

# Package ‘genoset’

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**Type** Package

**Title** Provides classes similar to ExpressionSet for copy number analysis

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**Description** Load, manipulate, and plot copynumber and BAF data. GenoSet class extends eSet by adding a ‘locData’ slot for a RangedData or GRAnegs object. This object contains feature genome location data and provides for efficient subsetting on genome location. CNSet and BAFSet extend GenoSet and require assayData matrices for Copy Number (cn) or Log-R Ratio (lrr) and B-Allele Frequency (baf) data. Implements and provides convenience functions for processing of copy number and B-Allele Frequency data.

**License** Artistic-2.0

**LazyLoad** yes

**Depends**

R (>= 2.10), BiocGenerics (>= 0.1.6), Biobase (>= 2.15.1), IRanges (>= 1.13.5), GenomicRanges

**Imports** methods, graphics, GenomicRanges

**Suggests** RUnit, DNACopy, stats

**Enhances** parallel

**biocViews** Infrastructure, DataRepresentation, Microarray, SNP, CopyNumberVariants

**Collate** ‘genoset-class.R’ ‘cnset-class.R’ ‘bafset-class.R’ ‘DataFrame-methods.R’ ‘test\_genoset\_package.R’ ‘utils.R’

**ByteCompile** TRUE

**R topics documented:**

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<i>genoset-package</i>	<i>GenoSet: An eSet for data with genome locations</i>
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### Description

Load, manipulate, and plot copynumber and BAF data. *GenoSet* class extends *eSet* by adding a "locData" slot for a *GRanges* or *RangedData* object. This object contains feature genome location data and provides for efficient subsetting on genome location. *CNSet* and *BAFSet* extend *GenoSet* and require assayData matrices for Copy Number (cn) or Log-R Ratio (lrr) and B-Allele Frequency (baf) data. Implements and provides convenience functions for processing of copy number and B-Allele Frequency data.

### See Also

*genoset-datasets* *GenoSet* *CNSet* *BAFSet*

---

<i>baf</i>	<i>Get baf data</i>
------------	---------------------

---

### Description

Get or Set the baf assayData slot

### Arguments

object            A *BAFset* object

### Details

Get or Set the baf assayData slot

### Value

matrix

### Author(s)

Peter M. Haverty

**Examples**

```
data(genoset)
baf(baf.ds) # Returns assayDataElement called "baf"
baf(baf.ds) <- baf2mbaf( baf(baf.ds) )
```

---

baf2mbaf

*Calculate mBAF from BAF*


---

**Description**

Calculate Mirrored B-Allele Frequency (mBAF) from B-Allele Frequency (BAF) as in Staaf et al., Genome Biology, 2008. BAF is converted to mBAF by folding around 0.5 so that is then between 0.5 and 1. HOM value are then made NA to leave only HET values that can be easily segmented. Values > hom.cutoff are made NA. Then, if genotypes (usually from a matched normal) are provided as the matrix 'calls' additional HOMs can be set to NA. The argument 'call.pairs' is used to match columns in 'calls' to columns in 'baf'.

**Usage**

```
baf2mbaf(baf, hom.cutoff = 0.95, calls = NULL,
         call.pairs = NULL)
```

**Arguments**

baf	numeric matrix of BAF values
hom.cutoff	numeric, values above this cutoff to be made NA (considered HOM)
calls	matrix of NA, CT, AG, etc. genotypes to select HETs (in normals). Dimnames must match baf matrix.
call.pairs	list, names represent target samples for HOMs to set to NA. Values represent columns in "calls" matrix.

**Value**

numeric matrix of mBAF values

**Author(s)**

Peter M. Haverty

**Examples**

```
data(genoset)
mbaf = baf2mbaf( baf(baf.ds), hom.cutoff=0.9 )
calls = matrix(sample(c("AT", "AA", "CG", "GC", "AT", "GG"), (nrow(baf.ds) * 2), replace=TRUE), ncol=2, dimnames=list(
mbaf = baf2mbaf( baf(baf.ds), hom.cutoff=0.9, calls = calls, call.pairs = list(K="L", L="L") ) # Sample L is matched
assayDataElement(baf.ds, "mbaf") = baf2mbaf( baf(baf.ds), hom.cutoff=0.9 ) # Put mbaf back into the BAFSet object
```

---

BAFSet *Create a BAFSet object*

---

### Description

This function is the preferred method for creating a new BAFSet object. Users are generally discouraged from calling "new" directly. This BAFSet function enforces the requirement for "lrr" and "baf" matrices. These and any other "..." arguments will become part of the assayData slot of the resulting object. "..." can be matrices or DataFrame objects (from the IRanges package). This function passes control to the "initGenoSet" method which performs argument checking including dimname matching among relevant slots and sets everything to genome order. Genome order can be disrupted by "[" or "[[" calls and will be checked by methods that require it.

