

# Package ‘GeneBreak’

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**License** GPL-2

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---

accessOptions,CopyNumberBreakPoints-method

*Access Object Data. This method lists possible functions to access the data of the object.*

---

## Description

Access Object Data. This method lists possible functions to access the data of the object.

## Usage

```
## S4 method for signature 'CopyNumberBreakPoints'
accessOptions(object)
```

## Arguments

object            An object of class CopyNumberBreakPoints or CopyNumberBreakPointGenes

## Value

prints text to screen

## Examples

```
data( copynumber.data.chr20 )
bp <- getBreakpoints( copynumber.data.chr20 )

accessOptions( bp )
```

---

addGeneAnnotation,CopyNumberBreakPoints-method  
*addGeneAnnotation*

---

## Description

Maps features to gene locations.

## Usage

```
## S4 method for signature 'CopyNumberBreakPoints'
addGeneAnnotation(object, geneAnnotation)
```

## Arguments

**object** An object of class [CopyNumberBreakPoints](#)

**geneAnnotation** An object of class GRanges or dataframe with at least four columns ("Gene", "Chromosome", "Start", "End")

## Details

The end of the first feature after gene start location up to and including the first feature after gene end location will be defined as gene-associated features. For hg18, hg19 and hg38 built-in gene annotation files obtained from ensembl can be used. Please take care to use a matching reference genome for your breakpoint data. In stead of using the built-in gene annotation files, feature-to-gene mapping can be based on an user-defined annotation file. The dataframe should contain at least these four columns: "Gene", "Chromosome", "Start" and "End".

## Value

Returns an object of class [CopyNumberBreakPointGenes](#) with gene annotation added.

## Examples

```
data( copynumber.data.chr20 )
data( ens.gene.ann.hg18 )

## other built-in gene annotations are:
# data( ens.gene.ann.hg19 )
# data( ens.gene.ann.hg38 )

bp <- getBreakpoints( copynumber.data.chr20 )
```

```

bp <- bpFilter( bp )
# input copynumber.data.chr20 is hg18 based
bp <- addGeneAnnotation( bp, ens.gene.ann.hg18 )

## options to inspect the data
bp
accessOptions( bp )

```

---

*bpFilter, CopyNumberBreakPoints-method*  
*bpFilter*

---

### Description

Selects breakpoints by filter criteria options.

### Usage

```

## S4 method for signature 'CopyNumberBreakPoints'
bpFilter(object, filter = "CNA-ass",
         threshold = NULL)

```

### Arguments

object	An object of class <a href="#">CopyNumberBreakPoints</a>
filter	Type of filter. This can be either "CNA-ass", "deltaSeg" or "deltaCall". <ul style="list-style-type: none"> <li>• CNA-ass: filter out breakpoints that are flanked by copy number neutral segments to obtain CNA-associated breakpoint locations</li> <li>• deltaSeg: selects for breakpoints where the log<sub>2</sub> ratio transition of the copy number segments exceeds the user-defined threshold</li> <li>• deltaCall: selects only breakpoints of discrete copy number states (amplification, gain, neutral, loss)</li> </ul>
threshold	Set the minimal log <sub>2</sub> ratio difference between segments. This parameter is required for the "deltaSeg" filter option

### Details

Filter options "CNA-ass" and "deltaCall" require calls in addition to segmented copynumber data (see input for `getBreakpoints()` )

### Value

Returns an object of class [CopyNumberBreakPoints](#) with breakpoint matrix replaced by filtered breakpoints.

**Examples**

```
data( copynumber.data.chr20 )
bp <- getBreakpoints( copynumber.data.chr20 )
bp <- bpFilter( bp, filter = "CNA-ass" )
bp <- bpFilter( bp, filter = "deltaSeg", threshold = 0.2 )

## options to inspect the data
bp
accessOptions( bp )
```

---

*bpGenes, CopyNumberBreakPointGenes-method*  
*bpGenes*

---

**Description**

Identifies genes affected by breakpoint locations.

