

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' 'summarizationSI.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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| | |
|---------------|---|
| callSummarize | <i>Defines which variables should be written back when calling a cn.farms run</i> |
|---------------|---|

Description

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

Usage

```
callSummarize(object, psInfo, summaryMethod, summaryParam, batchList = NULL,
  cores = 1, runtime = "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 |
| runtime | 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 | <i>cn.farms</i> |
|----------|-----------------|

Description

Wrapper for the cn.farms algorithm

Usage

```
cn.farms(filenamees, cores = 1, runtime = "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. |


```
summaryParam = summaryParam)
assayData(s1Data)$L_z[1:10, ]
combData <- combineData(s1Data, s1Data)
combData
```

createAnnotation *Creation of annotation files*

Description

Annotation files for cn.farms are created

Usage

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

Arguments

| | |
|------------|--|
| filename | 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(filename = 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 | <i>Does the whole cn.farms process in one call</i> |
|-----------------|--|

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

| | |
|------------|---|
| f1cSnp6Std | <i>Does a fragment length correction on intensities</i> |
|------------|---|

Description

Does a fragment length correction on intensities

Usage

```
f1cSnp6Std(y, fragmentLengths, targetFcn = NULL, subsetToFit = NULL,
  runtype = "ff", cores = 1, saveFile = "f1c", ...)
```

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, runtime = "ff", saveFile = "slDataFlc", ...)
```

Arguments

| | |
|----------|---|
| object | An instance of ExpressionSet |
| runtime | 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 which 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 runtime (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 | <i>Scales the range of the non-polymorphic data to the range of a given array.</i> |
|------------------|--|

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 | <i>Wrapper for the normalization functions</i> |
|---------------|--|

Description

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

Usage

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

Arguments

| | |
|------------|--|
| filenamees | 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")  
filenamees <- dir(path = celDir, full.names = TRUE)  
createAnnotation(filenamees = filenamees)  
normData <- normalizeCels(filenamees, method = "SOR")  
  
## End(Not run)
```

| | |
|---------------|--|
| normalizeNone | <i>Runs the SOR normalization on microarray data</i> |
|---------------|--|

Description

Runs the SOR normalization on microarray data

Usage

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

Arguments

| | |
|------------|--|
| filenamees | 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 | <i>Processes the non-polymorphic data</i> |
|-----------------|---|

Description

Normalization for non-polymorphic data for Affymetrix SNP5 and SNP6

Usage

```
normalizeNpData(filenamees, 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, runtime = "ff",
  saveFile = "seqNorm")
```

Arguments

| | |
|----------|---|
| object | an instance of ExpressionSet |
| annotDir | the directory where the annotation can be found |
| runtime | 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(filenamees, cores = 1, annotDir = NULL, alleles = FALSE,
  runtime = "ff", cys = 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 log ₂ 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 | <i>Creates a plot with known regions and a numeric vector</i> |
|------------|---|

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 | <i>Plots given regions by segments</i> |
|-------------|--|

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 variable. |
| 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 $cyc[1] \neq cyc[2]$. 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 $p(z_{lx_i})$ should be used for an estimation of the hidden variable. |
| 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 variable. |
| 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 = 0 (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 = 0 (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 neighbouring 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)
```

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