

# tilingArray

April 19, 2010

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`breakpointsPretend` *Accessor methods for breakpointsPretend objects - not to be called by the user.*

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## Description

Accessor methods for `breakpointsPretend` objects - not to be called by the user.

These functions are used in the interface between the `segmentation` class and the `confint.breakpointsfull` method of the `strucchange` package. This method calls `breakpoints` and `residuals` methods for its first argument, and since we pass an argument of S3 class `breakpointsPretend`, we can avoid the overhead of the corresponding methods for `breakpointsfull` objects. These functions are of no interest to the user.

## Usage

```
residuals.breakpointsPretend(object, breaks, ...)  
breakpoints.breakpointsPretend(obj, breaks, ...)
```

## Arguments

<code>object</code>	a <code>breakpointsPretend</code> object.
<code>obj</code>	a <code>breakpointsPretend</code> object.
<code>breaks</code>	dummy argument, is ignored.
<code>...</code>	further arguments.

## Value

residuals and breakpoints.

## Author(s)

W. Huber <huber@ebi.ac.uk>

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segmentation

*The class segmentation represents a segmentation result.*


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## Description

This class represents the result of a segmentation, usually a call to the function `segment`.

## Objects from the Class

Objects can be created by calls of the function `segment` or by calls of the form `new("segmentation", ...)`.

## Slots

**y:** A matrix with the data (the dependent variable(s)), see `segment`.

**x:** A numeric vector with the regressor variable. The length of this vector must be either the same as `nrow(y)`, or 0. The latter case is equivalent to `x=1:nrow(y)`.

**flag:** An integer vector, whose length must be either the same as `nrow(y)`, or 0. This can be used to *flag* certain probes for special treatment, for example by `plotAlongChrom`.

**breakpoints:** List of segmentations. The element `breakpoints[[j]]` corresponds to a segmentation fit of `j` segments, i.e. with `j-1` breakpoints. It is a matrix with `(j-1)` rows and 1 or 3 columns. It always contains a column named `estimate` with the point estimates. Optionally, it may contain columns `lower` and `upper` with the confidence intervals. The point estimates are the row indices in `y` where new segments start, for example: let `z=breakpoints[[j]]`, then the first segment is from row 1 to `z[1, "estimate"]-1`, the second from row `z[1, "estimate"]` to `z[2, "estimate"]-1`, and so on.

**logLik:** Numeric vector of the same length as `breakpoints`, containing the log-likelihood of the piecewise constant models under the data `y`.

**hasConfint:** Logical vector of the same length as `breakpoints`. TRUE if the confidence interval estimates are present, i.e. if the matrix `breakpoints[[j]]` has columns `lower` and `upper`.

**nrSegments:** A scalar integer, value must be either NA or between 1 and `length(breakpoints)`. Can be used to select one of the fits in `breakpoints` for special treatment, for example by `plotAlongChrom`.

## Methods

**confint** The method `confint(object, parm, level=0.95, het.reg=FALSE, het.err=FALSE, ...)` computes confidence intervals for the change point estimates of the segmentation. Typically, these were obtained from a previous call to the function `segment` that created the object. This is just a wrapper for the function `confint.breakpointsfull` from the `strucchange` package, which does all the hard computations. Parameters: `object` an object of class `segmentation`, `parm` an integer vector, it determines for which of the segmentation fits confidence intervals are computed. See also `segment`. The other parameters are directly passed on to `confint.breakpointsfull`.

**logLik** The method `logLik(object, penalty="none", ...)` returns the log-likelihoods of fitted models. Valid values for the argument `penalty` are `none`, `AIC` and `BIC`.

**plot** The method `plot(x, y, xlim, xlab="x", ylab="y", bpcol="black", bplty=1, pch=16, ...)` provides a simple visualization of the result of a segmentation. Parameters: `x` an object of class `segmentation`, `y` an integer between 1 and `length(x@breakpoints)`, selecting which of the fits contained in `x` to plot, `bpcol` and `bplty` color and line type of breakpoints. The plot shows the numeric data along with breakpoints and if available their confidence intervals.

**show** summary.

### Author(s)

Wolfgang Huber <huber@ebi.ac.uk>

### See Also

[segment](#)

### Examples

```
## generate random data with 5 segments:
y = unlist(lapply(c(0,3,0.5,1.5,5), function(m) rnorm(10, mean=m)))

seg = segment(y, maxseg=10, maxk=15)
seg = confint(seg, parm=c(3,4,5))

if(interactive())
  plot(seg, 5)

show(seg)
```

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comparisonPlot

*Plot a vertical layout of panels for the comparison of different along-chromosome profiles.*

---

### Description

This function is used for Figure 5 in the David et al. (PNAS 2006) paper and in the Huber et al. methods paper.

### Usage

```
comparisonPlot(x, y, xscale=range(x), yscale, anno, ticks, pch=20, cex=1, bgcol=
```

### Arguments

<code>x</code>	numeric vector.
<code>y</code>	list of numeric vector, each of same length as <code>x</code> .
<code>xscale</code>	numeric vector of length 2.
<code>yscale</code>	matrix with 2 rows and columns corresponding to the elements of <code>x</code> .
<code>anno</code>	dataframe with columns <code>start</code> , <code>end</code> , and <code>name</code> , each row corresponds to one gene CDS to be plotted at the bottom.
<code>ticks</code>	numeric vector, where to plot the ticks.

pch	A numeric or character vector indicating what sort of plotting symbol to use, see <a href="#">grid.points</a> .
cex	Multiplier applied to fontsize, see <a href="#">gpar</a> .
bgcol	Color to use as background for some of the plot panels.