**Usage**

```
## S4 method for signature 'CopyNumberBreakPointGenes'
bpGenes(object)
```

**Arguments**

object            An object of class [CopyNumberBreakPointGenes](#)

**Details**

This step requires feature-to-gene annotations added to the input object (see [?addGeneAnnotation](#)).

**Value**

Returns an object of class [CopyNumberBreakPointGenes](#) with gene-breakpoint information

**Examples**

```
data( copynumber.data.chr20 )
data( ens.gene.ann.hg18 )

bp <- getBreakpoints( copynumber.data.chr20 )
bp <- bpFilter( bp )
bp <- addGeneAnnotation( bp, ens.gene.ann.hg18 )
bp <- bpGenes( bp )

## options to inspect the data
bp
accessOptions( bp )
```

---

bpPlot, CopyNumberBreakPoints-method

*bpPlot*

---

## Description

Plots breakpoint frequencies per chromosome

## Usage

```
## S4 method for signature 'CopyNumberBreakPoints'  
bpPlot(object, plot.chr = NULL,  
        plot.ylim = 15, fdr.threshold = 0.1, add.jitter = FALSE)
```

## Arguments

object	An object of class <a href="#">CopyNumberBreakPoints</a> or <a href="#">CopyNumberBreakPointGenes</a>
plot.chr	A vector with chromosome(s) to plot. All chromosomes will be plotted when NULL is used.
plot.ylim	An integer giving the max y coordinate.
fdr.threshold	The FDR threshold to label recurrent breakpoint genes with their gene name
add.jitter	Logical. If TRUE, function jitter will be used for the y position of gene labels

## Details

The plot includes breakpoint locations and breakpoint gene frequencies. Genes that are recurrently affected are labeled with their gene name.

## Value

calls plot function

## Examples

```
data( copynumber.data.chr20 )  
data( ens.gene.ann.hg18 )  
bp <- getBreakpoints( copynumber.data.chr20 )  
bp <- bpFilter( bp )  
bp <- addGeneAnnotation( bp, ens.gene.ann.hg18 )  
bp <- bpGenes( bp )  
bp <- bpStats( bp )  
  
bpPlot( bp, c(20) )
```

---

bpStats,CopyNumberBreakPoints-method  
*bpStats*

---

### Description

Applies cohort-based statistics to identify genes and/or chromosomal locations that are recurrently affected by breakpoints.

### Usage

```
## S4 method for signature 'CopyNumberBreakPoints'  
bpStats(object, level = "gene",  
        method = "BH", fdr.threshold = 1)
```

### Arguments

object	An object of class <a href="#">CopyNumberBreakPointGenes</a>
level	The level at which to operate, this can be either "gene" (correcting for gene length) or "feature" (per probe/bin)
method	The FDR correction method to apply. This can be "BH" (applies Benjamini-Hochberg-type FDR correction) or "Gilbert" (for dedicated Benjamini-Hochberg-type FDR correction)
fdr.threshold	The threshold for FDR correction

### Details

The statistical method on gene-level corrects for covariates that may influence the probability to be a breakpoint gene including number of breakpoints in a profile, number of gene-associated features and gene length by gene-associated feature coverage. The statistical analysis includes multiple testing where standard Benjamini-Hochberg-type FDR correction will be performed by default. This less computational intensive method assumes a similar null-distribution for all candidate breakpoint events and satisfies for analysis on breakpoint location-level. For statistics on gene-level however, we recommend to apply the more comprehensive and powerful dedicated Benjamini-Hochberg-type FDR correction that accounts for discreteness in null-distribution (Gilbert, 2005) following correction for covariates that may influence the probability to be a breakpoint gene including number of breakpoints in a profile, number of gene-associated features and gene length by gene-associated feature coverage.

### Value

Returns an object of class [CopyNumberBreakPointGenes](#) with cohort based statistics added.

