

# Package ‘Starr’

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**Title** Simple tiling array analysis of Affymetrix ChIP-chip data

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**Depends** Ringo, affy, affxparser

**Imports** pspline, MASS, zlibbioc

**Description** Starr facilitates the analysis of ChIP-chip data, in particular that of Affymetrix tiling arrays. The package provides functions for data import, quality assessment, data visualization and exploration. Furthermore, it includes high-level analysis features like association of ChIP signals with annotated features, correlation analysis of ChIP signals and other genomic data (e.g. gene expression), peak-finding with the CMARRT algorithm and comparative display of multiple clusters of ChIP-profiles. It uses the basic Bioconductor classes ExpressionSet and probeAnno for maximum compatibility with other software on Bioconductor. All functions from Starr can be used to investigate preprocessed data from the Ringo package, and vice versa. An important novel tool is the the automated generation of correct, up-to-date microarray probe annotation (bpmmap) files, which relies on an efficient mapping of short sequences (e.g. the probe sequences on a microarray) to an arbitrary genome.

**License** Artistic-2.0

**biocViews** Microarray,OneChannel,DataImport,QualityControl,Preprocessing,ChIPchip

**LazyLoad** yes

## R topics documented:

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bpmmapToProbeAnno      *Creating a probeAnno object*

---

## Description

This function allows the user to create a probeAnno environment that holds the mapping between probes on the array and their genomic match position(s). The function takes an Affymetrix bpmmap file as input.

## Usage

```
bpmmapToProbeAnno(bpmmap, verbose=T, uniqueSeq=T)
```

**Arguments**

bpmap	Either a list, created by the function readBpmap() from the affy package. Or a path to the bpmap file.
verbose	should the progress be printed out?
uniqueSeq	If TRUE, probes sequences that occur more than once on the chip (and consequently match several positions on the genome) are set to 1 in the probeAnno object. Unique probes are set to 0. If false, all probes are set to 0. To identify all unique and multiple matching probes, a remapping of the probes to the genome is recommended.

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**Examples**

```
##
# dataPath <- system.file("extdata", package="Starr")
# bpmapChr1 <- readBpmap(file.path(dataPath, "Scerevisiae_tlg_chr1.bpmap"))

# probeAnnoChr1 <- bpmapToProbeAnno(bpmapChr1)
```

---

cmarrt.ma	<i>Compute moving average statistics by incorporating the correlation structure</i>
-----------	---

---

**Description**

This function extends the moving average approach by incorporating the correlation structure. It also outputs the p-values of the standardized moving average statistics under the Gaussian approximation.

**Usage**

```
cmarrt.ma(eSet, probeAnno, chr=NULL, M=NULL, frag.length, window.opt=fixed.probe)
```

**Arguments**

eSet	ExpressionSet containing the normalized ratio
probeAnno	probeAnno object with mapping
chr	which chromosome should be analysed? If chr==NULL, all chromosome in the probeAnno object are taken.
M	rough estimate of the percentage of bound probes. If unknown, leave it NULL.
frag.length	average fragment length from sonication.
window.opt	option for sliding window, either "fixed.probe" or "fixed.gen.dist". Default is 'fixed.probe'.

## Details

Computation using `window.opt = "fixed.probe"` calculates the moving average statistics within a fixed number of probes and is more efficient. Use this option if the tiling array is regular with approximately constant resolution. `window.opt="fixed.gen.dist"` computes the moving average statistics over a fixed genomic distance.

## Value

<code>data.sort</code>	datafile sorted by genomic position.
<code>ma</code>	unstandardized moving average(MA) statistics.
<code>z.cmarrt</code>	standardized MA under correlation structure.
<code>z.indep</code>	standardized MA under independence (ignoring correlation structure).
<code>pv.cmarrt</code>	p-values of probes under correlation.
<code>pv.indep</code>	p-values of probes under independence (ignoring correlation structure).

## Note

The p-values are obtained under the Gaussian approximation. Therefore, it is important to check the normal quantile-quantile plot if the Gaussian approximation is valid. The function also outputs the computation under independence (ignoring the correlation structure) for comparisons.

## Author(s)

Pei Fen Kuan, Adam Hinz

## References

P.F. Kuan, H. Chun, S. Keles (2008). CMARRT: A tool for the analysis of ChIP-chip data from tiling arrays by incorporating the correlation structure. *Pacific Symposium of Biocomputing* **13**:515-526.

## See Also

[plotcmarrt,cmarrt.peak](#)

## Examples

```
# dataPath <- system.file("extdata", package="Starr")
# bmapChr1 <- readBmap(file.path(dataPath, "Scerevisiae_tlg_chr1.bmap"))

# cels <- c(file.path(dataPath, "Rpb3_IP_chr1.cel"), file.path(dataPath, "wt_IP_chr1.cel"),
# file.path(dataPath, "Rpb3_IP2_chr1.cel"))
# names <- c("rpb3_1", "wt_1", "rpb3_2")
# type <- c("IP", "CONTROL", "IP")
# rpb3Chr1 <- readCelFile(bmapChr1, cels, names, type, featureData=TRUE, log.it=TRUE)

# ips <- rpb3Chr1$type == "IP"
# controls <- rpb3Chr1$type == "CONTROL"
```

```
# rpb3_rankpercentile <- normalize.Probes(rpb3Chr1, method="rankpercentile")
# description <- c("Rpb3vsWT")
# rpb3_rankpercentile_ratio <- getRatio(rpb3_rankpercentile, ips, controls, description, fkt=median, featureData=

# probeAnnoChr1 <- bmapToProbeAnno(bmapChr1)
# peaks <- cmarrt.ma(rpb3_rankpercentile_ratio, probeAnnoChr1, chr=NULL, M=NULL, 250, window.opt=fixed.probe)
```

---

cmarrt.peak

*Obtain bound regions for a given error rate control*


---

## Description

Obtain bound regions under a given error rate control using correction method from [p.adjust](#).