**Value**

Function is called for its side-effect.

**Author(s)**

W. Huber <[huber@ebi.ac.uk](mailto:huber@ebi.ac.uk)>

**References**

...

**Examples**

```
##
```

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costMatrix

*Segmentation cost matrix*

---

**Description**

This function calculates the cost matrix for the segmentation model

**Usage**

```
costMatrix(x, maxk)
```

**Arguments**

x	Numeric vector of length n or matrix with n rows and d columns, where n is the number of sample points and d the number of replicate measurements (e.g. from multiple arrays).
maxk	Positive integer.

**Details**

See the package vignette *Calculation of the cost matrix*.

**Value**

Matrix with maxk rows and length(x) columns.

**Author(s)**

W. Huber

**Examples**

```

d = 4
x = apply(matrix(rnorm(200), ncol=d), 2, cumsum)
maxk = 50

G = costMatrix(x, maxk=maxk)

G.pedestrian = matrix(NA, nrow=nrow(G), ncol=ncol(G))
for(i in 1:(ncol(G)))
  for(k in 1:min(nrow(G), nrow(x)-i+1))
    G.pedestrian[k, i] = (k*d-1)*var(as.vector(x[i:(i+k-1), ]))

stopifnot(identical(is.na(G), is.na(G.pedestrian)))
stopifnot(max(abs(G-G.pedestrian), na.rm=TRUE) <= 1e-6)

```

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findSegments	<i>Fit a piecewise constant curve to a sequence of numbers – OBSOLETE, please use function segment instead.</i>
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**Description**

This function is only here for backward compatibility - please use [segment](#).

The function fits a piecewise constant curve to a sequence of numbers using a simple least squares cost function and the dynamic programming algorithm described by Picard et al. (see reference).

**Usage**

```
findSegments(x, maxcp, maxk, verbose=TRUE)
```

**Arguments**

x	Numeric (real) vector.
maxcp	Integer (length 1): maximum number of segments (= 1 + maximum number of change points).
maxk	Integer (length 1): maximum length of a segment.
verbose	Logical: if this parameter has a positive value, various diagnostic output is printed.

**Details**

The complexity of the algorithm is  $\text{length}(x) * \text{maxk}$  in memory and  $\text{length}(x) * \text{maxk} * \text{maxcp}$  in time.

**Value**

An object of class "segmentation" A list with elements

J	likelihood criterion
th	matrix of segment start points
dat	the data used for the segmentation

call `normalizeByReference` the function call

.

See the vignette, and the paper cited below for details.

### Note

This function is deprecated and replaced by function `segment`, but still included for backward compability.

### Author(s)

W. Huber <huber@ebi.ac.uk>, Joern Toedling <toedling@ebi.ac.uk>

### References

A statistical approach for CGH microarray data analysis. Franck Picard, Stephane Robin, Marc Lavielle, Christian Vaisse, Gilles Celeux, Jean-Jacques Daudin, Rapport de recherche No. 5139, Mars 2004, Institut National de Recherche en Informatique et en Automatique (INRIA), ISSN 0249-6399. The code of this function is based on the Matlab implementation presented at [http://www.inapg.fr/ens\\_rech/mathinfo/recherche/mathematique/outil.html](http://www.inapg.fr/ens_rech/mathinfo/recherche/mathematique/outil.html), but it has evolved.

### Examples

```
x = rep( sin((0:4)/2*pi), each=3) + rnorm(3*5, sd=0.1)
res = findSegments(x, maxcp=6, maxk=15)
```

---

normalizeByReference

*Probe-specific normalization of hybridization intensities from an oligonucleotide microarray*

---

### Description

Adjust the hybridization intensities from an oligonucleotide microarray for probe-specific response effect by using one or several reference hybridizations. If `x` contains more than one array, `vsnMatrix` from the `vsn` package is called for between array normalization.

### Usage

```
normalizeByReference(x, reference, pm, background, refSig, nrStrata=10,
  cutoffQuantile=0.05, plotFileNames, verbose=FALSE)
```

### Arguments

<code>x</code>	ExpressionSet containing the data to be normalized.
<code>reference</code>	ExpressionSet with the same number of features as <code>x</code> , containing the reference signal, on the raw scale (non-logarithmic). This argument can be used to directly input the data from a set of replicate DNA hybridizations. Alternatively, the argument <code>refSig</code> can be specified.

<code>pm</code>	Indices specifying the perfect match features in <code>reference</code> (see Details). This can be either an integer vector with values between 1 and <code>nrow(exprs(reference))</code> or a logical vector.
<code>background</code>	Indices specifying a set of background features in <code>x</code> (see Details). This can be either an integer vector with values between 1 and <code>nrow(exprs(x))</code> or a logical vector.
<code>refSig</code>	A numeric vector of the same length as <code>pm</code> with estimates of probe response effects, on a logarithm-like scale. This argument can be specified alternatively to <code>reference</code> .
<code>nrStrata</code>	Integer (length 1), number of strata for the estimation of the background function.
<code>cutoffQuantile</code>	Numeric (length 1), the probes whose reference signal is below this quantile are thrown out.
<code>plotFileNames</code>	Character vector whose length is the same as the number of arrays in <code>x</code> . Optional, if missing, no plots are produced.
<code>verbose</code>	Logical of length 1, if TRUE, some messages about progress are printed.

