeFarmsExact` *Summarization Laplacian approach with exact computation*

Description

This function implements an exact Laplace FARMS algorithm.

Usage

```
summarizeFarmsExact(probes, mu = 1, weight = 0.001, weightSignal = 1,
  weightZ = 1, weightProbes = TRUE, cyc = c(10, 10), tol = 1e-05,
  weightType = "mean", centering = "median", rescale = FALSE,
  backscaleComputation = FALSE, maxIntensity = TRUE, refIdx, ...)
```

Arguments

`probes`	A matrix with numeric values.
`mu`	Hyperparameter value which allows to quantify different aspects of potential prior knowledge. Values near zero assumes that most positions do not contain a signal, and introduces a bias for loading matrix elements near zero. Default value is 0 and it's recommended not to change it.
`weight`	Hyperparameter value which determines the influence of the Gaussian prior of the loadings
`weightSignal`	Hyperparameter value on the signal.
`weightZ`	Hyperparameter value which determines how strong the Laplace prior of the factor should be at 0. Users should be aware, that a change of weightZ in comparison to the default parameter might also entail a need to change other parameters. Unexperienced users should not change weightZ.
`weightProbes`	Parameter (TRUE/FALSE), that determines, if the number of probes should additionally be considered in weight. If TRUE, weight will be modified.
`cyc`	Number of cycles. If the length is two, it is assumed, that a minimum and a maximum number of cycles is given. If the length is one, the value is interpreted as the exact number of cycles to be executed (minimum == maximum).
`tol`	States the termination tolerance if cyc[1]!=cyc[2]. Default is 0.00001.
`weightType`	Flag, that is used to summarize the probes of a sample.
`centering`	States how the data should be centered ("mean", "median"). Default is median.

rescale	Parameter (TRUE/FALSE), that determines, if moments in exact Laplace FARMS are rescaled in each iteration. Default is FALSE.
backscaleComputation	Parameter (TRUE/FALSE), that determines if the moments of hidden variables should be reestimated after rescaling the parameters.
maxIntensity	Parameter (TRUE/FALSE), that determines if the expectation value (=FALSE) or the maximum value (=TRUE) of p(z|x_i) should be used for an estimation of the hidden varaible.
refIdx	index or indices which are used for computation of the centering
...	Further parameters for expert users.

Value

A list including: the found parameters: lambda0, lambda1, Psi

the estimated factors: z (expectation), maxZ (maximum)

p: log-likelihood of the data given the found lambda0, lambda1, Psi (not the posterior likelihood that is optimized)

varzx: variances of the hidden variables given the data

KL: Kullback Leibler divergences between between posterior and prior distribution of the hidden variables

IC: Information Content considering the hidden variables and data

ICtransform: transformed Information Content

Case: Case for computation of a sample point (non-exception, special exception)

L1median: Median of the lambda vector components

intensity: back-computed summarized probeset values with mean correction

L_z: back-computed summarized probeset values without mean correction

rawCN: transformed values of L_z

SNR: some additional signal to noise ratio value

Author(s)

Andreas Mayr <mayr@bioinf.jku.at> and Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
x <- matrix(rnorm(100, 11), 20, 5)
summarizeFarmsExact(x)
```

summarizeFarmsExact2 *Summarization Laplacian approach with exact computation*

Description

This function implements an exact Laplace FARMS algorithm.

Usage

```
summarizeFarmsExact2(probes, mu = 1, weight = 0.5, weightSignal = 1,
  weightZ = 1, weightProbes = TRUE, cyc = c(10, 10), tol = 1e-05,
  weightType = "mean", centering = "median", rescale = FALSE,
  backscaleComputation = FALSE, maxIntensity = TRUE, refIdx, ...)
```

Arguments

probes	A matrix with numeric values.
mu	Hyperparameter value which allows to quantify different aspects of potential prior knowledge. Values near zero assumes that most positions do not contain a signal, and introduces a bias for loading matrix elements near zero. Default value is 0 and it's recommended not to change it.
weight	Hyperparameter value which determines the influence of the Gaussian prior of the loadings
weightSignal	Hyperparameter value on the signal.
weightZ	Hyperparameter value which determines how strong the Laplace prior of the factor should be at 0. Users should be aware, that a change of weightZ in comparison to the default parameter might also entail a need to change other parameters. Unexperienced users should not change weightZ.
weightProbes	Parameter (TRUE/FALSE), that determines, if the number of probes should additionally be considered in weight. If TRUE, weight will be modified.
cyc	Number of cycles. If the length is two, it is assumed, that a minimum and a maximum number of cycles is given. If the length is one, the value is interpreted as the exact number of cycles to be executed (minimum == maximum).
tol	States the termination tolerance if cyc[1]!=cyc[2]. Default is 0.00001.
weightType	Flag, that is used to summarize the probes of a sample.
centering	States how the data should be centered ("mean", "median"). Default is median.
rescale	Parameter (TRUE/FALSE), that determines, if moments in exact Laplace FARMS are rescaled in each iteration. Default is FALSE.
backscaleComputation	Parameter (TRUE/FALSE), that determines if the moments of hidden variables should be reestimated after rescaling the parameters.
maxIntensity	Parameter (TRUE/FALSE), that determines if the expectation value (=FALSE) or the maximum value (=TRUE) of p(z|x_i) should be used for an estimation of the hidden varaible.
refIdx	index or indices which are used for computation of the centering
...	Further parameters for expert users.

Value

A list including: the found parameters: lambda0, lambda1, Psi

the estimated factors: z (expectation), maxZ (maximum)

p: log-likelihood of the data given the found lambda0, lambda1, Psi (not the posterior likelihood that is optimized)

varzx: variances of the hidden variables given the data

KL: Kullback Leibler divergences between between posterior and prior distribution of the hidden variables

IC: Information Content considering the hidden variables and data

ICtransform: transformed Information Content

Case: Case for computation of a sample point (non-exception, special exception)

L1median: Median of the lambda vector components

intensity: back-computed summarized probeset values with mean correction

L_z: back-computed summarized probeset values without mean correction

rawCN: transformed values of L_z

SNR: some additional signal to noise ratio value

Author(s)

Andreas Mayr <mayr@bioinf.jku.at> and Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
x <- matrix(rnorm(100, 11), 20, 5)
summarizeFarmsExact(x)
```

