

# Package ‘SimBindProfiles’

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**Title** Similar Binding Profiles

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## Description

SimBindProfiles identifies common and unique binding regions in genome tiling array data. This package does not rely on peak calling, but directly compares binding profiles processed on the same array platform. It implements a simple threshold approach, thus allowing retrieval of commonly and differentially bound regions between datasets as well as events of compensation and increased binding.

**Depends** R (>= 2.10), methods, Ringo

**Imports** limma, mclust, Biobase

**biocViews** Microarray, Software

**License** GPL-3

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|                         | <i>Similar Binding Profiles, identifies common and unique regions in array genome tiling array data</i> |

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**Description**

SimBindProfiles, identifies common and unique binding regions in genome tiling array data. This package does not rely on peak calling, but directly compares binding profiles processed on the same array platform. It implements a simple threshold approach, thus allowing retrieving commonly and differentially bound regions between datasets as well as events of compensation and increased binding.

**Details**

Package: SimBindProfiles  
Type: Package  
License: GPL-3

**Author(s)**

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|                     |                                                     |
|---------------------|-----------------------------------------------------|
| compensationRegions | <i>Classify two Binding Profiles - Compensation</i> |
|---------------------|-----------------------------------------------------|

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**Description**

This function is used to classify three Binding Profiles into regions which are bound in data set one and two but not three.

**Usage**

```
compensationRegions(xSet, sgrset = c(1, 2, 3), bound.cutoff, diff.cutoff,  
  probes, probe.max.spacing, writeBedFile = TRUE)
```

**Arguments**

|                   |                                                                                         |
|-------------------|-----------------------------------------------------------------------------------------|
| xSet              | object of class ExpressionSet                                                           |
| sgrset            | vector of length 3; specifying which data sets to compare from the ExpressionSet        |
| bound.cutoff      | numeric; threshold above probes are considered “bound”                                  |
| diff.cutoff       | numeric; difference threshold to determine if objects uniquely bound                    |
| probes            | integer; minimum number of probes in a valid region                                     |
| probe.max.spacing | integer; maximum number of base pairs in a gap before splitting a region into 2 regions |
| writeBedFile      | logical; should bed file be written                                                     |

**Details**

Select probes with a signal above the bound.cutoff in data set 1 and 2 and below in set 3, and for which the average signal of set 1 and set2 is above the diff.cutoff compared to set 3. These probes are then filtered into regions using the probes and probe.max.spacing details. The score is calculated as mean (probes in region average(set 1 and set 2) minus set 3). Optional bed file formatted result files are written using the chosen options in the file names.

**Value**

data.frame with the following columns:

|             |                                             |
|-------------|---------------------------------------------|
| name        | name(s) of data set to which region belongs |
| class.group | class group, in this case only 1            |
| chr         | chromosome                                  |
| start       | start position of region                    |
| end         | end position of region                      |
| score       | score of region                             |
| nProbes     | number of probes in region                  |

**Author(s)**

Bettina Fischer, Robert Stojnic

**See Also**

[pairwiseRegions](#), [threewayRegions](#), [increasedBindingRegions](#)

**Examples**

```
dataPath <- system.file("data", package="SimBindProfiles")
load(file.path(dataPath, "SGR.RData"))
transcompABC <- compensationRegions(SGR, sgrset=c(1,2,3), bound.cutoff=1.86,
                                     diff.cutoff=1.4, probes=10, probe.max.spacing=200)
```

---

|                 |                                            |
|-----------------|--------------------------------------------|
| eSetScatterPlot | <i>Scatterplot of ExpressionSet object</i> |
|-----------------|--------------------------------------------|

---

## Description

Create a smooth scatterplot with correlation

## Usage

```
eSetScatterPlot(xSet)
```

## Arguments

|      |                               |
|------|-------------------------------|
| xSet | object of class ExpressionSet |
|------|-------------------------------|

## Details

Scatterplot and correlations of all data sets in ExpressionSet object

## Value

No useful return. The function is called for its side effect to produce the scatterplot.