### Details

The intensities in `x` are adjusted according to the reference values. Typically, the reference values are obtained by hybridizing a DNA sample to the array, so that the abundance of target is the same for all reference probes, and their signal can be used to estimate the probe sequence effect. A reference probe is a probe that perfectly matches the target genome exactly once. Usually, not all probes on a chip are reference probes, hence the subset of those that are is specified by the argument `pm`.

The background signal is estimated from the probes indicated by the argument `background`. They need to be a strict subset of the `reference` probes. I.e., they need to uniquely match the target organism's DNA, but are not expected to match any of its transcripts. A robust estimation method is used, so a small fraction of `background` probes that do hit transcripts is not harmful.

A limitation of this normalization method is that it only makes sense for the data from reference probes, NA values are returned for all other probes.

The functions `PMindex` and `BGindex` can be used to produce the `pm` and `background` arguments from a `probeAnno` environment such as provided in the  `davidTiling`  package.

To summarize, a reference probe (indicated by argument `pm`) is a probe that perfectly matches the target genome exactly once, a background probe (indicated by argument `background`) is a reference probe which we expect not to be transcribed. These should not be confused with what is called 'perfect match' and 'mismatch' probes in Affymetrix annotation.

### Value

A copy of `x` with the normalized intensities.

### Author(s)

W. Huber <huber@ebi.ac.uk>

### References

Huber W, Toedling J, Steinmetz, L. Transcript mapping with high-density oligonucleotide tiling arrays. *Bioinformatics* 22, 1963-1970 (2006).

**See Also**

PMindex, BGindex

**Examples**

```
## see vignette assessNorm.Rnw in inst/scripts directory
```

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otherStrand	<i>Return the name of the opposite strand</i>
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---

**Description**

Return the name of the opposite strand

**Usage**

```
otherStrand(x)
```

**Arguments**

x                    Character vector whose elements are "+" or "-".

**Details**

This is a rather trivial convenience function.

An alternative would be to code strands with integers  $-1$  and  $+1$ , in which case the inversion would be a trivial builtin operation. However, many genomic databases and input data files use the character string / factor notation.

**Value**

Character vector of same length as x, with strands reversed.

**Author(s)**

W. Huber <huber@ebi.ac.uk>

**Examples**

```
otherStrand(c("+", "-"))
```



---

plotAlongChromLegend

*Plot a legend for genomic features*


---

## Description

Plot a legend for genomic features

## Usage

```
plotAlongChromLegend(vpr, nr=2,
  featureColorScheme=1,
  featureExclude=c("chromosome", "nucleotide_match", "insertion"),
  mainLegend, cexLegend=0.35, cexMain=1)
```

## Arguments

vpr	vector specifying where to place the legend in figure (set up by using the <code>viewport</code> function from the <code>grid</code> package. When this function is called directly by the user this argument should be left missing.
nr	numeric scalar, specifying the number of rows to plot legend over (default value is 2).
featureColorScheme	numeric scalar, used to select a color scheme for the boxes representing genomic features such as coding sequences, ncRNAs etc. Currently the only value supported is 1.
featureExclude	character vector of names of feature types (in <code>gff</code> ) that should not be plotted. Default is "chromosome", "nucleotide_match" and "insertion". Additional possible candidates include: "ARS", "repeat_region", "repeat_family" and "nc_primary_transcript".
mainLegend	character vector specifying legend title.
cexLegend	numeric scalar specifying the magnification to be used for the legend text relative to the current text size.
cexMain	numeric scalar specifying the magnification to be used for the legend title relative to the current text size.

## Details

This function is usually called by `plotAlongChrom` when `doLegend` is `TRUE`. It can also be called directly by the user to produce a separate legend.

The following features are included in the legend (unless excluded using the `featureExclude` option): "chromosome", "nucleotide\_match", "pseudogene", "uORF", "nc\_primary\_transcript", "region", "repeat\_family", "repeat\_region", "transposable\_element", "transposable\_element", "ARS", "centromere", "telomere", "insertion", "CDS", "CDS\_dubious", "ncRNA", "tRNA", "snRNA", "rRNA", "snoRNA", "binding\_site" and "TF\_binding\_site".

## Author(s)

Wolfgang Huber <huber@ebi.ac.uk>

**Examples**

```
## plotAlongChromLegend(mainLegend="Legend")
```

---

```
plotAlongChrom      Plot signals and segmentation for a region of a chromosome
```

---

**Description**

Plot signals and segmentation for a region of a chromosome

**Usage**

```
plotAlongChrom(segObj, y, probeAnno, gff,
  isDirectHybe=FALSE,
  what = c("dots"), ## "heatmap"
  chr, coord, highlight,
  colors, doLegend=FALSE,
  featureExclude=c("chromosome", "nucleotide_match", "insertion"),
  featureColorScheme=1, extras,
  rowNamesHeatmap, rowNamesExtras, ylab, ylabExtras, main,
  colHeatmap=colorRamp(brewer.pal(9, "YlGnBu")),
  colExtras=colorRamp(brewer.pal(9, "Reds")),
  sepPlots=FALSE, reOrder=TRUE, ...)
```