## Usage

```
cmarrt.peak(cmarrt.ma, alpha, method, minrun, asCherList=FALSE)
```

## Arguments

cmarrt.ma	output object from <a href="#">cmarrt.ma</a> .
alpha	error rate control for declaring bound region.
method	correction method inherited from <a href="#">p.adjust</a> .
minrun	minimum number of probes to be called a bound region.
asCherList	If TRUE, result is returned as class cherList. See <a href="#">Ringo</a> , for further description.

## Details

The function returns two objects, `cmarrt.bound` and `indep.bound`. Each object is a list of bound regions which can be accessed by `$chr` (chromosome), `$peak.start` (start coordinate of each bound region), `$peak.stop` (stop coordinate of each bound region), `$n.probe` (number of probes within each bound region), `$min.pv` (minimum p-values of each bound region), `$ave.pv` (average p-values of each bound region).

## Value

<code>cmarrt.bound</code>	list of bound regions obtained under correlation structure.
<code>indep.bound</code>	list of bound regions obtained under independence (ignoring correlation).

## Note

The list of bound regions obtained under independence (ignoring the correlation structure) is for comparison. It is not recommended to use this list for downstream analysis.

## Author(s)

Pei Fen Kuan, Adam Hinz

**References**

P.F. Kuan, H. Chun, S. Keles (2008). CMARRT: A tool for the analysis of ChIP-chip data from tiling arrays by incorporating the correlation structure. *Pacific Symposium of Biocomputing* **13**:515-526.

**See Also**

[cmarrt.ma,p.adjust](#)

**Examples**

```
# dataPath <- system.file("extdata", package="Starr")
# bmapChr1 <- readBmap(file.path(dataPath, "Scerevisiae_tlg_chr1.bmap"))

# cels <- c(file.path(dataPath, "Rpb3_IP_chr1.cel"), file.path(dataPath, "wt_IP_chr1.cel"),
# file.path(dataPath, "Rpb3_IP2_chr1.cel"))
# names <- c("rpb3_1", "wt_1", "rpb3_2")
# type <- c("IP", "CONTROL", "IP")
# rpb3Chr1 <- readCelFile(bmapChr1, cels, names, type, featureData=TRUE, log.it=TRUE)

# ips <- rpb3Chr1$type == "IP"
# controls <- rpb3Chr1$type == "CONTROL"

# rpb3_rankpercentile <- normalize.Probes(rpb3Chr1, method="rankpercentile")
# description <- c("Rpb3vsWT")
# rpb3_rankpercentile_ratio <- getRatio(rpb3_rankpercentile, ips, controls, description, fkt=median, featureData=

# probeAnnoChr1 <- bmapToProbeAnno(bmapChr1)
# peaks <- cmarrt.ma(rpb3_rankpercentile_ratio, probeAnnoChr1, chr=NULL, M=NULL, 250, window.opt=fixed.probe)
# peaklist <- cmarrt.peak(peaks)
```

---

correlationPlot

*correlation of ChIP signals to other data*

---

**Description**

`correlationPlot` The `correlationPlot` can be used to visualize e.g. the correlation between the mean binding intensity of specific regions around annotated features and gene expression. The regions around the annotated features, that should be analyzed are defined in a data frame. Each row represents one region. In the upper panel of the plot, the correlation is plotted in a barplot. In the lower panel, the annotated feature and the regions defined in the data frame are shown.

**Usage**

```
correlationPlot(regions, labels=c("start", "stop"), ...)
```

**Arguments**

<code>regions</code>	a data frame, containing four columns. Every row defines one region to be analyzed and is plotted in the lower panel. <code>pos=start</code> , <code>upstream=500</code> and <code>downstream=500</code> mean characterize the region 500 bp upstream and downstream around the start of the feature. The <code>pos</code> columns is a character with values out of <code>c("start", "region", "end")</code> . <code>upstream</code> and <code>downstream</code> are integers, indicating how many bases upstream and downstream from the specified position in the feature are included. <code>level</code> is an integer, that says at which level the rectangle in the lower device should be plotted. The numeration goes from the bottom to the ceiling. <code>cor</code> is the correlation of the region, which is plotted in the upper panel.
<code>labels</code>	a character vector which holds the names of the borders of the annotated region. (e.g. <code>c("TSS", "TTS")</code> for transcripts)
<code>...</code>	parameters, that are passed to <code>barplot</code> (for plotting the upper panel)

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**See Also**

[barplot](#)

**Examples**

```
## Constructing an example data frame
pos <- c("start", "start", "start", "region", "region", "region", "region", "stop", "stop", "stop")
upstream <- c(500, 0, 250, 0, 0, 500, 500, 500, 0, 250)
downstream <- c(0, 500, 250, 0, 500, 0, 500, 0, 500, 250)
level <- c(1, 1, 2, 3, 4, 5, 6, 1, 1, 2)
cor <- seq(-1,1, length=10)
info <- data.frame(pos=pos, upstream=upstream, downstream=downstream, level=level, cor=cor, stringsAsFactors=FALSE)
rownames(info) <- letters[1:10]

## Generate plot
correlationPlot(info)
```

---

densityscatter

*Compute density of a scatterplot*

---

**Description**

A 2d density is computed by `kde2D`.

**Usage**

```
densityscatter(x,y,pch=19,cex=1,ncol=30,grid=100,palette="heat", add=F,...)
```

**Arguments**

x	x coordinate of data
y	y coordinate of data
pch	type of point
cex	A numerical value giving the amount by which plotting text and symbols should be magnified relative to the default
grid	Number of grid points in each direction
ncol	number of colors
palette	color palette to choose
add	should data points be added to an existing plot?
...	parameters passed to plot or points

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**See Also**

[kde2dplot](#)

**Examples**

```
##
points = 10^4
x <- rnorm(points/2)
x = c(x,x+2.5)
y <- x + rnorm(points,sd=0.8)
x = sign(x)*abs(x)^1.3
densityscatter(x,y)
```

---

expressionByFeature     *Getting expression value by feature from an ExpressionSet*

---

**Description**

This function gets the expression of a specified feature (e.g. orf, gene) from an ExpressionSet.