### References

Gilbert,P.B. (2005) A modified false discovery rate multiple-comparisons procedure for discrete data, applied to human immunodeficiency virus genetics. *Journal of the Royal Statistical Society Series C-Applied Statistics*, 54, 143-158.

### Examples

```
data( copynumber.data.chr20 )
data( ens.gene.ann.hg18 )
bp <- getBreakpoints( copynumber.data.chr20 )
bp <- bpFilter( bp )
bp <- addGeneAnnotation( bp, ens.gene.ann.hg18 )
bp <- bpGenes( bp )
bp <- bpStats( bp )

## options to inspect the data
bp
accessOptions( bp )
```

---

breakpointData,CopyNumberBreakPoints-method

*Access Object breakpointData. This method returns a dataframe with breakpoint values per feature.*

---

### Description

Access Object breakpointData. This method returns a dataframe with breakpoint values per feature.

### Usage

```
## S4 method for signature 'CopyNumberBreakPoints'
breakpointData(object)
```

### Arguments

object            An object of class CopyNumberBreakPoints

### Value

a dataframe with breakpoint values

### Examples

```
data( copynumber.data.chr20 )
bp <- getBreakpoints( copynumber.data.chr20 )

breakpointData( bp )
```

---

breakpointsPerGene,CopyNumberBreakPointGenes-method

*Access Object breakpointsPerGene. This method returns a dataframe with breakpoints per gene.*

---

### Description

Access Object breakpointsPerGene. This method returns a dataframe with breakpoints per gene.

### Usage

```
## S4 method for signature 'CopyNumberBreakPointGenes'  
breakpointsPerGene(object)
```

### Arguments

object            An object of class CopyNumberBreakPoints

### Value

a dataframe with breakpoints per gene

### Examples

```
data( copynumber.data.chr20 )  
data( ens.gene.ann.hg18 )  
bp <- getBreakpoints( copynumber.data.chr20 )  
bp <- bpFilter( bp )  
bp <- addGeneAnnotation( bp, ens.gene.ann.hg18 )  
bp <- bpGenes( bp )  
  
breakpointsPerGene( bp )
```

---

callData,CopyNumberBreakPoints-method

*Access Object callData. This method returns a dataframe with feature call values.*

---

### Description

Access Object callData. This method returns a dataframe with feature call values.

### Usage

```
## S4 method for signature 'CopyNumberBreakPoints'  
callData(object)
```

**Arguments**

object            An object of class CopyNumberBreakPoints

**Value**

a dataframe with feature call values

**Examples**

```
data( copynumber.data.chr20 )  
bp <- getBreakpoints( copynumber.data.chr20 )  
  
callData( bp )
```

---

copynumber.data.chr18 *CGHcall Example copynumber data hg18 chr18*

---

**Description**

A test dataset containing copynumber data of chromosome 18 for the GeneBreak package (hg18 based). This copy number aberration (CNA) data was obtained by analysis of 200 array-CGH (Agilent 180k) samples from advanced colorectal cancers.

**Usage**

```
data( copynumber.data.chr18 )
```

**Format**

An object of class cghCall

**Value**

An object of class cghCall

---

copynumber.data.chr20 *CGHcall Example copynumber data hg18 chr20*

---

**Description**

A test dataset containing chromosome 20 copynumber data for the GeneBreak package (hg18 based). This copy number aberration (CNA) data was obtained by analysis of 200 array-CGH (Agilent 180k) samples from advanced colorectal cancers.

**Usage**

```
data( copynumber.data.chr20 )
```

**Format**

An object of class cghCall

**Value**

An object of class cghCall

---

copynumber.data.chr21 *CGHcall Example copynumber data hg18 chr21*

---

**Description**

A test dataset containing chromosome 21 copynumber data for the GeneBreak package (hg18 based). This copy number aberration (CNA) data was obtained by analysis of 200 array-CGH (Agilent 180k) samples from advanced colorectal cancers.