**Arguments**

segObj	Either an environment or an object of S4 class <code>segmentation</code> . See <i>Details</i> .
y	a numeric vector or matrix containing the signal to be plotted. See <i>Details</i> .
probeAnno	environment with probe annotations. See <i>Details</i> , and package <code>daavidTiling</code> for an example.
gff	data frame with genome annotation from the GFF file.
isDirectHybe	logical scalar: if TRUE, the mapping of probes to genomic strands is reversed with respect to the default. This is appropriate for data from a direct RNA hybridization that used no reverse transcription.
what	character scalar indicating which signal visualization to plot. Can be either <code>dots</code> to plot each probe intensity with a point, or <code>heatmap</code> to produce a color-scale representation of the intensities.
chr	integer of length 1 indicating the chromosome number to plot.
coord	integer vector of length 2 containing the start and end coordinates (in bases) for the plot.
highlight	(optional) list with two elements: a single numeric value <code>coord</code> and a character <code>strand</code> . If present, this position is marked by a vertical red bar on the coordinate axis. The color can be changed using the <code>colors</code> argument below.
colors	(optional) named character vector. If missing, a default color scheme is used: <code>c("+="#00441b", "-="#081d58", "duplicated"="grey", "cp"="#101010", "highlight"="red", "threshold"="grey")</code> , where the first three elements refer to the colors of data points and the last three to the colors of lines in the plot.

doLegend	logical: should the plot contain a legend?
featureExclude	character vector of names of feature types (in <code>gff</code> ) that should not be plotted. Default is "chromosome", "nucleotide_match" and "insertion". Additional possibilities include: "ARS", "repeat_region", "repeat_family" and "nc_primary_transcript".
featureColorScheme	numeric scalar, used to select a color scheme for the boxes representing genomic features such as coding sequences, ncRNAs etc. Currently the only value supported is 1 (see <code>plotAlongChromLegend</code> or <code>plotFeatures</code> for further information).
extras	a matrix containing additional values to be plotted along the chromosome in a separate panel (such as p-values). This option is only available when <code>y</code> is specified. These values should be on the scale [0,1].
rowNamesHeatmap	character vector of row names for the main heatmap.
rowNamesExtras	character vector of row names for the extra heatmap.
ylab	character label for y-axis of main plot.
ylabExtras	character label for y-axis on <code>extras</code> panel (if specified).
main	character: plot title.
colHeatmap	function describing color scheme for the main heatmap plot (defaults to <code>YlGnBu</code> from <code>RColorBrewer</code> package).
colExtras	function describing color scheme for the extra heatmap plot (if specified) (defaults to <code>Reds</code> from <code>RColorBrewer</code> package).
sepPlots	logical scalar. If <code>TRUE</code> , each column of intensities in <code>segObj</code> or <code>y</code> is plotted separately (maximum of 3) in the same figure. When <code>FALSE</code> , the average is plotted. This argument is only used when <code>what</code> is set to <code>dots</code> .
reOrder	logical scalar (only used when <code>sepPlots</code> is <code>TRUE</code> ). If <code>TRUE</code> , the first column of intensities is printed at the bottom of each plot, and the subsequent columns are plotted above. If <code>FALSE</code> , the first appears at the top, and the subsequent columns are plotted below.
...	further arguments that can be passed to the functions that implement the <code>what</code> option above (see <code>plotSegmentationDots</code> and <code>plotSegmentationHeatmap</code> ) or <code>gff</code> plotting (see <code>plotFeatures</code> and <code>plotAlongChromLegend</code> ).

## Details

*Intensities:* There are two alternative, mutually exclusive ways of providing the intensities that are to be plotted to this function.

1. Via the parameters `y` and `probeAnno`. In this case, `y` is a matrix of intensities, whose rows correspond to probes on the array, and its columns to different conditions, time points, etc. It is also acceptable that `y` is provided as a vector, in which case it is converted to an `nrow(y) × 1` matrix. `probeAnno` is an environment whose elements correspond to target sequences (e.g. chromosome strands) and that contain integer vectors of length `nrow(y)` with information about the probes: start and end positions of their alignment to the target sequence, their row indices in `y`, the type of alignment (is it perfect? is it unique?). For example, the start positions and indices of probes for the + strand of chromosome 1 would be described by environment elements "1.+start" and "1.+index".

2. Via the parameter `segObj`.

*segObj*: This can be either an object of S4 class `segmentation` or an environment that by convention contains a certain set of objects. Future work on this package will focus on the S4 class `segmentation`. The `environment` option is provided for backward compatibility.

*Explanation of the environment*: the intended workflow is as follows: Use the script `segment.R` (in the `inst/scripts` directory of this package) to generate segmentations. This can be run in parallel on several processors, separately for each chromosome and strand. The results of this are stored in files of the name `1.+ .rda`, `1.- .rda`, `2.+ .rda`, and so forth, typically within a dedicated directory. Then use the script `readSegments.R` to collect the R objects in these `.rda` files into the environment. It contains three types of data:

- microarray intensities in along-chromosome order.
- the segmentation objects (output of `findSegments`).
- a dataframe named `segScore` with segment scores; it can be missing iff `nrBasesPerSeg` is present,
- a numeric scalar named `theThreshold`, which is used to draw a horizontal "threshold" line in the plot.

... and the different signal visualization methods (what *option*): If `what=="dots"`, the argument `showConfidenceIntervals` can be a logical scalar to choose whether vertical dashed lines are drawn for the confidence interval. In any case, these are only drawn if they are present in the segmentation object in `segObj`.