**Usage**

```
expressionByFeature(eSet, fkt, method="median")
```



**Arguments**

eSet	An ExpressionSet, containing the normalized expression values
fkt	Function to convert the featureNames (e.g. affy IDs) of eSet to the required features (e.g. ORFs)
method	If one feature (e.g. ORF) has more than one feature (e.g. affy ID) on the chip, the mean/median over the intensities is taken

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**See Also**

[mget](#)

---

filterGenes

*Filter Features/Genes*

---

**Description**

This function filters genes and other annotated features with respect to length, overlaps and distance to other features.

**Usage**

```
filterGenes(gffAnno, distance_us=500, distance_ds=500, minLength=-Inf, maxLength=Inf)
```

**Arguments**

gffAnno	a data frame containing the annotation
distance_us	how many basepairs upstream to the feature should not overlap with other features.
distance_ds	how many basepairs downstream to the feature should not overlap with other features.
minLength	minimal length of the feature
maxLength	maximal length of the feature

**Value**

a character vector with the names of the features, that passed the filter.

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

## Examples

```
##
# dataPath <- system.file("extdata", package="Starr")
# transcriptAnno <- read.gffAnno(file.path(dataPath, "transcriptAnno.gff"), feature="transcript")
# filtered_transcripts <- filterGenes(transcriptAnno, distance_us = 0, distance_ds = 0, minLength = 1000)
```

---

getMeans

*Get mean ChIP-signal over annotated features*

---

## Description

getMeans calculates the mean ChIP-signal over annotated features

## Usage

```
getMeans(eSet, probeAnno, geneAnno, regions)
```

## Arguments

eSet	an ExpressionSet
probeAnno	a probeAnno object for the given ExpressionSet
geneAnno	a data frame containing the annotation of the features of interest
regions	a data frame, containing four columns. The pos column is a character with values out of c("start", "region", "end"). upstream and downstream are integers, indicating how many bases upstream and downstream from the specified position in the feature are included. level is an integer, that says at which level the rectangle in the lower device should be plotted. The numeration goes from the bottom to the ceiling. cor is the correlation of the region, which is plotted in the upper panel.

## Value

a list. Each entry contains the mean signals over the specified regions (in the regions data frame) of all features in geneAnno.

## Author(s)

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

## See Also

[getProfiles](#)

**Examples**

```
##
# dataPath <- system.file("extdata", package="Starr")
# bmapChr1 <- readBmap(file.path(dataPath, "Scerevisiae_tlg_chr1.bmap"))

# cels <- c(file.path(dataPath,"Rpb3_IP_chr1.cel"), file.path(dataPath,"wt_IP_chr1.cel"),
# file.path(dataPath,"Rpb3_IP2_chr1.cel"))
# names <- c("rpb3_1", "wt_1","rpb3_2")
# type <- c("IP", "CONTROL", "IP")
# rpb3Chr1 <- readCelFile(bmapChr1, cels, names, type, featureData=TRUE, log.it=TRUE)

# ips <- rpb3Chr1$type == "IP"
# controls <- rpb3Chr1$type == "CONTROL"

# rpb3_rankpercentile <- normalize.Probes(rpb3Chr1, method="rankpercentile")
# description <- c("Rpb3vsWT")
# rpb3_rankpercentile_ratio <- getRatio(rpb3_rankpercentile, ips, controls, description, fkt=median, featureData=TRUE)

# probeAnnoChr1 <- bmapToProbeAnno(bmapChr1)

# transcriptAnno <- read.gffAnno(file.path(dataPath, "transcriptAnno.gff"), feature="transcript")
# filtered_orfs <- filterGenes(transcriptAnno, distance_us = 0, distance_ds = 0, minLength = 1000)

# pos <- c("start", "start", "start", "region", "region","region","region", "stop","stop","stop")
# upstream <- c(500, 0, 250, 0, 0, 500, 500, 500, 0, 250)
# downstream <- c(0, 500, 250, 0, 500, 0, 500, 0, 500, 250)
# info <- data.frame(pos=pos, upstream=upstream, downstream=downstream, stringsAsFactors=FALSE)
# means_rpb3 <- getMeans(rpb3_rankpercentile_ratio, probeAnnoChr1, transcriptAnno[which(transcriptAnno$name %in%
```

---

getProfiles

*Get profiles of ChIP-signal over annotated features*


---

**Description**

This function associates the measured ChIP signals to annotated features and stores the profile of each feature in a list. Each profile is divided in three parts. The first entry is "upstream", which saves the signal upstream of start. Then follows "region", which is from start to end and then "downstream", which stores the signals downstream of end.

**Usage**

```
getProfiles(eSet, probeAnno, gffAnno, upstream, downstream, feature="ORF", borderNames, method, sameLe
```

**Arguments**

eSet	an ExpressionSet, containing on sample.
probeAnno	a probeAnno object for the given ExpressionSet
gffAnno	a data frame containing the annotation of the features of interest

upstream	how many basepairs upstream of the feature start (feature start on the crick strand is end in gffAnno) should be taken.
downstream	how many basepairs downstream of the feature start (feature end on the crick strand is start in gffAnno) should be taken.
feature	name of the features (e.g. ORF, transcript, rRNA, ...)
borderNames	names of the borders, flanking the feature (e.g. c("start", "stop"))
method	Two methods are available. "middle", just takes the middle position of each probe and its corresponding value. This method should be used if the whole genome is tiled in an high resolution. "basewise" calculates for each base the mean of all probes overlapping with this position.
fill	if "middle" is chosen the distance of the taken values equals the probe spacing on the chip. To avoid errors, because of regions lacking of probes, one can fill up these regions with NAs.
distance	if method "middle" and fill==TRUE are chosen, distance is the max distance of no value occuring before filling in one NA.
spacing	probe spacing on the chip. Only used for filling up with NAs in method "middle".
sameLength	if method "middle" is chosen it can occur that the length of the upstream/downstream region vary a little. If sameLength==TRUE, upstream/downstream regions get all the same length.