**Usage**

```
data( copynumber.data.chr21 )
```

**Format**

An object of class cghCall

**Value**

An object of class cghCall

---

CopyNumberBreakPointGenes-class

*An S4 class to represent a CopyNumberBreakPointGenes object*

---

## Description

An S4 class to represent a CopyNumberBreakPointGenes object

## Slots

geneAnnotation A data.frame with original gene annotation input

geneData A data.frame with gene information added by package methods

featuresPerGene A list with the associated features per gene

breakpointsPerGene A matrix with breakage status per gene

## Accessors

- `callData( object )` Returns feature call values
- `segmentData( object )` Returns feature segment values
- `breakpointData( object )` Returns feature breakpoint values
- `sampleNames( object )` Returns vector with sample names
- `namesFeatures( object )` Returns vector with feature names
- `featureChromosomes( object )` Returns vector of feature chromosomes
- `featureInfo( object )` Returns feature data/information
- `geneChromosomes( object )` Returns vector of gene chromosomes
- `geneInfo( object )` Returns gene data/information
- `featuresPerGene( object )` Returns a list of genes with coupled features
- `breakpointsPerGene( object )` Returns gene break status
- `recurrentGenes( object )` Returns recurrently broken genes

## Methods

- `getBreakpoints` Builds the [CopyNumberBreakPoints](#) object from copynumber data and detects breakpoint locations
- `bpFilter` Selects breakpoints by filter criteria options
- `addGeneAnnotation` Maps features to gene locations
- `bpGenes` Identifies genes affected by breakpoint locations
- `bpStats` Applies cohort-based statistics to identify genes and/or chromosomal locations that are recurrently affected by breakpoints
- `bpPlot` Plots breakpoint frequencies per chromosome

**Author(s)**

E. van den Broek and S. van Lieshout

**Examples**

```
data( copynumber.data.chr20 )
data( ens.gene.ann.hg18 )
bp <- getBreakpoints( copynumber.data.chr20 )
bp <- bpFilter( bp )
bp <- addGeneAnnotation( bp, ens.gene.ann.hg18 )
bp <- bpGenes( bp )
bp <- bpStats( bp )
bpPlot( bp, c(20) )
```

---

CopyNumberBreakPoints-class

*An S4 class to represent a CopyNumberBreakPoints object.*

---

**Description**

An S4 class to represent a CopyNumberBreakPoints object.

**Slots**

segmDiff A matrix with breakpoints based on segment values

callDiff A matrix with breakpoints based on call values

segments A matrix with segmented copy number values

calls A matrix with copy number calls

featureAnnotation A dataframe with predefined information about the features (usually probes or bins)

featureData A dataframe with calculated information about the features (usually probes or bins)

**Accessors**

- callData( object ) Returns feature call values
- segmentData( object ) Returns feature segment values
- breakpointData( object ) Returns feature breakpoint values
- sampleNames( object ) Returns vector with sample names
- namesFeatures( object ) Returns vector with feature names
- featureChromosomes( object ) Returns vector of feature chromosomes
- featureInfo( object ) Returns feature data/information

## Methods

- `getBreakpoints` Builds the `CopyNumberBreakPoints` object from copynumber data and detects breakpoint locations
- `bpFilter` Selects breakpoints by filter criteria options
- `bpStats` Applies cohort-based statistics to identify chromosomal locations that are recurrently affected by breakpoints
- `bpPlot` Plots breakpoint frequencies per chromosome

## Author(s)

E. van den Broek and S. van Lieshout

## Examples

```
data( copynumber.data.chr20 )
data( ens.gene.ann.hg18 )
bp <- getBreakpoints( copynumber.data.chr20 )
bp <- bpFilter( bp )
bp <- bpStats( bp , level = 'feature' , method = 'BH' )
bpPlot( bp, c(20) )
```

---

ens.gene.ann.hg18

*Gene Annotation hg18*

---

## Description

A dataset containing the gene locations based on human genome reference hg18 that was obtained from BioMart.