### Author(s)

Wolfgang Huber <huber@ebi.ac.uk>

### Examples

```
## 1. see viewSegmentation.R script in the inst/scripts directory
## 2. (newer): segmentation.Rnw
```

---

plotFeatures

*Plot genomic features for a region along a chromosome*

---

### Description

Plot genomic features for a region along a chromosome

### Usage

```
plotFeatures(gff, chr, xlim, strand, vpr, featureColorScheme=1,
             featureExclude=c("chromosome", "nucleotide_match", "insertion"),
             featureNoLabel=c("uORF", "CDS"), ...)
```

**Arguments**

gff	data frame with genome annotation from the GFF file.
chr	integer of length 1 specifying the chromosome to plot the features for.
xlim	integer of length 2 with start and end coordinates (in bases) for plotting.
strand	character scalar which should be set to either + or - to indicate which strand of DNA to plot the features from.
vpr	which viewport to plot the features in.
featureColorScheme	numeric scalar, used to select a color scheme for the boxes representing genomic features such as coding sequences, ncRNAs etc. Currently the only value supported is 1.
featureExclude	character vector of names of feature types (in gff) that should not be plotted. Default is "chromosome", "nucleotide_match" and "insertion". Additional possible candidates include: "ARS", "repeat_region", "repeat_family" and "nc_primary_transcript".
featureNoLabel	character vector, names of feature types (in gff) that should not be labelled with their names (if they are plotted).
...	additional arguments.

**Details**

This function is called by `plotAlongChrom` when the `gff` argument has been specified. It should not be called directly by the user.

**Author(s)**

Wolfgang Huber <huber@ebi.ac.uk>

---

plotPenLL

*Plot the log-likelihood and penalized log-likelihoods (AIC, BIC)*

---

**Description**

Plot the log-likelihood and two versions of penalized log-likelihoods (AIC, BIC) for a segmentation object.

**Usage**

```
plotPenLL(seg, extrabar=numeric(0), type="b", lty=1, pch=16, lwd=2, ...)
```

**Arguments**

seg	A <a href="#">segmentation</a> object.
extrabar	In addition to the location of maximal BIC, vertical bars are drawn at these x-positions as well.
type, pch, lty, lwd, ...	Get passed on to <a href="#">matplot</a> .

**Details**

This function is used in the vignette: *How to use the segment function to fit a piecewise constant curve.*

**Value**

The function is called for its side effect, which is creating a plot in the current graphics device.

**Author(s)**

Wolfgang Huber <huber@ebi.ac.uk>

**Examples**

```
x = rep( sin((0:4)/2*pi), each=3) + rnorm(3*5, sd=0.1)
res = segment(x, maxseg=8, maxk=15)
plotPenLL(res)
```

---

```
plotSegmentationDots
```

*Plot points for a region along a chromosome*

---

**Description**

Plot points for a region along a chromosome

**Usage**

```
plotSegmentationDots(dat, xlim, ylim, ylab, threshold=NA,
                     chr=1, strand="+", vpr, colors, main,
                     pointSize=unit(0.6, "mm"), showConfidenceIntervals=TRUE,
                     sepPlots=FALSE, cexAxisLabel=1, cexAxis=1,...)
```

**Arguments**

dat	list containing data to be plotted (see <i>Details</i> section below for particulars).
xlim	integer vector of length 2 with start and end coordinates (in bases) for plotting.
ylim	numeric vector containing the y limits of the plot.
ylab	character scalar (if sepPlots=FALSE) or vector containing y-axis label(s).
threshold	numeric scalar indicating the threshold of expression (default value is NA, for no threshold. If a value is supplied, it is subtracted from the intensity measures in dat\$y).
chr	integer of length 1 indicating the chromosome to be plot (defaults to 1).
strand	character scalar which should be set to either + or - to indicate which strand of DNA to plot the intensity values from (defaults to "+").
vpr	which viewport to plot the figure in. If this function is called directly by the user this argument should be left missing.

<code>colors</code>	named character vector, optional. If missing, a default color scheme is used: <code>c("+="#00441b", "-="#081d58", "duplicated"="grey", "cp"="#101010", "highlight"="red", "threshold"="grey")</code> , where the first three elements refer to the colors of data points and the last three to the colors of lines in the plot.
<code>main</code>	character vector specifying plot title.
<code>pointSize</code>	an object of class <code>unit</code> which specifies the size of each point. Default value is <code>unit(0.6, "mm")</code> .
<code>showConfidenceIntervals</code>	logical scalar indicating whether confidence intervals for each change-point are to be plotted (only available once segmentation has occurred).
<code>sepPlots</code>	logical scalar indicating whether the intensities are plotted separately for each array (if <code>dat\$y</code> has multiple columns). Defaults to <code>FALSE</code> , in which case the average intensity for each probe is plotted. When <code>TRUE</code> , up to 3 arrays can be plotted separately (more than 3 gets crowded).
<code>cexAxisLabel</code>	numeric scalar specifying the magnification to be used for the y-axis label relative to the current test size.
<code>cexAxis</code>	numeric scalar specifying the magnification to be used for the y-axis annotation relative to the current text size.
<code>...</code>	additional arguments.

### Details

This function is called by `plotAlongChrom` when the argument `what` is set to `dots`. Although this function can be called directly by the user, this is not recommended.

The `dat` list contains the following items: items `x`: x-coordinates (in bases) along chromosome,

1. `y`: intensity matrix of probes along chromosome,
2. `flag`: indicates probe uniqueness in the genome. Possibilities are 3: multiple perfect matches, 2: has no PM but one or more near-matches, 1: has exactly one PM and some near-matches in the genome, 0: has exactly one PM and no near-matches.
3. `extras`: (optional) matrix of additional values (such as test-statistics/p-values) to be plotted.