### Usage

```
BAFSet(locData, lrr = NULL, baf = NULL, pData = NULL,
       annotation = "", universe, assayData = NULL, ...)
```

### Arguments

locData	A GRanges or RangedData object specifying feature chromosome locations. featureNames (names or rownames) are required to match featureNames of assayData.
lrr	numeric matrix of copy number data with rownames matching featureNames and colnames matching sampleNames
baf	numeric matrix of B-Allele Frequency data with rownames matching featureNames and colnames matching sampleNames
pData	A data frame with rownames matching all data matrices
annotation	character, string to specify chip/platform type
universe	character, a string to specify the genome universe for locData. Overrides any universe/genome data in locData.
assayData	assayData, usually an environment
...	More matrix or DataFrame objects to include in assayData slot

### Details

The BAFSet class is deprecated. Please use GenoSet. BAFSet only added the baf/lrr getter/setter functions, which are redundant with x[, , 'baf'] and x[, , 'lrr'] now.

### Value

A BAFSet object

### Author(s)

Peter M. Haverty

**See Also**

bafset-class, genoset-class

**Examples**

```
test.sample.names = LETTERS[11:13]
probe.names = letters[1:10]
locData.rd = RangedData(ranges=IRanges(start=c(1,4,3,2,5:10),width=1,names=probe.names),space=c(rep("chr1",4),
bs = BAFSet(
  locData=locData.rd,
  lrr=matrix(1:30,nrow=10,ncol=3,dimnames=list(probe.names,test.sample.names)),
  baf=matrix(31:60,nrow=10,ncol=3,dimnames=list(probe.names,test.sample.names)),
  pData=data.frame(matrix(LETTERS[1:15],nrow=3,ncol=5,dimnames=list(test.sample.names,letters[1:5]))),
  annotation="SNP6"
)
```

---

BAFSet-class

*Class "BAFSet"*

---

**Description**

A BAFSet is an extension of GenoSet that requires 'baf' and 'lrr' assayData element

**Objects from the Class**

Objects can be created by calls of the form `new("BAFSet", assayData, phenoData, featureData, experimentData, ...)`. However, as per BioConductor standard practice the object creation function `BAFSet` is recommended.

**Slots**

**locData:** Object of class "RangedData" Feature locations on the genome  
**assayData:** Object of class "AssayData" ~~  
**phenoData:** Object of class "AnnotatedDataFrame" ~~  
**featureData:** Object of class "AnnotatedDataFrame" ~~  
**experimentData:** Object of class "MIxS" ~~  
**annotation:** Object of class "character" ~~  
**protocolData:** Object of class "AnnotatedDataFrame" ~~  
**.\_\_classVersion\_\_:** Object of class "Versions" ~~

**Extends**

Class "[GenoSet](#)", directly. Class "[eSet](#)", by class "GenoSet", distance 2.

**Methods**

```

show signature(object = "BAFSet"): ...
baf signature(object = "BAFSet"): Getter for 'baf' assayDataElement
baf<- signature(object = "BAFSet", value = "matrix"): setter for 'baf' assayDataElement
genoPlot signature(x = "BAFSet", y = "ANY"): Plot data along the genome. Defaults to 'lrr'
  assayDataElement.
lrr signature(object = "BAFSet"): Getter for 'lrr' assayDataElement
lrr<- signature(object = "BAFSet", value = "matrix"): Setter for 'lrr' assayDataElement

```

**Author(s)**

Peter M. Haverly <phaverly@gene.com>

**See Also**

[BAFSet](#), [CNSet](#), [GenoSet](#)

**Examples**

```

showClass("BAFSet")
test.sample.names = LETTERS[11:13]
probe.names = letters[1:10]
locData.gr = GRanges(ranges=IRanges(start=c(1,4,3,2,5:10),width=1,names=probe.names),seqnames=c(rep("chr1",4),r
bs = BAFSet(
  locData=locData.gr,
  lrr=matrix(1:30,nrow=10,ncol=3,dimnames=list(probe.names,test.sample.names)),
  baf=matrix(31:60,nrow=10,ncol=3,dimnames=list(probe.names,test.sample.names)),
  pData=data.frame(matrix(LETTERS[1:15],nrow=3,ncol=5,dimnames=list(test.sample.names,letters[1:5]))),
  annotation="SNP6"
)