## Usage

```
data( ens.gene.ann.hg18 )
```

## Format

A data.frame

## Details

Dataframe with 5 columns:

- Gene: ensembl gene name
- EnsID: ensembl gene id
- Chromosome: Genomic Chromosome
- Start: Genomic start of gene
- End: Genomic end of gene

**Value**

data.frame

---

ens.gene.ann.hg19      *Gene Annotation hg19*

---

**Description**

A dataset containing the gene locations based on human genome reference hg19 that was obtained from BioMart.

**Usage**

```
data( ens.gene.ann.hg19 )
```

**Format**

A data.frame

**Details**

Dataframe with 5 columns:

- Gene: ensembl gene name
- EnsID: ensembl gene id
- Chromosome: Genomic Chromosome
- Start: Genomic start of gene
- End: Genomic end of gene

**Value**

data.frame

ens.gene.ann.hg38      *Gene Annotation hg38*

---

### Description

A dataset containing the gene locations based on human genome reference hg38 that was obtained from BioMart.

### Usage

```
data( ens.gene.ann.hg38 )
```

### Format

A data.frame

### Details

Dataframe with 5 columns:

- Gene: ensembl gene name
- EnsID: ensembl gene id
- Chromosome: Genomic Chromosome
- Start: Genomic start of gene
- End: Genomic end of gene

### Value

data.frame

---

featureChromosomes,CopyNumberBreakPoints-method

*Access Object featureChromosomes. This method returns a vector with feature chromosomes.*

---

### Description

Access Object featureChromosomes. This method returns a vector with feature chromosomes.

### Usage

```
## S4 method for signature 'CopyNumberBreakPoints'  
featureChromosomes(object)
```

**Arguments**

object            An object of class CopyNumberBreakPoints

**Value**

a vector with feature chromosomes

**Examples**

```
data( copynumber.data.chr20 )
bp <- getBreakpoints( copynumber.data.chr20 )
featureChromosomes( bp )
```

---

featureInfo,CopyNumberBreakPoints-method

*Access Options featureInfo. This method returns a dataframe with feature annotations.*

---

**Description**

Access Options featureInfo. This method returns a dataframe with feature annotations.

**Usage**

```
## S4 method for signature 'CopyNumberBreakPoints'
featureInfo(object)
```

**Arguments**

object            of class CopyNumberBreakPoints

**Value**

data.frame with feature annotations

**Examples**

```
data( copynumber.data.chr20 )
data( ens.gene.ann.hg18 )
bp <- getBreakpoints( copynumber.data.chr20 )
bp <- bpFilter( bp )
bp <- addGeneAnnotation( bp, ens.gene.ann.hg18 )
bp <- bpGenes( bp )

featureInfo( bp )
```

---

featuresPerGene, CopyNumberBreakPointGenes-method

*Access Object featuresPerGene. This method returns a vector with gene-related features for a particular gene.*

---

### Description

Access Object featuresPerGene. This method returns a vector with gene-related features for a particular gene.

### Usage

```
## S4 method for signature 'CopyNumberBreakPointGenes'
featuresPerGene(object, geneName = NULL)
```

### Arguments

object	An object of class CopyNumberBreakPoints
geneName	Exact Gene name as in the annotation

### Value

a vector with gene-related features

### Examples

```
data( copynumber.data.chr20 )
data( ens.gene.ann.hg18 )
bp <- getBreakpoints( copynumber.data.chr20 )
bp <- bpFilter( bp )
bp <- addGeneAnnotation( bp, ens.gene.ann.hg18 )
bp <- bpGenes( bp )

featuresPerGene( bp, geneName="PCMTD2" )
```

---

GeneBreak

*GeneBreak: A package for gene breakpoint detection on copy number aberration data*

---

### Description

The GeneBreak package performs cohort based recurrent gene breakpoint detection on copynumber data. It is possible to use the output of the function [CGHcall](#) from the package [CGHcall](#) or the function [callBins](#) from the package [QDNAseq](#) as the input for this analysis.