### Author(s)

Wolfgang Huber <huber@ebi.ac.uk>

---

`plotSegmentationHeatmap`

*Plot a heatmap diagram for a region along a chromosome*

---

### Description

Plot a heatmap diagram for a region along a chromosome

**Usage**

```
plotSegmentationHeatmap(dat, xlim, ylab, rowNames,
                        chr=1, strand="+", vpr, colors,
                        colHeatmap=colorRamp(brewer.pal(9, "YlGnBu")),
                        showConfidenceIntervals=TRUE,
                        just=c("left", "centre"),
                        main, ...)
```

**Arguments**

<code>dat</code>	list containing data to be plotted (see <i>Details</i> section below for particulars).
<code>xlim</code>	integer vector of length 2 with start and end coordinates (in bases) for plotting.
<code>ylab</code>	character scalar specifying y-axis label.
<code>rowNames</code>	character vector specifying a name for each row in the heatmap plot.
<code>chr</code>	integer of length 1 indicating the chromosome to plot (defaults to 1).
<code>strand</code>	character scalar which should be set to either + or - to indicate which strand of DNA to plot the intensity values from (defaults to "+").
<code>vpr</code>	which viewport to plot the figure in. If this function is called directly by the user this argument should be left missing.
<code>colors</code>	named character vector, optional. If missing, a default color scheme is used: <code>c("+="#00441b", "-="#081d58", "duplicated"="grey", "cp"="#101010", "highlight"="red", "threshold"="grey")</code> , where the first three elements refer to colors of data points and the last three to those of lines in the plot.
<code>colHeatmap</code>	function describing color scheme for the heatmap plot (defaults to YlGnBu from RColorBrewer package).
<code>showConfidenceIntervals</code>	logical scalar indicating whether confidence intervals for each change-point are to be plotted (only available once segmentation has occurred).
<code>just</code>	character vector specifying the justification of the supplied values to the given coordinates; setting the first entry to "left" indicates that the supplied x-coordinates are the start positions of the probes, change this to "centre" if the x-coordinates are the probe middle positions. Usually the second entry should be "centre" (see <a href="#">grid.rect</a> )
<code>main</code>	character vector specifying plot title.
<code>...</code>	additional arguments.

**Details**

This function is called by `plotAlongChrom` if the argument `what` is set to `heatmap`. Although this function can be called directly by the user, this is not recommended. The `dat` list contains the following items:

- `x` x-coordinates (in bases) along chromosome
- `y` intensity matrix of probes along chromosome
- `flag` indicates probe uniqueness in the genome. Possibilities are 3: multiple perfect matches, 2: has no PM but one or more near-matches, 1: has exactly one PM and some near-matches in the genome, 0: has exactly one PM and no near-matches.
- `extras` (optional) matrix of additional values (such as test-statistics/p-values) to be plotted



**Author(s)**

Wolfgang Huber <huber@ebi.ac.uk>

---

PMindex

*Find the index of the exact match (PM) or background probes from a probeAnno environment*

---

**Description**

Find the index of the exact match (PM) or background probes from a probeAnno environment

**Usage**

```
PMindex(probeAnno)
BGindex(probeAnno)
```

**Arguments**

probeAnno environment with probe annotations. See package davidTiling for an example (?probeAnno).

**Details**

These functions extract the exact match probes (PM) or background probes (from intergenic regions outside of known annotations) indices from probeAnno. These indices can be used to select the relevant rows of intensity data from the ExpressionSet object for plotting and normalization.

**Value**

Numeric vector of indices.

**Author(s)**

Matt Ritchie <ritchie@ebi.ac.uk>

**Examples**

```
## library(davidTiling)
## data(davidTiling)
## data(probeAnno)
## pmind <- PMindex(probeAnno)
## mmind <- MMindex(probeAnno)
## bgind <- BGindex(probeAnno)
## boxplot(as.data.frame(log2(exprs(davidTiling))[pmind,]), outline=FALSE)
```

---

`posMin`*Find the smallest positive number in a vector*

---

**Description**

Find the smallest positive number in a vector

**Usage**

```
posMin(x, ...)
```

**Arguments**

`x`                    Numeric vector.  
`...`                Further arguments that get passed on to `min`.

**Details**

This is a rather trivial convenience function.

**Value**

Numeric of length 1.

**Author(s)**

W. Huber <huber@ebi.ac.uk>

**Examples**

```
x = runif(5)
posMin(x-0.5)
posMin(x-2)
```

---

`qcPlots`*Generate simple diagnostic plots for Affymetrix tiling array data*

---

**Description**

Generate simple diagnostic plots for Affymetrix tiling array data

**Usage**

```
qcPlots(x, html=TRUE, plotdir=NULL, probeAnno, gff,
        chr=4, coord=c(230000,245000),
        nr = 2560, nc = 2560,
        ylimchrom=c(5,16), nucleicAcid, pminindex, pgm=TRUE,
        ext=".cel", ranks=FALSE, ...)
```