### Value

a list with the following entries

ID	the ID/name of the sample
upstream	number of basepairs, taken upstream of the feature
downstream	number of basepairs, taken upstream of the feature
method	method used
borderNames	names of the borders
feature	feature type (e.g. "ORF")
profile	a list which contains all profiles of the features in the gffAnno. Each entry consists of a list with the elements "upstream", "region", "downstream".

### Author(s)

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

### See Also

[fill](#), [fillNA](#), [mapFeatures](#), [getIntensities](#), [getFeature](#), [fill.getProfilesByBase](#)

**Examples**

```
##
# dataPath <- system.file("extdata", package="Starr")
# bmapChr1 <- readBmap(file.path(dataPath, "Scerevisiae_tlg_chr1.bmap"))

# cels <- c(file.path(dataPath, "Rpb3_IP_chr1.cel"), file.path(dataPath, "wt_IP_chr1.cel"),
# file.path(dataPath, "Rpb3_IP2_chr1.cel"))
# names <- c("rpb3_1", "wt_1", "rpb3_2")
# type <- c("IP", "CONTROL", "IP")
# rpb3Chr1 <- readCelFile(bmapChr1, cels, names, type, featureData=TRUE, log.it=TRUE)

# ips <- rpb3Chr1$type == "IP"
# controls <- rpb3Chr1$type == "CONTROL"

# rpb3_rankpercentile <- normalize.Probes(rpb3Chr1, method="rankpercentile")
# description <- c("Rpb3vsWT")
# rpb3_rankpercentile_ratio <- getRatio(rpb3_rankpercentile, ips, controls, description, fkt=median, featureData=TRUE)

# probeAnnoChr1 <- bmapToProbeAnno(bmapChr1)
# transcriptAnno <- read.gffAnno(file.path(dataPath, "transcriptAnno.gff"), feature="transcript")

# profile <- getProfiles(rpb3_rankpercentile_ratio, probeAnnoChr1, transcriptAnno, 500, 500, feature="transcript")
```

---

getRatio

*Building ratio over experiments*


---

**Description**

This function calculates the ratio over experiments.

**Usage**

```
getRatio(eSet, ip, control, description, fkt=median, featureData=F)
```

**Arguments**

eSet	An ExpressionSet, containing the logged raw intensities
ip	a boolean or integer vector, that indicate, which columns in the matrix are IP experiments
control	a boolean or integer vector, that indicate, which columns in the matrix are CONTROL or REFERENCE experiments
description	description of the new data (e.g. IPvsCONTROL)
fkt	mean or median to calculate the averaged intensity over replicates
featureData	if TRUE, featureData is added to the new ExpressionSet

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**Examples**

```
##
# dataPath <- system.file("extdata", package="Starr")
# bmapChr1 <- readBpmap(file.path(dataPath, "Scerevisiae_tlg_chr1.bpmap"))

# cels <- c(file.path(dataPath, "Rpb3_IP_chr1.cel"), file.path(dataPath, "wt_IP_chr1.cel"),
# file.path(dataPath, "Rpb3_IP2_chr1.cel"))
# names <- c("rpb3_1", "wt_1", "rpb3_2")
# type <- c("IP", "CONTROL", "IP")
# rpb3Chr1 <- readCelFile(bmapChr1, cels, names, type, featureData=TRUE, log.it=TRUE)

# ips <- rpb3Chr1$type == "IP"
# controls <- rpb3Chr1$type == "CONTROL"

# rpb3_rankpercentile <- normalize.Probes(rpb3Chr1, method="rankpercentile")
# description <- c("Rpb3vsWT")
# rpb3_rankpercentile_ratio <- getRatio(rpb3_rankpercentile, ips, controls, description, fkt=median, featureData=
```

---

heatmapplot

*heatmapplot*

---

**Description**

Heatmap representation of binding profiles

**Usage**

```
heatmapplot(profiles, colpal=c("black", "dark blue", "dark green", "green", "gold", "yellow"), abl=NULL,
```

**Arguments**

profiles	a list of profiles returned by getProfiles(). Features must have same lengths.
colpal	color palette for intensity coding
abl	positions of vertical lines that are added to the panel
subset	subset of genes in the list that should be plotted

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

---

list2matrix	<i>Convert profile list to matrix</i>
-------------	---------------------------------------

---

**Description**

This function converts the list of profiles generated by the `getProfiles` function to a matrix, if all entries have the same length.

**Usage**

```
list2matrix(profiles)
```

**Arguments**

`profiles` a list, generated by the `getProfiles`

**Value**

a list with with a matrix at the entry profile.

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

---

makeProbeAnno	<i>Creating a probeAnno object</i>
---------------	------------------------------------

---

**Description**

Creates a `probeAnno` object (package: `Ringo`) from a given Affymetrix `bpmmap` file or a Nimblegen POS file. The `posToProbeAnno` function from the `Ringo` package is called to build the object.

**Usage**

```
makeProbeAnno(posFile=NULL, bpmmap=NULL, probeIDAsStrings=F)
```

**Arguments**

`posFile` path to the POS file

`bpmmap` Either a list, created by the function `readBpmmap()` from the `affy` package, or a path to the `bpmmap` file.

`probeIDAsStrings` should the mapping of the probes to the rows in the `assayData` be integers or characters.

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**See Also**

[posToProbeAnno](#), [readBpmap](#)

---

makeSplines

*Fit splines to profiles*

---

**Description**

This function uses the pspline package to fit splines to each entry in a list of profiles.

**Usage**

```
makeSplines(profiles, df=1000)
```

**Arguments**

profiles            a list as it is created by the getProfiles package.  
df                    the degree of freedom of the fit

**Value**

a list as it is created by the getProfiles function.