## Author(s)

Bettina Fischer

## See Also

[plot](#), [smoothScatter](#)

## Examples

```
dataPath <- system.file("data", package = "SimBindProfiles")
load(file.path(dataPath, "SGR.RData"))
eSetScatterPlot(SGR)
```

---

|                 |                              |
|-----------------|------------------------------|
| findBoundCutoff | <i>Find the bound.cutoff</i> |
|-----------------|------------------------------|

---

**Description**

Define the bound.cutoff using either the normalNull or the twoGaussiansNull method.

**Usage**

```
findBoundCutoff(xSet, method = c("normalNull", "twoGaussiansNull"), mean.method = "mode",  
  pvalue = FALSE, fdr = FALSE, pvalPlot = FALSE)
```

**Arguments**

|             |                                                                                                         |
|-------------|---------------------------------------------------------------------------------------------------------|
| xSet        | object of class ExpressionSet                                                                           |
| method      | a character string equal to "normalNull" or "twoGaussiansNull"                                          |
| mean.method | a character string equal to "mode" or "zero". This is used in combination with the "normalNull" method. |
| pvalue      | decimal specifying the p-value cutoff (either pvalue or fdr can be used not both!)                      |
| fdr         | decimal specifying the fdr cutoff (either pvalue or fdr can be used not both!)                          |
| pvalPlot    | logical, if TRUE the pvalue histogram is written                                                        |

**Details**

We implemented two methods to set the bound.cutoff, probes above this threshold are considered "bound". The twoGaussiansNull method established in the Ringo package (Toedling et al., 2007), by which the data is assumed to follow a mixture of two Gaussian distributions. The one Gaussian with the lower mean value is assumed to be the null distribution and probe levels are assigned p-values based on this null distribution. Alternatively the user can select the normalNull method instead which assumes the null distribution is normal and symmetrical around the mode (or zero). For both methods the user can decide if the resulting p-values are to be adjusted for multiple testing (fdr) or selected by a p-value threshold. The function also provides QC plots for the twoGaussiansNull and an optional p-value histogram.

**Value**

Returns a numeric

**Note**

Please note that the use of the package "mclust" is only free for strict academic use (see the license of "mclust" here: <http://www.stat.washington.edu/mclust/license.txt>). The alternative function normalNull does not have this restriction.

**Author(s)**

Bettina Fischer

## References

Toedling J., Skylar O., Krueger T, Fischer J.J., Sperling S., Huber W. 2007 Ringo - an R/Bioconductor package for analyzing ChIP-chip readouts. BMC Bioinformatics, 8:221

## Examples

```
dataPath <- system.file("data",package="SimBindProfiles")
load(file.path(dataPath,"SGR.RData"))
bound.cutoff <- findBoundCutoff(SGR, method="twoGaussiansNull", fdr=0.25)
```

---

increasedBindingRegions

*Classify two Binding Profiles - Increased Binding*

---

## Description

This function is used to classify two Binding Profiles into regions which are more bound in one data set than the other.

## Usage

```
increasedBindingRegions(xSet, sgrset = c(1, 2), bound.cutoff, diff.cutoff, probes,
  probe.max.spacing, writeBedFile = TRUE)
```

## Arguments

|                   |                                                                                         |
|-------------------|-----------------------------------------------------------------------------------------|
| xSet              | object of class ExpressionSet                                                           |
| sgrset            | vector of length 2; specifying which data sets to compare from the ExpressionSet        |
| bound.cutoff      | numeric; threshold above probes are considered "bound"                                  |
| diff.cutoff       | numeric; difference threshold to determine if object 1 and object 2 are uniquely bound  |
| probes            | integer; minimum number of probes in a valid region                                     |
| probe.max.spacing | integer; maximum number of base pairs in a gap before splitting a region into 2 regions |
| writeBedFile      | logical; should a bed file be written                                                   |

## Details

Probe signal values above the bound.cutoff threshold for both data sets are compared where set 1 is above the diff.cutoff of set 2. These probes are then filtered into regions using the probes and probe.max.spacing details. The score is calculated as mean (probes in region set 1 minus set 2). Optional bed file formatted result files are written using the chosen options in the file names.