**Arguments**

<code>x</code>	ExpressionSet containing the data to be plotted.
<code>html</code>	logical scalar. If <code>TRUE</code> an html summary page 'qcsummary.htm' is generated. If <code>FALSE</code> , no summary page is generated.
<code>plotdir</code>	optional character string specifying the filepath where the plots will be saved. Defaults to current working directory.
<code>probeAnno</code>	environment with probe annotations. See package <code>daavidTiling</code> for an example ( <code>?probeAnno</code> ).
<code>gff</code>	data frame with genome annotation from the GFF file.
<code>chr</code>	integer of length 1 indicating the chromosome number to plot.
<code>coord</code>	integer vector of length 2 containing the start and end coordinates (in bases) for the along chromosome intensity plot.
<code>nr</code>	integer, indicating the number of probes in each row on the array (2560 for yeast tiling arrays).
<code>nc</code>	integer, indicating the number of probes in each column on the array (2560 for yeast tiling arrays).
<code>ylimchrom</code>	numeric vector containing the y limits of the along chromosome intensity plot.
<code>nucleicAcid</code>	character vector or factor indicating what sample has been hybridised to each array. Used to color the boxplots and smoothed histograms of intensities.
<code>pmindex</code>	integer vector of indices of PM probes in <code>x</code> . If missing, this information is extracted from <code>probeAnno</code> .
<code>pgm</code>	logical scalar. If <code>TRUE</code> , image plots will be saved as .pgm files. Otherwise ( <code>FALSE</code> ), they are converted to jpegs. On windows machines, this argument should be set to <code>TRUE</code> .
<code>ext</code>	character string indicating the file extension.
<code>ranks</code>	logical scalar. If <code>TRUE</code> , imageplots will show ranks of standardised probe intensities. Otherwise ( <code>FALSE</code> , default), the standardised probe intensities are plotted.
<code>...</code>	further arguments that can be passed to the plotting function <code>plotSegmentationDots</code> .

**Details**

This function creates boxplots, smoothed histogram (density) plots, imageplots and along chromosome plots of the raw (log base 2) probe intensity data.

An html page called 'qcsummary.htm' which displays the results, is created when `html=TRUE`.

Imageplots of standardised intensities (i.e. (probe intensity - minimum probe intensity) divided by the difference between the maximum and minimum probe intensities, all on log base 2 scale) or the ranks of these standardised intensities are plotted depending on the `ranks` argument.

The individual plots are named by replacing the file extension (specified by `ext`) of each 'celfile.ext', with 'density.png' for smoothed histogram plots, 'gencoord.jpg', for along chromosome plots and either 'log.pgm' ('log.jpg' if `pgm=FALSE`) or 'rank.pgm' ('rank.jpg' if `pgm=FALSE`) for the imageplots, depending on the `ranks` argument.

**Author(s)**

Matt Ritchie <ritchie@ebi.ac.uk> and Wolfgang Huber <huber@ebi.ac.uk>

**Examples**

```
## library(davidTiling)
## data(davidTiling)
## data(probeAnno)
## qcPlots(davidTiling, probeAnno)
```

---

readCel2eSet	<i>Read celfiles into an ExpressionSet object.</i>
--------------	--

---

**Description**

This is a wrapper for [ReadAffy](#) that returns an [ExpressionSet](#) object rather than an Affy-Batch. This is particularly usefiles for arrays for which we have or need no CDF environment.

**Usage**

```
readCel2eSet(filename, adf, path=".", rotated=FALSE, ...)
```

**Arguments**

filename	Character vector with CEL file names. Either filename or adf need to be specified, but not both.
adf	Object of class <a href="#">AnnotatedDataFrame</a> .
path	Character scalar with path to CEL files.
rotated	Logical scalar, see details.
...	Further arguments that are passed on to <code>new("ExpressionSet")</code> .

**Details**

The `rotate` options allows to deal with different versions of the scanner software. Older versions rotated the image by 90 degrees, newer ones do not. Use the default `rotated=FALSE` for CEL files produced by the newer version.

**Value**

[ExpressionSet](#) object.

**Author(s)**

W. Huber

**Examples**

```
## To test the rotation, look at the scatterplot between two DNA hybes
## that were measured with scanner software that rotated (041120) and did
## not rotate (060125)
##
## cp /ebi/research/huber/Projects/tilingArray/Celfiles/041120_S96genDNA_re-hybe.cel.gz ~
## cp /ebi/research/huber/Projects/allelicTranscription/celfiles_allelictrans/060125_S96_
## cd ~/p/tmp
```

```
## gunzip 041120_S96genDNA_re-hybe.cel.gz
## unzip 060125_S96_genomicDNA.zip
##
## Not run:
library("affy")
options(error=recover)

e1 = readCel2eSet("041120_S96genDNA_re-hybe.cel", rotated=TRUE)
e2 = readCel2eSet("060125_S96_genomicDNA.CEL")

smoothScatter(log(exprs(e1)), log(exprs(e2)), nrpoints=0)

## End(Not run)
```

---

sampleStep

*Sampling of ascending numbers to ensure minimal spacing.*

---

### Description

Given a vector of ascending numbers and a step width, sample the numbers such that the difference between consecutive numbers is greater than or equal to `step`.

### Usage

```
sampleStep(x, step)
```

### Arguments

<code>x</code>	Numeric or integer vector.
<code>step</code>	Numeric scalar.

### Details

The simple algorithm works greedily from `x[1]` to `x[length(x)]`. First, `x[1]` is selected. Then, if `x[i]` is selected, all numbers `x[j]` with `j>i` and `x[j]-x[i]<step` are dropped. Then, `i` is set to the smallest `j` with `x[j]-x[i]>=step`.

### Value

A logical vector of the same length as `x`, representing the selected subsample.

### Author(s)

W. Huber <huber@ebi.ac.uk>

### Examples

```
x = sort(as.integer(runif(20)*100))
sel = sampleStep(x, step=10)
x
x[sel]
```

---

segChrom	<i>Fit a piecewise constant curve to along chromosome data (wrapper function)</i>
----------	---

---

### Description

Wrapper around the `segment` function for each strand of one or more chromosomes specified by the user. It does some typical preprocessing and I/O.

