

# cn.farms

May 17, 2012

---

<code>callSummarize</code>	<i>Defines which variables should be written back when calling a <code>cn.farms</code> 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

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

---

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", runtime = "ff",
            saveFile = "combData")
```

## Arguments

object01	An instance of <a href="#">ExpressionSet</a> either with SNP or non-polymorphic data
object02	An instance of <a href="#">ExpressionSet</a> 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.
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.
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(filenamees = NULL, annotation = NULL,  
annotDir = NULL, checks = TRUE)
```

## Arguments

filenamees	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")  
filenamees <- dir(path = celDir, full.names = TRUE)  
createAnnotation(filenamees = filenamees)  
  
## 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)$data
```

---

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

---

**Description**

Works for all kind of Affymetrix SNP arrays

**Usage**

```
doCnFarmsSingle(cefiles, samplenames, normalization)
```

**Arguments**

**cefiles**            The cefiles 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	<i>Does a fragment length correction on intensities</i>
------------	---

---

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

---

**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	<i>Does a fragment length correction</i>
--------------	--

---

**Description**

Does a fragment length correction

**Usage**

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

**Arguments**

object	An instance of <a href="#">ExpressionSet</a>
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 which are used for probeset summarization

### Author(s)

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

---

mlSummarization      *Does summarization*

---

## Description

Does 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**    summaryParam

**callParam**       callParam

**returnValues**    List with return values.

**saveFile**        Name of the file to save. For possible values see summaryMethod.

## Value

Some data

## 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$cyt <- c(20)
mlData <- mlSummarization(slData, windowMethod, windowParam,
  summaryMethod, summaryParam)
assayData(mlData)
```

---

normAdd	<i>Extracts info from the package name</i>
---------	--

---

**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

*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(filenamees,
  method = c("SOR", "quantiles", "none"), cores = 1,
  alleles = FALSE, runtime = "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.
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.
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	<i>Runs the SOR normalization on microarray data</i>
---------------	--

---

## 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(filenamees, cores = 1, annotDir = NULL,  
  runtime = "ff", saveFile = "npData",  
  method = c("baseline", "quantiles", "none"))
```

### Arguments

filenamees	the absolute path of the CEL files as a list
cores	number of cores for used for parallelization
annotDir	Optional annotation directory.
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.
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")  
filenamees <- dir(path = celDir, full.names = TRUE)  
createAnnotation(filenamees = filenamees)  
npData <- normalizeNpData(filenamees)  
  
## End(Not run)
```

---

normalizeQuantiles *Normalization Quantiles*

---

**Description**

Normalization Quantiles

**Usage**

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

**Arguments**

filenamees	filenamees
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 <a href="#">ExpressionSet</a>
annotDir	the directory where the annotation 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	<i>Runs the SOR normalization on microarray data</i>
--------------	--

---

**Description**

Runs the SOR normalization on microarray data

**Usage**

```
normalizeSor(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>



---

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](http://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 <a href="#">graphics</a> ).
lwd	The line width, a positive number, defaulting to 1 (see <a href="#">graphics</a> ).
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, max = 255),
  pointSize = 0.75, pointType = 4,
  bandwidth = c(0.01, 1000), nbin = 100)
```

**Arguments**

object	an instance of <a href="#">ExpressionSet</a>
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 <a href="#">ExpressionSet</a>
segments	An instance of <a href="#">ExpressionSet</a> 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 <a href="#">ExpressionSet</a> .
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/s1Data.RData", package = "cn.farms"))
plotSmoothScatter(s1Data[, 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 <a href="#">ExpressionSet</a>
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 <a href="#">ExpressionSet</a>
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: <a href="#">cn.farms</a> , <a href="#">cn.farms</a> or <a href="#">cn.farms</a>
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. For possible values see summaryMethod.
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)
```

---

```
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 $p(z x_i)$ 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)
```

---

```
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 $cyc[1] \neq cyc[2]$ . 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 $p(z x_i)$ 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)
```

---

```
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 <code>cyc[1]!=cyc[2]</code> . 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**

<code>probes</code>	A matrix with numeric values.
<code>weight</code>	Hyperparameter value in the range of [0,1] which determines the influence of the prior.
<code>mu</code>	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.
<code>cyc</code>	Number of cycles for the EM algorithm.
<code>tol</code>	States the termination tolerance. Default is 0.00001.
<code>weightType</code>	Flag, that is used to summarize the loading matrix. The default value is set to mean.
<code>init</code>	Parameter for estimation.
<code>correction</code>	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)
<code>minNoise</code>	States the minimal noise. Default is 0.35.
<code>centering</code>	States how the data is centered. Default is median.
<code>refIdx</code>	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

<code>probes</code>	A matrix with numeric values.
<code>weight</code>	Hyperparameter value in the range of [0,1] which determines the influence of the prior.
<code>mu</code>	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.
<code>cyc</code>	Number of cycles for the EM algorithm.
<code>weightType</code>	Flag, that is used to summarize the loading matrix. The default value is set to mean.
<code>init</code>	Parameter for estimation.
<code>correction</code>	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)
<code>spuriousCorrelation</code>	Numeric value for suppression of spurious correlation.
<code>minNoise</code>	States the minimal noise. Default is 0.35.
<code>centering</code>	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**

<code>phInf</code>	The locations on the chromosomes.
<code>windowSize</code>	Size of how many Locations should be combined.
<code>overlap</code>	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

callSummarize, 1  
cn.farms, 22  
combineData, 2  
createAnnotation, 3  
createMatrix, 4  
  
distributionDistance, 4  
dnaCopySf, 5  
doCnFarmsSingle, 6  
  
ExpressionSet, 2, 5, 8, 10, 13, 14, 16,  
19–22  
  
flcSnp6Std, 7  
flcStd, 7  
fragLengCorr, 8  
  
getFragmentSet, 9  
getSingleProbeSetSize, 9  
graphics, 18  
  
mlSummarization, 10  
  
normAdd, 11  
normalizeAverage, 11  
normalizeCels, 12  
normalizeNone, 13  
normalizeNpData, 14  
normalizeQuantiles, 15  
normalizeSequenceEffect, 15  
normalizeSor, 16  
  
plotDendrogram, 17  
plotDensity, 17  
plotEvalIc, 18  
plotRegions, 19  
plotSmoothScatter, 20  
plotViolines, 21  
  
slSummarization, 22  
sparseFarmsC, 23  
summarizeFarmsExact, 22, 27  
summarizeFarmsExact2, 24  
summarizeFarmsExact3, 25  
summarizeFarmsGaussian, 29  
  
summarizeFarmsMethods, 30  
summarizeFarmsStatistics, 30  
summarizeFarmsVariational, 31  
summarizeWindowBps, 32  
summarizeWindowMethods, 33  
summarizeWindowStd, 33