```

---

BAFSet.to.ExpressionSets

*Make a pair of ExpressionSets from a BAFSet*

---

**Description**

Often it is convenient to have a more standard "ExpressionSet" rather than a BAFSet. For example, when using infrastructure dependent on the ExpressionSet slots, like limma or ExpressionSetOnDisk. This will create a list of two ExpressionSets, one each for the baf and lrr data. To make a single ExpressionSet, with the lrr data in the exprs slot and the baf data as an additional member of assayData, use the standard coercion `eset = as(bafset,"ExpressionSet")`.

**Usage**

```
BAFSet.to.ExpressionSets(bs)
```

**Arguments**

bs                    A BAFset object

**Details**

BAFSet.toExpressionSets has been deprecated. Please use `as(x, 'ExpressionSet')`.

**Value**

A list with one ExpressionSet each for the baf and lrr data in the BAFset object

**Author(s)**

Peter M. Haverty

**Examples**

```
data(genoset)
eset.list = BAFSet.to.ExpressionSets(baf.ds)
```

---

boundingIndices

*Find indices of features bounding a set of chromosome ranges/genes*

---

**Description**

This function is similar to `findOverlaps` but it guarantees at least two features will be covered. This is useful in the case of finding features corresponding to a set of genes. Some genes will fall entirely between two features and thus would not return any ranges with `findOverlaps`. Specifically, this function will find the indices of the features (first and last) bounding the ends of a range/gene (start and stop) such that  $first \leq start < stop \leq last$ . Equality is necessary so that multiple conversions between indices and genomic positions will not expand with each conversion. Ranges/genes that are outside the range of feature positions will be given the indices of the corresponding first or last index rather than 0 or  $n + 1$  so that genes can always be connected to some data.

**Usage**

```
boundingIndices(starts, stops, positions,
  valid.indices = TRUE, all.indices = FALSE, offset = 0)
```

**Arguments**

starts                integer vector of first base position of each query range

stops                 integer vector of last base position of each query range

positions             Base positions in which to search

valid.indices        logical, TRUE assures that the returned indices don't go off either end of the array, i.e. 0 becomes 1 and  $n+1$  becomes  $n$



offset	integer, value to add to all returned indices. For the case where positions represents a portion of some larger array (e.g. a chr in a genome)
all.indices	logical, return a list containing full sequence of indices for each query

### Details

This function uses some tricks from `findIntervals`, where is for  $k$  queries and  $n$  features it is  $O(k * \log(n))$  generally and  $\sim O(k)$  for sorted queries. Therefore will be dramatically faster for sets of query genes that are sorted by start position within each chromosome. The index of the stop position for each gene is found using the left bound from the start of the gene reducing the search space for the stop position somewhat. This function has important differences from `boundingIndices2`, which uses `findInterval`: `boundingIndices` does not check for NAs or unsorted data in the subject positions. Also, the positions are kept as integer, where `boundingIndices2` (and `findInterval`) convert them to doubles. These assumptions are safe for position info coming from a `GenoSet`, `GRanges`, or `RangedData`.

### Value

integer matrix of 2 columns for start and stop index of range in data or a list of full sequences of indices for each query (see `all.indices` argument)

### Author(s)

Peter M. Haverty <phaverty@gene.com>

### See Also

Other "range summaries": [boundingIndices2](#), [boundingIndicesByChr](#), [rangeColMeans](#), [rangeSampleMeans](#)

### Examples

```
starts = seq(10,100,10)
boundingIndices( starts=starts, stops=starts+5, positions = 1:100 )
```

---

boundingIndices2	<i>Find indices of features bounding a set of chromosome ranges/genes</i>
------------------	---

---

### Description

This function is similar to `findOverlaps` but it guarantees at least two features will be covered. This is useful in the case of finding features corresponding to a set of genes. Some genes will fall entirely between two features and thus would not return any ranges with `findOverlaps`. Specifically, this function will find the indices of the features (first and last) bounding the ends of a range/gene (start and stop) such that  $first \leq start \leq stop \leq last$ . Equality is necessary so that multiple conversions between indices and genomic positions will not expand with each conversion. This function uses `findIntervals`, which is for  $k$  queries and  $n$  features is  $O(k * \log(n))$  generally and  $\sim O(k)$  for sorted queries. Therefore will be dramatically faster for sets of query genes that are sorted by start position within each chromosome. This should give performance for  $k$  genes and  $n$  features that is  $\sim O(k)$

for starts and  $O(k * \log(n))$  for stops and  $\sim O(k * \log(n))$  overall. Ranges/genes that are outside the range of feature positions will be given the indices of the corresponding first or last index rather than 0 or  $n + 1$  so that genes can always be connected to some data.