### Usage

```
segChrom(y, probeAnno, chr=1:17, strands=c("+", "-"),
         nrBasesPerSegment = 1500, maxk = 3000, step = 7, confint = FALSE,
         confintLevel = 0.95, useLocks=TRUE, verbose=TRUE, savedir)
```

### Arguments

<code>y</code>	ExpressionSet or matrix containing the data to be segmented.
<code>probeAnno</code>	an object of class <code>probeAnno</code> (defined in the <code>Ringo</code> package) or an environment with probe annotations. For the latter, see the package <code>davidTiling</code> for an example ( <code>?probeAnno</code> ).
<code>chr</code>	integer scalar or vector specifying which chromosome(s) to segment.
<code>strands</code>	character scalar or vector specifying which strands to segment; can also be NA.
<code>nrBasesPerSegment</code>	integer (length 1): the parameter <code>maxseg</code> of the <code>segment</code> function is calculated as the length of the chromosome divided by <code>nrBasesPerSegment</code> . Thus, it determines the average segment length in the finest segmentation.
<code>maxk</code>	passed on to the function <code>segment</code> .
<code>step</code>	integer scalar, indicating the minimum distance between consecutive probes. In cases when probes are offset by less than <code>step</code> bases, the probes are sampled to achieve the desired spacing.
<code>confint</code>	logical scalar. If TRUE, confidence intervals for each change-point are calculated.
<code>confintLevel</code>	numeric scalar between 0 and 1 indicating the probability level for the confidence intervals that are calculated for each change-point.
<code>useLocks</code>	logical scalar. Should a file locking mechanism be used that allows for a simple-minded parallelization of this function.
<code>verbose</code>	logical scalar. Should we be chatty about our progress?
<code>savedir</code>	character scalar. If specified, resulting <code>segmentation</code> objects are saved (with <code>save</code> ) to this directory.

### Details

This function is a wrapper for the `segment` function. It is provided in this package for illustration. For applications to different datasets, you will likely need to adapt it to some extent, please refer to its source code.

**Value**

An environment containing S4 objects of class "segmentation" called "1.+", "1.-", etc. (depending on the values in `chr` and `strands`), where "+" and "-" indicate the strand and the preceding number refers to the chromosome. If `savedir` is specified, there is also the side-effect that a series of files "1.+rda", "1.-rda", etc. is saved in that directory.

**Author(s)**

Wolfgang Huber <whuber@embl.de>

**Examples**

```
## Not run:
  library("davidTiling")
  data("davidTiling")
  data("probeAnno")
  isDNA = seq(1:3)
  yn = normalizeByReference(davidTiling[,-isDNA], davidTiling[,isDNA], probeAnno=probeAnno)
  seg = segChrom(yn, probeAnno) ## this will take a while to run!

## End(Not run)
```

---

segment	<i>Fit a piecewise constant curve: segmentation by dynamic programming</i>
---------	--

---

**Description**

The function fits a piecewise constant curve to one or multiple sequences of measurements, using a least squares cost function and an O(n) dynamic programming algorithm (see references).

**Usage**

```
segment(y, maxseg, maxk)
```

**Arguments**

<code>y</code>	Numeric matrix. Rows correspond to the <code>x</code> -variable, columns to replicate measurements at the same value of <code>x</code> . Breakpoints are fitted along the <code>x</code> -axis. For example, the <code>x</code> -variable can be genomic coordinates or time. The segmentation will be along the rows of <code>y</code> .
<code>maxseg</code>	integer of length 1, maximum number of segments (= 1 + maximum number of change points).
<code>maxk</code>	integer of length 1, maximum length of a single segment.

**Details**

The complexity of the algorithm is  $\text{length}(x) * \text{maxk}$  in memory and  $\text{length}(x) * \text{maxk} * \text{maxseg}$  in time.

**Value**

An object of class `segmentation`.

**Author(s)**

W. Huber <huber@ebi.ac.uk>

**References**

- [1] Transcript mapping with high-density oligonucleotide tiling arrays. Huber W, Toedling J, Steinmetz, L. *Bioinformatics* 22, 1963-1970 (2006).
- [2] A statistical approach for CGH microarray data analysis. Franck Picard, Stephane Robin, Marc Lavielle, Christian Vaisse, Gilles Celeux, Jean-Jacques Daudin. *BMC Bioinformatics*. 2005 Feb 11; 6:27.

**Examples**

```
x = rep( sin((0:4)/2*pi), each=3) + rnorm(3*5, sd=0.1)
res = segment(x, maxseg=6, maxk=15)
```

---

tilingArray-package

*tilingArray package overview*

---

**Description**

tilingArray package overview

**Details**

The package provides some functionalities that can be useful for the analysis of high-density tiling microarray data (such as Affymetrix genechips) for measuring transcript abundance and architecture. The main functionalities of the package are:

- The `segmentation` class for representing partitionings of a linear series of data (such as microarray intensity readings along a chromosome strand).
- The function `segment` for fitting piecewise constant models using a dynamic programming algorithm that is both fast and exact, and `confint` for calculating confidence intervals using the `strucchange` package. Please see the vignette *Segmentation demo* in the file `inst/doc/segmentation.pdf` (source file `inst/scripts/segmentation.Rnw`).
- The function `plotAlongChrom` for generating pretty plots of segmentations along with genomic features. Please also see the vignette *Segmentation demo*.
- The function `normalizeByReference` for probe-sequence dependent response adjustment from a (set of) reference hybridizations. Please see the vignette *Assessing signal/noise ratio before and after normalization* in the file `inst/doc/assessNorm.pdf` (source file `inst/scripts/assessNorm.Rnw`).

**Author(s)**

W. Huber <huber@ebi.ac.uk>



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