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**See Also**

[smooth.Pspline](#), [predict.smooth.Pspline](#)

**Examples**

```
##  
# dataPath <- system.file("extdata", package="Starr")  
# bpmapChr1 <- readBpmap(file.path(dataPath, "Scerevisiae_tlg_chr1.bpmap"))  
  
# cels <- c(file.path(dataPath, "Rpb3_IP_chr1.cel"), file.path(dataPath, "wt_IP_chr1.cel"),  
# file.path(dataPath, "Rpb3_IP2_chr1.cel"))  
# names <- c("rpb3_1", "wt_1", "rpb3_2")  
# type <- c("IP", "CONTROL", "IP")  
# rpb3Chr1 <- readCelFile(bpmapChr1, cels, names, type, featureData=TRUE, log.it=TRUE)  
  
# ips <- rpb3Chr1$type == "IP"
```



```

# controls <- rpb3Chr1$type == "CONTROL"

# rpb3_rankpercentile <- normalize.Probes(rpb3Chr1, method="rankpercentile")
# description <- c("Rpb3vsWT")
# rpb3_rankpercentile_ratio <- getRatio(rpb3_rankpercentile, ips, controls, description, fkt=median, featureData=

# probeAnnoChr1 <- bmapToProbeAnno(bmapChr1)
# transcriptAnno <- read.gffAnno(file.path(dataPath, "transcriptAnno.gff"), feature="transcript")

# profile <- getProfiles(rpb3_rankpercentile_ratio, probeAnnoChr1, transcriptAnno, 500, 500, feature="transcript")
# profile_splines <- makeSplines(profile)

```

---

normalize.Probes	<i>Normalization of probes</i>
------------------	--------------------------------

---

## Description

Normalization of probe intensities with a given method.

## Usage

```
normalize.Probes(eSet, method=NULL, ratio=FALSE, ip, control, description, fkt=median, featureData=FA
```

## Arguments

eSet	An ExpressionSet, containing the logged raw intensities
method	character string specifying the normalization method to be used. Choices are "none", "scale", "quantile", "Aquantile", "Gquantile", "Rquantile", "Tquantile", "vsn", "rankpercentile", "loess", "subtract".
ratio	if TRUE, the ratios are calculated.
ip	a boolean vector, indicating which sample are IP experiments
control	a boolean vector, indicating which sample are CONTROL experiments
description	description of the normalized data
fkt	function to chose for averaging over replicates
featureData	should the featureData of eSet be passed to the new ExpressionSet?
targets	vector, factor or matrix of length twice the number of arrays, used to indicate target groups if method="Tquantile"
arrays	Subset of experiments (colnames in ExpressionSet) in the ExpressionSet, that are supposed to be normalized separately.
...	arguments, that should be passed to the normalization methods.

## Details

The procedure calls different functions from this package or from `affy` and `limma`, depending on the method.

**none** Calls `normalizeWithinArrays` with `method="none"` from package `limma`.

**scale** Calls `normalizeWithinArrays` with `method="scale"` from package `limma`.

**quantile** Calls `normalizeBetweenArrays` with `method="quantile"` from package `limma`.

**Gquantile** Calls `normalizeBetweenArrays` with `method="Gquantile"` from package `limma`.

**Rquantile** Calls `normalizeBetweenArrays` with `method="Rquantile"` from package `limma`.

**Tquantile** Calls `normalizeBetweenArrays` with `method="Tquantile"` from package `limma`.

**Rquantile** Calls `normalizeBetweenArrays` with `method="Rquantile"` from package `limma`.

**vsn** Calls `normalizeBetweenArrays` with `method="vsn"` from package `limma`.

**loess** Calls `normalize.loess` from package `affy`.

**rankpercentile** Calls `rankPercentile.normalize` from this package.

**subtract** Calls `subtract` from this package.

## Author(s)

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

## See Also

[normalizeBetweenArrays](#), [normalize.loess](#), [subtract](#), [rankPercentile.normalize](#)

## Examples

```
##
# dataPath <- system.file("extdata", package="Starr")
# bmapChr1 <- readBpmap(file.path(dataPath, "Scerevisiae_tlg_chr1.bpmap"))

# cels <- c(file.path(dataPath, "Rpb3_IP_chr1.cel"), file.path(dataPath, "wt_IP_chr1.cel"),
# file.path(dataPath, "Rpb3_IP2_chr1.cel"))
# names <- c("rpb3_1", "wt_1", "rpb3_2")
# type <- c("IP", "CONTROL", "IP")
# rpb3Chr1 <- readCelFile(bmapChr1, cels, names, type, featureData=TRUE, log.it=TRUE)

# rpb3_rankpercentile <- normalize.Probes(rpb3Chr1, method="rankpercentile")
```

---

plotBoxes	<i>boxplots of experiments</i>
-----------	--------------------------------

---

**Description**

Generates a boxplot of the of the given experiments.

**Usage**

```
plotBoxes(eSet, col=NULL)
```

**Arguments**

eSet	Either an ExpressionSet or a matrix, containing the data.
col	color, to fill the boxes

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**See Also**

[boxplot](#)

**Examples**

```
##  
mat <- matrix(rnorm(1000000), ncol=2)  
colnames(mat) <- c("Sample1", "Sample2")  
mat[,1] <- mat[,1]-2  
plotBoxes(mat)
```

---

plotcmarrt	<i>Histogram of p-values and normal QQ plots for standardized MA statistics</i>
------------	---

---

**Description**

Plot the histograms of p-values and normal QQ plots under correlation structure and independence.

**Usage**

```
plotcmarrt(cmarrt.ma, freq=FALSE)
```

**Arguments**

cmarrt.ma      output object from [cmarrt.ma](#).  
 freq          see ?hist

**Details**

Diagnostic plots for comparing the distribution of standardized MA statistics under correlation and independence.

**Value**

Histogram of p-values and normal QQ plots under correlation structure and independence.

**Note**

If the normal quantile-quantile plot deviates from the reference line for unbound probes, this indicates that Gaussian approximation is not suitable for analyzing this data.