## GeneBreak functions

Analysis starts with the function `getBreakpoints` and continues with:  
`bpFilter` to exclude certain breakpoints from the analysis  
`addGeneAnnotation` to add gene location information  
`bpGenes` to determine which features (probes/bins) are related to which genes  
`bpStats` to determine which gene breaks are recurrent in the cohort

---

geneChromosomes,CopyNumberBreakPointGenes-method

*Access Object geneChromosomes. This method returns a vector with gene chromosomes.*

---

## Description

Access Object geneChromosomes. This method returns a vector with gene chromosomes.

## Usage

```
## S4 method for signature 'CopyNumberBreakPointGenes'  
geneChromosomes(object)
```

## Arguments

object            An object of class CopyNumberBreakPoints

## Value

vector with gene chromosomes

## Examples

```
data( copynumber.data.chr20 )  
data( ens.gene.ann.hg18 )  
bp <- getBreakpoints( copynumber.data.chr20 )  
bp <- bpFilter( bp )  
bp <- addGeneAnnotation( bp, ens.gene.ann.hg18 )  
bp <- bpGenes( bp )  
  
geneChromosomes( bp )
```

---

geneInfo, CopyNumberBreakPointGenes-method

*Access Options geneInfo. This method returns a dataframe with gene annotations.*

---

### Description

Access Options geneInfo. This method returns a dataframe with gene annotations.

### Usage

```
## S4 method for signature 'CopyNumberBreakPointGenes'
geneInfo(object)
```

### Arguments

object                    of class CopyNumberBreakPointGenes

### Value

data.frame with gene annotations

### Examples

```
data( copynumber.data.chr20 )
data( ens.gene.ann.hg18 )
bp <- getBreakpoints( copynumber.data.chr20 )
bp <- bpFilter( bp )
bp <- addGeneAnnotation( bp, ens.gene.ann.hg18 )

geneInfo( bp )
```

---

getBreakpoints

*getBreakpoints*

---

### Description

Builds the [CopyNumberBreakPoints](#) object from copynumber data and detects breakpoint locations.

### Usage

```
getBreakpoints(data, data2 = NULL, first.rm = TRUE)
```

**Arguments**

<code>data</code>	An object of class <b>cghCall</b> or an object of class <b>QDNAseqCopyNumbers</b> or a <code>data.frame</code> containing feature annotations ("Chromosome", "Start", "End", "FeatureName") followed by copy number segment values (rows are features, columns are subjects).
<code>data2</code>	A "data.frame" containing copy number calls following feature annotations with the four columns ("Chromosome", "Start", "End", "FeatureName", ...). This is optional and allows CNA-associated breakpoint filtering. (see <code>?bpFilter</code> )
<code>first.rm</code>	Remove the first 'artificial' breakpoint of the first DNA segment for each chromosome (default: <code>first.rm=TRUE</code> )

**Details**

The accuracy of chromosomal breakpoint locations depends on the quality and genomic resolution of processed copy number data. For CNA input data, we recommend to use established computational methods for CNA detection such as 'CGHcall' (Van De Wiel et al., 2007) for array-CGH or 'QDNAseq' (Scheinin et al., 2014) for MPS data, which both use the implemented Circular Binary Segmentation algorithm (Olshen et al. 2004).

**Value**

Returns an object of class [CopyNumberBreakPoints](#).

**References**

- Van De Wiel, M.A. et al. (2007) CGHcall: calling aberrations for array CGH tumor profiles. *Bioinformatics*, 23, 892-894.
- Scheinin, I. et al. (2014) DNA copy number analysis of fresh and formalin-fixed specimens by shallow whole-genome sequencing with identification and exclusion of problematic regions in the genome assembly. *Genome Research*, 24, 2022-2032.
- Olshen, A.B. et al. (2004) Circular binary segmentation for the analysis of array-based DNA copy number data. *5*, 557-572.