`summarizeFarmsExact3` *Summarization Laplacian approach with exact computation*

Description

This function implements an exact Laplace FARMS algorithm.

Usage

```
summarizeFarmsExact3(probes, mu = 1, weight = 100, weightSignal = 1,
  weightZ = 30, weightProbes = TRUE, updateSignal = FALSE, cyc = c(10,
  10), tol = 1e-05, weightType = "mean", centering = "median",
  rescale = FALSE, backscaleComputation = FALSE, maxIntensity = TRUE,
  refIdx, ...)
```

Arguments

probes	A matrix with numeric values.
mu	Hyperparameter value which allows to quantify different aspects of potential prior knowledge. Values near zero assumes that most positions do not contain a signal, and introduces a bias for loading matrix elements near zero. Default value is 0 and it's recommended not to change it.
weight	Hyperparameter value which determines the influence of the Gaussian prior of the loadings
weightSignal	Hyperparameter value on the signal.
weightZ	Hyperparameter value which determines how strong the Laplace prior of the factor should be at 0. Users should be aware, that a change of weightZ in comparison to the default parameter might also entail a need to change other parameters. Unexperienced users should not change weightZ.
weightProbes	Parameter (TRUE/FALSE), that determines, if the number of probes should additionally be considered in weight. If TRUE, weight will be modified.
updateSignal	updateSignal.
cyc	Number of cycles. If the length is two, it is assumed, that a minimum and a maximum number of cycles is given. If the length is one, the value is interpreted as the exact number of cycles to be executed (minimum == maximum).
tol	States the termination tolerance if cyc[1]!=cyc[2]. Default is 0.00001.
weightType	Flag, that is used to summarize the probes of a sample.
centering	States how the data should be centered ("mean", "median"). Default is median.
rescale	Parameter (TRUE/FALSE), that determines, if moments in exact Laplace FARMS are rescaled in each iteration. Default is FALSE.
backscaleComputation	Parameter (TRUE/FALSE), that determines if the moments of hidden variables should be reestimated after rescaling the parameters.
maxIntensity	Parameter (TRUE/FALSE), that determines if the expectation value (=FALSE) or the maximum value (=TRUE) of p(z|x_i) should be used for an estimation of the hidden varaible.
refIdx	index or indices which are used for computation of the centering
...	Further parameters for expert users.

Value

A list including: the found parameters: lambda0, lambda1, Psi

the estimated factors: z (expectation), maxZ (maximum)

p: log-likelihood of the data given the found lambda0, lambda1, Psi (not the posterior likelihood that is optimized)

varzx: variances of the hidden variables given the data

KL: Kullback Leibler divergences between between posterior and prior distribution of the hidden variables

IC: Information Content considering the hidden variables and data

ICtransform: transformed Information Content

Case: Case for computation of a sample point (non-exception, special exception)

L1median: Median of the lambda vector components

intensity: back-computed summarized probeset values with mean correction

L_z: back-computed summarized probeset values without mean correction

rawCN: transformed values of L_z

SNR: some additional signal to noise ratio value

Author(s)

Andreas Mayr <mayr@bioinf.jku.at> and Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
x <- matrix(rnorm(100, 11), 20, 5)
summarizeFarmsExact(x)
```

---

summarizeFarmsGaussian

Summarization Gaussian approach

Description

This function runs the FARMS algorithm.

Usage