**Author(s)**

Pei Fen Kuan, Adam Hinz

**References**

P.F. Kuan, H. Chun, S. Keles (2008). CMARRT: A tool for the analysis of ChIP-chip data from tiling arrays by incorporating the correlation structure. *Pacific Symposium of Biocomputing* **13**:515-526.

**See Also**

[cmarrt.ma,qqnorm](#)

**Examples**

```
# dataPath <- system.file("extdata", package="Starr")
# bmapChr1 <- readBpmap(file.path(dataPath, "Scerevisiae_tlg_chr1.bpmap"))

# cels <- c(file.path(dataPath, "Rpb3_IP_chr1.cel"), file.path(dataPath, "wt_IP_chr1.cel"),
# file.path(dataPath, "Rpb3_IP2_chr1.cel"))
# names <- c("rpb3_1", "wt_1", "rpb3_2")
# type <- c("IP", "CONTROL", "IP")
# rpb3Chr1 <- readCelFile(bmapChr1, cels, names, type, featureData=TRUE, log.it=TRUE)

# ips <- rpb3Chr1$type == "IP"
# controls <- rpb3Chr1$type == "CONTROL"

# rpb3_rankpercentile <- normalize.Probes(rpb3Chr1, method="rankpercentile")
# description <- c("Rpb3vsWT")
# rpb3_rankpercentile_ratio <- getRatio(rpb3_rankpercentile, ips, controls, description, fkt=median, featureData=

# probeAnnoChr1 <- bpmapToProbeAnno(bpmapChr1)
```

```
# peaks <- cmarrt.ma(rpb3_rankpercentile_ratio, probeAnnoChr1, chr=NULL, M=NULL, 250, window.opt=fixed.probe)
# plotcmarrt(peaks)
```

---

plotDensity                    *density plots of experiments*

---

### Description

Generates a plot, showing the densities of the experiments.

### Usage

```
plotDensity(eSet, oneDevice=T, main="")
```

### Arguments

eSet	an ExprsionSet or a matrix, containing the data
oneDevice	should all lines be plotted to one device?
main	head of the plot

### Author(s)

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

### See Also

[plot.default, density](#)

### Examples

```
##
mat <- matrix(rnorm(1000000), ncol=2)
colnames(mat) <- c("Sample1", "Sample2")
mat[,1] <- mat[,1]-2
plotDensity(mat)
```

---

plotGCbias                      *Visualize GC-Bias of Hybridization*

---

**Description**

Generates a plot showing the GC-bias of the hybridization.

**Usage**

```
plotGCbias(intensity, sequence, main="")
```

**Arguments**

intensity	a vector of type numeric, containing the measured intensities.
sequence	a vector of type character, containing the sequences.
main	head of the plot

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**See Also**

[boxplot](#)

**Examples**

```
##
sequence <- unlist(lapply(1:50000, function(x) {paste(sample(c("A","T","C","G"),prob=c(0.3,0.3,0.2,0.2),25,repL
values <- runif(50000,min=-2,max=2)
plotGCbias(values, sequence)
```

---

plotImage                      *Reconstruct the array image*

---

**Description**

Function to visualize spatial distribution of raw intensities on Affymetrix Oligoarrays.

**Usage**

```
plotImage(CEL)
```

**Arguments**

CEL	a character, specifying the path to the CEL file
-----	--

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**See Also**

[readCel,levelplot](#)

**Examples**

```
# dataPath <- system.file("extdata", package="Starr")
# plotImage(file.path(dataPath,"Rpb3_IP_chr1.cel"))
```

---

plotMA

*M versus A plot*

---

**Description**

A matrix of M vs. A plots of each pair (ip, control) is produced.

**Usage**

```
plotMA(eSet, ip=NULL, control=NULL, col=NULL)
```

**Arguments**

eSet	an ExpressionSet or matrix, containing the data
ip	an integer, or boolean vector, that indicates, which columns in the ExpressionSet are IP experiments
control	an integer, or boolean vector, that indicates, which columns in the ExpressionSet are CONTROL or REFERENCE experiments
col	color, to fill the boxes

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**See Also**

[ma.plot](#)

**Examples**

```
##
mat <- matrix(rnorm(1000000), ncol=4)
colnames(mat) <- c("Sample1", "Sample2", "Sample3", "Sample4")
mat[,1] <- mat[,1]^2
plotMA(mat, c(TRUE, FALSE, TRUE, FALSE), c(FALSE, TRUE, FALSE, TRUE))
```

---

plotPosBias	<i>Bias of hybridzation, depending on base position in sequence.</i>
-------------	--

---

**Description**

plotPosBias generates a plot showing the bias of hybridzation, depending on base position in sequence.

**Usage**

```
plotPosBias(intensity, sequence, main="", ylim)
```

**Arguments**

intensity	a vector of type numeric, containing the measured intensities
sequence	a vector of type character, containing the sequeeces
main	head of the plot
ylim	ylim of plot

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**Examples**

```
##  
sequence <- unlist(lapply(1:50000, function(x) {paste(sample(c("A","T","C","G"),prob=c(0.3,0.3,0.2,0.2),25,repL  
values <- runif(50000,min=-2,max=2)  
plotPosBias(values, sequence)
```

---

plotProfiles	<i>Plotting ChIP profiles of one or more clusters</i>
--------------	---

---

**Description**

plotProfiles plots the ChIP profiles of one or more clusters. Additionally on can display the distribution of e.g. gene expression in the clusters.