### Usage

```
boundingIndices2(starts, stops, positions, offset = NULL)
```

### Arguments

starts	numeric or integer, first base position of each query range
stops	numeric or integer, last base position of each query range
positions	Base positions in which to search
offset	integer, value to add to all returned indices. For the case where positions represents a portion of some larger array (e.g. a chr in a genome)

### Value

integer matrix of 2 columns for start and stop index of range in data

### Author(s)

Peter M. Haverty

### See Also

Other "range summaries": [boundingIndices](#), [boundingIndicesByChr](#), [rangeColMeans](#), [rangeSampleMeans](#)

### Examples

```
starts = seq(10,100,10)
boundingIndices2( starts=starts, stops=starts+5, positions = 1:100 )
```

---

boundingIndicesByChr *Find indices of features bounding a set of chromosome ranges/genes, across chromosomes*

---

### Description

Finds subject ranges corresponding to a set of genes (query ranges), taking chromosome into account. Specifically, this function will find the indices of the features (first and last) bounding the ends of a range/gene (start and stop) such that  $first \leq start < stop \leq last$ . Equality is necessary so that multiple conversions between indices and genomic positions will not expand with each conversion. Ranges/genes that are outside the range of feature positions will be given the indices of the corresponding first or last index on that chromosome, rather than 0 or  $n + 1$  so that genes can always be connected to some data. Checking the left and right bound for equality will tell you when a query is off the end of a chromosome.

**Usage**

```
boundingIndicesByChr(query, subject)
```

**Arguments**

query	GRanges or something coercible to GRanges
subject	RangedData

**Details**

This function uses some tricks from `findIntervals`, where is for  $k$  queries and  $n$  features it is  $O(k * \log(n))$  generally and  $\sim O(k)$  for sorted queries. Therefore will be dramatically faster for sets of query genes that are sorted by start position within each chromosome. The index of the stop position for each gene is found using the left bound from the start of the gene reducing the search space for the stop position somewhat.

This function differs from `boundingIndices` in that 1. it uses both start and end positions for the subject, and 2. query and subject start and end positions are processed in blocks corresponding to chromosomes.

Both query and subject must be in at least weak genome order (sorted by start within chromosome blocks).

**Value**

integer matrix with two columns corresponding to indices on left and right bound of queries in subject

**Author(s)**

Peter M. Haverty <phaverty@gene.com>

**See Also**

Other "range summaries": [boundingIndices](#), [boundingIndices2](#), [rangeColMeans](#), [rangeSampleMeans](#)

---

bounds2Rle

*Convert bounding indices into a Rle*

---

**Description**

Given a matrix of first/last indices, like from `boundingIndicesByChr`, and values for each range, convert to a Rle. This function takes the expected length of the Rle,  $n$ , so that any portion of the full length not covered by a first/last range will be a run with the value NA. This is typical in the case where data is segmented with CBS and some of the data to be segmented is NA.

**Usage**

```
bounds2Rle(bounds, values, n)
```

**Arguments**

bounds	matrix, two columns, with first and last index, like from boundingIndicesByChr
values	ANY, some value to be associated with each range, like segmented copy number.
n	integer, the expected length of the Rle, i.e. the number of features in the genome/target ranges processed by boundingIndicesByChr.

**Value**

Rle

**Author(s)**

Peter M. Haverty

**See Also**

Other "segmented data": [runCBS](#), [segPairTable](#), [segPairTable](#), [segPairTable](#), [segs2RangedData](#), [segs2Rle](#), [segs2RleDataFrame](#), [segTable](#), [segTable](#), [segTable](#)

---

chr

*Look up chromosome for each feature*

---

**Description**

Chromosome name for each feature

**Arguments**

object GRanges, RangedData or GenoSet

**Details**

Get chromosome name for each feature. Returns character, not the factor 'space'.