**Examples**

```
data( copynumber.data.chr20 )
breakpoints <- getBreakpoints( data = copynumber.data.chr20 )

## or alternatively
library(CGHcall)
cgh <- copynumber.data.chr20
segmented <- data.frame( Chromosome=chromosomes(cgh), Start=bpstart(cgh),
  End=bpend(cgh), FeatureName=rownames(cgh), segmented(cgh))
called <- data.frame( Chromosome=chromosomes(cgh), Start=bpstart(cgh),
  End=bpend(cgh), FeatureName=rownames(cgh), calls(cgh))
breakpoints <- getBreakpoints( data = segmented, data2 = called )

## options to inspect the data
breakpoints
```

```
accessOptions( breakpoints )
```

---

```
namesFeatures, CopyNumberBreakPoints-method
```

*Access Object namesFeatures. This method returns a vector with feature names.*

---

### Description

Access Object namesFeatures. This method returns a vector with feature names.

### Usage

```
## S4 method for signature 'CopyNumberBreakPoints'
namesFeatures(object)
```

### Arguments

object            An object of class CopyNumberBreakPoints

### Value

a vector with feature names

### Examples

```
data( copynumber.data.chr20 )
bp <- getBreakpoints( copynumber.data.chr20 )

namesFeatures( bp )
```

---

```
recurrentGenes, CopyNumberBreakPointGenes-method
```

*Access Options recurrentGenes. This method returns a dataframe that contains genes that are recurrently affected across samples based on a FDR threshold.*

---

### Description

Access Options recurrentGenes. This method returns a dataframe that contains genes that are recurrently affected across samples based on a FDR threshold.

### Usage

```
## S4 method for signature 'CopyNumberBreakPointGenes'
recurrentGenes(object,
  fdr.threshold = 0.1, summarize = TRUE, order.column = "FDR")
```

**Arguments**

object            Output of bpStats(): an object of class CopyNumberBreakPointGenes  
 fdr.threshold    A numeric Genes with lower FDR are returned  
 summarize        A logical to determine whether to only output a selection of columns  
 order.column     Name of the column to sort output on

**Value**

data.frame with genes recurrently affected by breakpoints

**Examples**

```
data( copynumber.data.chr20 )
data( ens.gene.ann.hg18 )
bp <- getBreakpoints( copynumber.data.chr20 )
bp <- bpFilter( bp )
bp <- addGeneAnnotation( bp, ens.gene.ann.hg18 )
bp <- bpGenes( bp )
bp <- bpStats( bp )

recurrentGenes( bp )
```

---

sampleNames,CopyNumberBreakPoints-method

*Access Object sampleNames. This method returns a vector with sample names.*

---

**Description**

Access Object sampleNames. This method returns a vector with sample names.

**Usage**

```
## S4 method for signature 'CopyNumberBreakPoints'
sampleNames(object)
```

**Arguments**

object            An object of class CopyNumberBreakPoints

**Value**

a vector with sample names

**Examples**

```
data( copynumber.data.chr20 )
bp <- getBreakpoints( copynumber.data.chr20 )

sampleNames( bp )
```

---

segmentData,CopyNumberBreakPoints-method

*Access Object segmentData. This method returns a dataframe with segment values.*

---

**Description**

Access Object segmentData. This method returns a dataframe with segment values.

**Usage**

```
## S4 method for signature 'CopyNumberBreakPoints'
segmentData(object)
```

**Arguments**

object            An object of class CopyNumberBreakPoints

**Value**

a dataframe with segment values

**Examples**

```
data( copynumber.data.chr20 )
bp <- getBreakpoints( copynumber.data.chr20 )

segmentData( bp )
```

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