**Usage**

```
plotProfiles(profiles, mfcol=NULL, mfrow=NULL, ylab="intensity", xlab="position", histograms=NULL, cl
```



**Arguments**

profiles	a list constructed by the function getProfiles().
mfc01	see ?par
mfrow	see ?par
ylab	see ?par
xlab	see ?par
histograms	a list of named vectors. Density plots are created for every vector and cluster.
cluster	A named integer vector, that maps the features to the cluster.
profileplot	should a clusterplot be shown?
meanprofile	should the mean profiles of each cluster be plotted??
...	arguments, passed to plot.default

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**See Also**

[density](#), [profileplot](#)

**Examples**

```
##
samples = 100
probes = 63
clus = matrix(rnorm(probes*samples,sd=1),ncol=probes)
clus= rbind( t(t(clus)+sin(1:probes/10))+1:nrow(clus)/samples , t(t(clus)+sin(pi/2+1:probes/10))+1:nrow(clus)/samples)
clustering = kmeans(clus,3)$cluster
names(clustering) <- 1:length(clustering)

profiles <- apply(clus, 1, function(x) {list(upstream=x[1:20], region=x[21:43], downstream=x[44:63])})
names(profiles) <- 1:length(clustering)
profiles <- list(profile=profiles, upstream=20, downstream=20, borderNames=c("start", "stop"))

plotProfiles(profiles, cluster=clustering, ylim=c(-1,2.5), type="l", lwd=2)
```

---

plotRatioScatter

*Plot ratios of all possible combinations of IP and CONTROL*

---

**Description**

A matrix of pairwise scatterplots of the ratios is created. The lower panel shows the correlation of the data.

**Usage**

```
plotRatioScatter(eSet, ip, control, density=F, sample=NULL, cluster=T, cex=1)
```

**Arguments**

eSet	an ExpressionSet or matrix, containing the data
ip	an integer, or boolean vector, that indicates, which columns in the ExpressionSet are IP experiments
control	an integer, or boolean vector, that indicates, which columns in the ExpressionSet are CONTROL or REFERENCE experiments
density	if TRUE, a density scatter plot is plotted. This plot shows the density of the data.
sample	An integer, indicating the number of subsamples to take for the density scatter-plot. This is only recommended if the data is very large, as the density computation takes some time. #
cluster	if cluster=T, the experiments are clustered and similar experiments are plotted together.
cex	see ?par

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**See Also**

[pairs](#), [densityscatter](#)

**Examples**

```
##
points <- 10^4
x <- rnorm(points/2)
x <- c(x,x+2.5)
x <- sign(x)*abs(x)^1.3
y <- x + rnorm(points,sd=0.8)
z <- y*2
mat <- matrix(c(x,y,z), ncol=3)
colnames(mat) <- c("A", "B1", "B2")
plotRatioScatter(mat, c(TRUE, FALSE, FALSE), c(FALSE, TRUE, TRUE), density=TRUE)
```

---

`plotScatter`*High level scatterplot of experiments*

---

**Description**

A matrix of pairwise scatterplots is created. The lower panle shows the correlation of the data.

**Usage**

```
plotScatter(eSet, density=F, cluster=T, sample=NULL, cex=1)
```

**Arguments**

<code>eSet</code>	an ExprssionSet or matrix, containing the data
<code>density</code>	if TRUE, a density scatter plot is plotted. This plot shows the density of the data.
<code>sample</code>	An integer, indicating the number of subsamples to take for the density scatterplot. This is only recommended if the data is very large, as the density computation takes some time.
<code>cluster</code>	if <code>cluster=T</code> , the experiments are clustered and similiar experiments are plotted together.
<code>cex</code>	see <code>?par</code>

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**See Also**

[pairs](#), [densityscatter](#)

**Examples**

```
##
points <- 10^4
x <- rnorm(points/2)
x <- c(x,x+2.5)
x <- sign(x)*abs(x)^1.3
y <- x + rnorm(points,sd=0.8)
mat <- matrix(c(x,y), ncol=2)
colnames(mat) <- c("a", "b")
plotScatter(mat, density=TRUE)
```

profileplot

*Visualize clusters***Description**

Visualization of a set of “profiles” (i.e. a consecutive series of measurements like a time series, or the DNA binding levels along different positions on a gene). The profiles are given as the rows of a (samples x positions) matrix that contains the measurements. Instead of plotting a line for each profile (row of the matrix), the q-quantiles for each position (column of the matrix) are calculated, where q runs through a set of representative quantiles. Then for each q, a line of q-quantiles is plotted along the positions. Color coding of the quantile profiles aids the interpretation of the plot: There is a color gradient from the median profile to the 0 (=min) resp. 1(=max) quantile.

**Usage**

```
profileplot(cluster, label=NULL, at=NULL, main = "", xlim=NULL, xlab = "", xaxt = "s", xlabel = NULL, las
```

**Arguments**

cluster	a (samples x columns) matrix with numerical entries. Each sample row is understood as a consecutive series of measurements. Missing values are not allowed so far
label	if multiple clusters should be plotted in one diagram, the cluster labels for each item are given in this vector
at	optional vector of length ncol(cluster), default = 1:ncol(cluster). Specifies the x-values at which the positions will be plotted.
main	the title of the plot, standard graphics parameter
xlim	xlimits, standard graphics parameter
xlab	x-axis legend, standard graphics parameter
xaxt	should an x axis be plotted at all? (= "n" if not), standard graphics parameter
xlabels	character vector. If specified, this text will be added at the “at”-positions as x-axis labels.
las	direction of the xlabels text. las=1: horizontal text, las=2: vertical text
ylim	ylimits, standard graphics parameter
ylab	y-axis legend, standard graphics parameter
fromto	determines the smallest and the largest quantile that are plotted in colors, more distant values are plotted as outliers
colpal	either "red", "green", "blue" (predefined standard color palettes in profileplot), or a vector of colors to be used instead.
nrcolors	not very important. How many colors will the color palette contain? Usually, the default = 25 is sufficient
outer.col	color of the outlier lines, default = "light grey". For no outliers, choose outer.col="none"
add.quartiles	should the quartile lines be plotted (grey/black)? default=TRUE
add	should the profile plot be added to the current plot? Defaults to FALSE
separate	should each cluster, be plotted in a separate window? Defaults to TRUE

**Author(s)**

Achim Tresch, Benedikt Zacher <tresch@lmb.uni-muenchen.de>

**Examples**

```
sampls = 100
probes = 63
at = (-31:31)*14
clus = matrix(rnorm(probes*sampls,sd=1),ncol=probes)
clus= rbind( t(t(clus)+sin(1:probes/10))+1:nrow(clus)/sampls , t(t(clus)+sin(pi/2+1:probes/10))+1:nrow(clus)/sampls)
labs = paste("cluster",kmeans(clus,4)$cluster)

profileplot(clus,main="All data",fromto=c(0,1))
profileplot(clus,label=labs,main="Clustered data",colpal=c("heat","blue","red","topo"),add.quartiles=FALSE)
profileplot(clus,main="Same data, 4 clusters in one plot\n color gradient fromto = c(0.4,0.6), no outliers plotted"
colpal=c("heat","blue","red","green"),outer.col="none")
```

---

read.gffAnno

*Reading gff annotation*

---

**Description**

This functions reads the annotation from a gff file.