**Value**

data.frame with the following columns:

|             |                                             |
|-------------|---------------------------------------------|
| name        | name(s) of data set to which region belongs |
| class.group | class group, in this case only 1            |
| chr         | chromosome                                  |
| start       | start position of region                    |
| end         | end position of region                      |
| score       | score of region                             |
| nProbes     | number of probes in region                  |

**Author(s)**

Bettina Fischer, Robert Stojnic

**See Also**

[pairwiseRegions](#), [compensationRegions](#), [threewayRegions](#), [plotBoundProbes](#)

**Examples**

```
dataPath <- system.file("data",package="SimBindProfiles")
load(file.path(dataPath,"SGR.RData"))
overcompBC <- increasedBindingRegions(SGR, sgrset=c(2,3), bound.cutoff=1.86, diff.cutoff=1.4,
  probes=10, probe.max.spacing=200)
```

---

|                 |                                      |
|-----------------|--------------------------------------|
| pairwiseRegions | <i>Classify two Binding Profiles</i> |
|-----------------|--------------------------------------|

---

**Description**

Classify two Binding Profiles into unique and common binding regions and write results to bed files.

**Usage**

```
pairwiseRegions(xSet, sgrset = c(1, 2), bound.cutoff, diff.cutoff, probes, probe.max.spacing, writeBed
```

**Arguments**

|              |                                                                                        |
|--------------|----------------------------------------------------------------------------------------|
| xSet         | object of class ExpressionSet                                                          |
| sgrset       | vector of length 2; specifying which data sets to compare from the ExpressionSet       |
| bound.cutoff | numeric; threshold above probes are considered “bound”                                 |
| diff.cutoff  | numeric; difference threshold to determine if object 1 and object 2 are uniquely bound |

|                   |                                                                                         |
|-------------------|-----------------------------------------------------------------------------------------|
| probes            | integer; minimum number of probes in a valid region                                     |
| probe.max.spacing | integer; maximum number of base pairs in a gap before splitting a region into 2 regions |
| writeBedFile      | logical; should bed file be written                                                     |

## Details

Probe signal values above the bound.cutoff in both data are classified as common bound. Probes which are above the bound.cutoff and in one data and higher than the diff.cutoff to the other data are called unique. Then these probes are then filtered into regions using the probes and probe.max.spacing details. The score for the unique regions is calculated as mean (probes in region set 1 minus set 2), or vise versa. The score for the common region is the mean (probes in region (set 1 plus set 2)/2). Optional bed file formatted result files are written using the choosen options in the file names.

## Value

data.frame with the following columns:

|             |                                                             |
|-------------|-------------------------------------------------------------|
| name        | name(s) of data set to which region belongs                 |
| class.group | class group; 1, 2 or 3 for common regions between both sets |
| chr         | chromosome                                                  |
| start       | start position of region                                    |
| end         | end position of region                                      |
| score       | score of region                                             |
| nProbes     | number of probes in region                                  |

## Author(s)

Bettina Fischer, Robert Stojnic

## See Also

[compensationRegions](#), [increasedBindingRegions](#), [threewayRegions](#)

## Examples

```
dataPath <- system.file("data",package="SimBindProfiles")
load(file.path(dataPath,"SGR.RData"))
pairAB <- pairwiseRegions(SGR, sgrset=c(1,2), bound.cutoff=1.86, diff.cutoff=1.4,
  probes=10, probe.max.spacing=200)
```



---

|                 |                                   |
|-----------------|-----------------------------------|
| plotBoundProbes | <i>Plot coloured bound probes</i> |
|-----------------|-----------------------------------|

---

**Description**

Scatterplot of bound probes in colour based on the method.