```
summarizeFarmsGaussian(probes, weight = 0.15, mu = 0, cyc = 10,
  tol = 1e-04, weightType = "mean", init = 0.6, correction = 0,
  minNoise = 0.35, centering = "median", refIdx)
```

Arguments

probes	A matrix with numeric values.
weight	Hyperparameter value in the range of [0,1] which determines the influence of the prior.
mu	Hyperparameter value which allows to quantify different aspects of potential prior knowledge. Values near zero assumes that most genes do not contain a signal, and introduces a bias for loading matrix elements near zero. Default value is 0.
cyc	Number of cycles for the EM algorithm.
tol	States the termination tolerance. Default is 0.00001.
weightType	Flag, that is used to summarize the loading matrix. The default value is set to mean.
init	Parameter for estimation.

correction	Value that indicates whether the covariance matrix should be corrected for negative eigenvalues which might emerge from the non-negative correlation constraints or not. Default = O (means that no correction is done), 1 (minimal noise (0.0001) is added to the diagonal elements of the covariance matrix to force positive definiteness), 2 (Maximum Likelihood solution to compute the nearest positive definite matrix under the given non-negative correlation constraints of the covariance matrix)
minNoise	States the minimal noise. Default is 0.35.
centering	States how the data is centered. Default is median.
refIdx	index or indices which are used for computation of the centering

Value

A list containing the results of the run.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
x <- matrix(rnorm(100, 11), 20, 5)
summarizeFarmsGaussian(x)
```

---

summarizeFarmsMethods *Lists methods for possible FARMS summarization*

Description

Possible FARMS summarization

Usage

```
summarizeFarmsMethods()
```

Value

Returns a data frame with all possible FARMS calls.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
summarizeFarmsMethods()
```

summarizeFarmsStatistics

Mean or median instead of the FARMS model

Description

Mean or median instead of the FARMS model

Usage

```
summarizeFarmsStatistics(probes, type = "median", ...)
```

Arguments

probes	A matrix with numeric values.
type	The statistic which you want to apply.
...	Further parameters

Value

Some data

Author(s)

Andreas Mitterecker

summarizeFarmsVariational

Summarization variational Laplacian approach

Description

This function runs the FARMS algorithm.

Usage

```
summarizeFarmsVariational(probes, weight = 0.15, mu = 0, cyc = 10,
  weightType = "median", init = 0.6, correction = 0, minNoise = 0.35,
  spuriousCorrelation = 0.3, centering = "median")
```

Arguments

probes	A matrix with numeric values.
weight	Hyperparameter value in the range of [0,1] which determines the influence of the prior.
mu	Hyperparameter value which allows to quantify different aspects of potential prior knowledge. Values near zero assumes that most genes do not contain a signal, and introduces a bias for loading matrix elements near zero. Default value is 0.

cyc	Number of cycles for the EM algorithm.
weightType	Flag, that is used to summarize the loading matrix. The default value is set to mean.
init	Parameter for estimation.
correction	Value that indicates whether the covariance matrix should be corrected for negative eigenvalues which might emerge from the non-negative correlation constraints or not. Default = O (means that no correction is done), 1 (minimal noise (0.0001) is added to the diagonal elements of the covariance matrix to force positive definiteness), 2 (Maximum Likelihood solution to compute the nearest positive definite matrix under the given non-negative correlation constraints of the covariance matrix)
spuriousCorrelation	Numeric value for suppression of spurious correlation.
minNoise	States the minimal noise. Default is 0.35.
centering	States how the data is centered. Default is median.

Value

A list containing the results of the run.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
x <- matrix(rnorm(100, 11), 20, 5)
summarizeFarmsVariational(x)
```

---

summarizeWindowBps *Combines neighbouring locations to windows*

Description

Combines neighbouring locations to windows

Usage

```
summarizeWindowBps(phInf, fixedBps = 10000, upperLimit = 6)
```

Arguments

phInf	The locations on the chromosomes.
fixedBps	Size of the window in basepairs.
upperLimit	Maximal number of neigbouring locations to combine.

Value

Indices for summarization

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
## create toy physical data
sizeTmp <- 30
phInf <- data.frame(
        chrom = rep("15", sizeTmp),
        start = seq(from = 1, by = 300, length.out = sizeTmp),
        end = seq(from = 3600, by = 300, length.out = sizeTmp),
        man_fsetid = paste("SNP_A-", seq(sizeTmp)+1000, sep = ""))
summarizeWindowBps(phInf)
```

---

summarizeWindowMethods *Lists methods for possible window methods*

Description

Function to list how neighbouring positions can be combined.

Usage

```
summarizeWindowMethods()
```

Value

Returns a data frame with all possible methods.

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
summarizeWindowMethods()
```

---

summarizeWindowStd *Combines neighbouring locations to windows*

Description

Combines neighbouring locations to windows

Usage

```
summarizeWindowStd(phInf, windowSize = 3, overlap = TRUE)
```

Arguments

phInf	The locations on the chromosomes.
windowSize	Size of how many Locations should be combined.
overlap	States if the windows should overlap.

Value

Indices for summarization

Author(s)

Djork-Arne Clevert <okko@clevert.de> and Andreas Mitterecker <mitterecker@bioinf.jku.at>

Examples

```
## create toy physical data
sizeTmp <- 30
phInf <- data.frame(
        chrom = rep("15", sizeTmp),
        start = seq(from = 1, by = 300, length.out = sizeTmp),
        end = seq(from = 3600, by = 300, length.out = sizeTmp),
        man_fsetid = paste("SNP_A-", seq(sizeTmp)+1000, sep = ""))
summarizeWindowStd(phInf)
```

Index