**Usage**

```
read.gffAnno(gffFile, feature=NULL)
```

**Arguments**

gffFile	path to file
feature	feature to select ("character"). If feature="gene", then only rows, representing this feature are read.

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**Examples**

```
##
# dataPath <- system.file("extdata", package="Starr")
# transcriptAnno <- read.gffAnno(file.path(dataPath, "transcriptAnno.gff"), feature="transcript")
```

---

readCelFile	<i>Read raw intensities from CEL files</i>
-------------	--

---

### Description

Function to read the raw intensities of the perfect match probes (PM) of Affymetrix CEL files into an ExpressionSet. This function is used to read one-color data. For two-color data use the functions from the Ringo package.

### Usage

```
readCelFile(bpmap, cel_files, names, type, experimentData=NULL, featureData=T, log.it=T, phenodata=NULL)
```

### Arguments

bpmap	Either a list, created by the function readBpmap() from the affy package, or the path to the bpmap file.
cel_files	a character vector, specifying the path to the CEL files
names	a character vector, containing the names of the experiments
type	a character vector, containing the type of experiment, e.g. "IP" for an Immunoprecipitation, or "CONTROL" for a control or reference experiment was done
experimentData	This must be an object of type MIAME, which details information about e.g., the investigator or lab where the experiment was done, an overall title, and other notes
featureData	If TRUE, a featureData object is added to the ExpressionSet, containing information about the chromosome, position in the genome and sequence of the features
log.it	If TRUE, logged intensities are read
phenodata	data.frame, containing columns name, type, CEL.

### Value

Returns raw intensity values in form of an ExpressionSet with additional information:

assayData	This object contains the measured probe intensities.
phenoData	contains further description of the experiments, such as names or type
featureData	containing information about the chromosome, position in the genome and sequence of the features
experimentData	details information about e.g., the investigator or lab where the experiment was done

### Author(s)

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**See Also**

[readCelIntensities](#), [xy2indices](#)

**Examples**

```
##
# dataPath <- system.file("extdata", package="Starr")
# bmapChr1 <- readBmap(file.path(dataPath, "Scerevisiae_tlg_chr1.bmap"))

# cels <- c(file.path(dataPath, "Rpb3_IP_chr1.cel"), file.path(dataPath, "wt_IP_chr1.cel"),
# file.path(dataPath, "Rpb3_IP2_chr1.cel"))
# names <- c("rpb3_1", "wt_1", "rpb3_2")
# type <- c("IP", "CONTROL", "IP")
# rpb3Chr1 <- readCelFile(bmapChr1, cels, names, type, featureData=TRUE, log.it=TRUE)
```

---

remap

*Remap reporter sequences to the genome and create a new bmap file*


---

**Description**

This function remaps the reporter sequences on the chip on the genome and outputs a new bmap annotation, containing only unique matches to the genome. A remapping is recommended if the bmap file was built on an outdated genome, or if sequences, that match the genome more than once should be excluded.

**Usage**

```
remap(bmap=NULL, seqs=NULL, nseq=NULL, path="", complementary=FALSE, reverse=FALSE, reverse_compleme
```

**Arguments**

bmap	A list, created by the function <code>readBmap()</code> from the <code>affy</code> package.
nseq	Number of sequences, that are searched in one iteration.
seqs	Sequences to search as a character vector
path	path to genomic fasta files
complementary	If TRUE, the sequences are searched in the complementary strand of the text
reverse	If TRUE, the sequences are searched in the reverse strand of the text
reverse_complementary	If TRUE, the sequences are searched in the reverse complementary strand of the text
return_bmap	If TRUE, the output is a list in bmap format

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

**Examples**

```
# dataPath <- system.file("extdata", package="Starr")

# bmapChr1 <- readBpmap(file.path(dataPath, "Scerevisiae_tlg_chr1.bpmap"))
# newbmap <- remap(bmapChr1, nseq=5000000, path=dataPath, reverse_complementary=TRUE, return_bmap=TRUE)
```

---

writeGFF                      *write ChIP-chip data to a gff file*

---

**Description**

This function writes the all columns of the assayData to a gff file.

**Usage**

```
writeGFF(expressionSet, probeAnno, file)
```

**Arguments**

expressionSet	an ExpressionSet object
probeAnno	a probeAnno object
file	path to write to

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

---

writePosFile                      *Creating a pos file*

---

**Description**

Writes a Nimblegen pos file from a given Affymetrix bpmap file.

**Usage**

```
writePosFile(bpmap, file)
```

**Arguments**

bpmap	Either a list, created by the function readBpmap() from the affy package. Or a path to the bpmap file.
file	a character, specifying the path to the file to be written

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>



---

writeWIG	<i>write ChIP-chip data to a *.wig file</i>
----------	---

---

**Description**

This function writes the all columns of the assayData to a wiggle file.

**Usage**

```
writeWIG(expressionSet, probeAnno, file, chr=NULL, probeLength=NULL)
```

**Arguments**

expressionSet	an ExpressionSet object
probeAnno	a probeAnno object
file	path to write to
chr	subset of chromosomes in probeAnno. If specified, only the subset is written to the file.
probeLength	length of the probes on the chip.

**Author(s)**

Benedikt Zacher <zacher@lmb.uni-muenchen.de>

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