**Usage**

```
plotBoundProbes(xSet, sgrset, method=c("pairwise", "compensation", "increasedBinding"),
  bound.cutoff, diff.cutoff, cols=NULL, pcex=2)
```

**Arguments**

|              |                                                                                                      |
|--------------|------------------------------------------------------------------------------------------------------|
| xSet         | object of class ExpressionSet                                                                        |
| sgrset       | integer; specifying which data set to use from the ExpressionSet                                     |
| method       | a character string equal to "pairwise", "increasedBinding", "compensation"                           |
| bound.cutoff | numeric; threshold above probes are considered "bound"                                               |
| diff.cutoff  | numeric; difference threshold to determine if object 1 and object 2 are uniquely bound               |
| cols         | vector of colours to highlight probes, otherwise colours are set by default                          |
| pcex         | a numerical vector giving the amount by which probe symbols should be scaled relative to the default |

**Details**

Scatterplot of the bound probes in colour based on the selected method

**Value**

Coloured scatter plot

**Author(s)**

Bettina Fischer

**See Also**

[plot](#), [pairwiseRegions](#), [compensationRegions](#), [increasedBindingRegions](#)

**Examples**

```
dataPath <- system.file("data", package="SimBindProfiles")
load(file.path(dataPath, "SGR.RData"))
plotBoundProbes(SGR, sgrset=c(1,2), method="pairwise", bound.cutoff=1.86, diff.cutoff=1.4)
```

---

|                   |                                             |
|-------------------|---------------------------------------------|
| probeAnnoFromESet | <i>Build a probeAnno from ExpressionSet</i> |
|-------------------|---------------------------------------------|

---

## Description

Build a probeAnno from ExpressionSet.

## Usage

```
probeAnnoFromESet(eSet, probeLength)
```

## Arguments

|             |                                           |
|-------------|-------------------------------------------|
| eSet        | object of class ExpressionSet             |
| probeLength | integer; specifying probe length on array |

## Details

Creates a probeAnno object from ExpressionSet object. The function uses the PROBE\_ID, CHROMOSOME and POSITION information store in the ExpressionSet object.

## Value

An object of class probeAnno holding the mapping between probes and genomic positions.

## Author(s)

Bettina Fischer

## See Also

[probeAnno-class](#)

## Examples

```
dataPath <- system.file("data", package="SimBindProfiles")
load(file.path(dataPath, "SGR.RData"))
probeAnno <- probeAnnoFromESet(SGR, probeLength=50)
```

---

|                 |                                        |
|-----------------|----------------------------------------|
| probeLengthPlot | <i>Plot the probe length frequency</i> |
|-----------------|----------------------------------------|

---

**Description**

Plot the probe length frequency.

**Usage**

```
probeLengthPlot(xSet, sgrset = 1, chr = NULL, bound.cutoff, probe.max.spacing = 200, xlim.max = 25)
```

**Arguments**

|                   |                                                                                            |
|-------------------|--------------------------------------------------------------------------------------------|
| xSet              | object of class ExpressionSet                                                              |
| sgrset            | integer; specifying which data set to use from the ExpressionSet                           |
| chr               | probes from which chromosome to be used, default NULL means all probes                     |
| bound.cutoff      | numeric; threshold above probes are considered “bound”                                     |
| probe.max.spacing | integer; maximum amount of base pairs at which bound probes are condensed into one region. |
| xlim.max          | integer; maximum number of probes plotted along the x-axis                                 |

**Details**

Plot the probe length frequency per regions based on a bound.cutoff value.

**Value**

Plot of frequency of the number of probes within bound regions

**Author(s)**

Bettina Fischer

**See Also**

[plot](#)

**Examples**

```
dataPath <- system.file("data", package="SimBindProfiles")
load(file.path(dataPath, "SGR.RData"))
probeLengthPlot(SGR, sgrset=1, chr=NULL, bound.cutoff=1.2, probe.max.spacing=200, xlim.max=50)
```

---

|              |                      |
|--------------|----------------------|
| readSgrFiles | <i>Read sgr data</i> |
|--------------|----------------------|

---

## Description

Function to read sgr files into a list object, quantile normalise signal.

## Usage

```
readSgrFiles(X, dataPath = getwd(), fileExt=".txt", normalise = TRUE)
```

## Arguments

|           |                                                       |
|-----------|-------------------------------------------------------|
| X         | object of class ExpressionSet                         |
| dataPath  | path to the directory holding the data sgr data files |
| normalise | logical, should data be quantil normalised            |
| fileExt   | character specifying the filename extension           |

## Details

The function reads the data files in sgr file tab delimited format: chr, position, signal. All data sets must be from the same array platform and have the same chromosome names and positions. The data is read and then quantile normalised and stored as an ExpressionSet.

## Value

Returns normalized, transformed values as an object of class ExpressionSet

## Author(s)

Bettina Fischer

## See Also

[ExpressionSet](#)

## Examples

```
sgrfiles <- c("SoxNDam_trunc", "SoxN-DDam_trunc", "DDam_trunc")
dataPath <- system.file("extdata", package="SimBindProfiles")
readTestSGR <- readSgrFiles(X=sgrfiles, dataPath)
```

SGR

*A Sample Data object***Description**

The SGR dataset consists of three data sets stored in an ExpressionSet object. These are SoxN-Dam, SoxN-DDam and DDam with probes located on chromosome X between 1-6000000 bp. The precomputed dataset contains precomputed objects for the bound.cutoff, compR and increasedR to save time for building the vignette.

**Usage**

```
data(SGR)
data(precomputed)
```

**Format**

An ExpressionSet object, with three data sets.

**Examples**

```
data(SGR)
data(precomputed)
```

threewayRegions

*Classify three Binding Profiles***Description**

Classify three Binding Profiles into unique and common binding regions and write results to bed files.

**Usage**

```
threewayRegions(xSet, sgrset = c(1, 2, 3), bound.cutoff, diff.cutoff,
  probes, probe.max.spacing, writeBedFile=TRUE)
```

**Arguments**

|              |                                                                                  |
|--------------|----------------------------------------------------------------------------------|
| xSet         | object of class ExpressionSet                                                    |
| sgrset       | vector of length 3; specifying which data sets to compare from the ExpressionSet |
| bound.cutoff | numeric; threshold above probes are considered “bound”                           |
| diff.cutoff  | numeric; difference threshold to determine if objects are uniquely bound         |
| probes       | integer; minimum number of probes in a valid region                              |

|                   |                                                                                         |
|-------------------|-----------------------------------------------------------------------------------------|
| probe.max.spacing | integer; maximum number of base pairs in a gap before splitting a region into 2 regions |
| writeBedFile      | logical; should a bed file be written                                                   |

### Details

Signal values are flagged as bound and unbound, and then the bound probes are classified into 7 groups: class.group=1: unique probes in object 1; class.group=2: unique probes in object 2; class.group=3: unique probes in object 3; class.group=4: common probes in object 1+2; class.group=5: common probes in object 2+3; class.group=6: common probes in object 1+3; class.group=7: common probes in object 1+2+3. The classified probes are then filtered into regions using the probes and probe.max.spacing details. For scores calculations please refer to the pairwiseRegions function. Optional bed file formatted result files are written using the choosen options in the file names.

### Value

|             |                                             |
|-------------|---------------------------------------------|
| name        | name(s) of data set to which region belongs |
| class.group | class group; 1 to 7, see details above      |
| chr         | chromosome                                  |
| start       | start position of region                    |
| end         | end position of region                      |
| score       | score of region                             |
| nProbes     | number of probes in region                  |

### Author(s)

Bettina Fischer, Robert Stojnic

### See Also

[pairwiseRegions](#), [compensationRegions](#), [increasedBindingRegions](#)

### Examples

```
dataPath <- system.file("data",package="SimBindProfiles")
load(file.path(dataPath,"SGR.RData"))
threewayRegions(SGR, sgrset=c(1,2,3), bound.cutoff=1.86, diff.cutoff=1.4,
  probes=10, probe.max.spacing=200)
```

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