**Value**

character vector of chromosome positions for each feature

**Author(s)**

Peter Haverty

**Examples**

```

test.sample.names = LETTERS[11:13]
probe.names = letters[1:10]
gs = GenoSet(
  locData=RangedData(ranges=IRanges(start=1:10,width=1,names=probe.names),space=c(rep("chr1",4),rep("chr3",2),
  cn=matrix(31:60,nrow=10,ncol=3,dimnames=list(probe.names,test.sample.names)),
  pData=data.frame(matrix(LETTERS[1:15],nrow=3,ncol=5,dimnames=list(test.sample.names,letters[1:5]))),
  annotation="SNP6"
)
chr(gs) # c("chr1","chr1","chr1","chr1","chr3","chr3","chrX","chrX","chrX","chrX")
chr(locData(gs)) # The same

```

---

chrIndices

*Get a matrix of first and last index of features in each chromosome*


---

**Description**

Sometimes it is handy to know the first and last index for each chr. This is like chrInfo but for feature indices rather than chromosome locations. If chr is specified, the function will return a sequence of integers representing the row indices of features on that chromosome.

**Arguments**

object	GenoSet, RangedData, or GRanges
chr	character, specific chromosome name

**Value**

data.frame with "first" and "last" columns

**Author(s)**

Peter M. Haverty

**Examples**

```

data(genoset)
chrIndices(genoset.ds)
chrIndices(locData(genoset.ds)) # The same

```

---

chrInfo                      *Chromosome Information*

---

**Description**

Get chromosome start and stop positions

**Arguments**

object                      A GenoSet object or similar

**Details**

Provides a matrix of start, stop and offset, in base numbers for each chromosome.

**Value**

list with start and stop position, by ordered chr

**Author(s)**

Peter Haverty

**Examples**

```
data(genoset)
chrInfo(genoset.ds)
chrInfo(locData(genoset.ds)) # The same
```

---

chrNames                      *Get list of unique chromosome names*

---

**Description**

Get list of unique chromosome names

**Arguments**

object                      RangedData or GenoSet

**Value**

character vector with names of chromosomes

**Author(s)**

Peter M. Haverty

**Examples**

```

test.sample.names = LETTERS[11:13]
probe.names = letters[1:10]
gs = GenoSet(
  locData=RangedData(ranges=IRanges(start=1:10,width=1,names=probe.names),space=c(rep("chr1",4),rep("chr3",2)),
    cn=matrix(31:60,nrow=10,ncol=3,dimnames=list(probe.names,test.sample.names)),
  pData=data.frame(matrix(LETTERS[1:15],nrow=3,ncol=5,dimnames=list(test.sample.names,letters[1:5]))),
  annotation="SNP6"
)
chrNames(gs) # c("chr1","chr3","chrX")
chrNames(locData(gs)) # The same
chrNames(gs) = sub("^chr","",chrNames(gs))

```

---

chrOrder

*Order chromosome names in proper genome order*


---

**Description**

Chromosomes make the most sense orded by number, then by letter.

**Usage**

```
chrOrder(chr.names)
```

**Arguments**

chr.names      character, vector of unique chromosome names

**Value**

character vector of chromosome names in proper order

**Author(s)**

Peter M. Haverty

**See Also**

Other "genome ordering": [isGenomeOrder](#), [isGenomeOrder](#), [isGenomeOrder](#), [toGenomeOrder](#), [toGenomeOrder](#), [toGenomeOrder](#), [toGenomeOrder](#)

**Examples**

```
chrOrder(c("chr5","chrX","chr3","chr7","chrY")) # c("chr3","chr5","chr7","chrX","chrY")
```

---

cn	<i>Get or Set the cn assayData slot</i>
----	---

---

**Description**

Get or Set the cn assayData slot

**Arguments**

object            A BAFset object

**Value**

matrix

**Author(s)**

Peter M. Haverty

**Examples**

```
data(genoset)
cn(cn.ds) # Returns assayDataElement called "cn"
cn(cn.ds) <- cn(cn.ds) + 5
```

---

cn2lr	<i>Take vector or matrix of copynumber values, convert to log2ratios Utility function for converting copynumber units (2 is normal) to log2ratio units (two is normal)</i>
-------	--

---

**Description**

Take vector or matrix of copynumber values, convert to log2ratios Utility function for converting copynumber units (2 is normal) to log2ratio units (two is normal)

**Usage**

```
cn2lr(x)
```

**Arguments**

x                    numeric data in copynumber units

**Value**

data of same type as "x" transformed into log2ratio units



**Author(s)**

Peter M. Haverty <phaverty@gene.com>

**See Also**

lr2cn

---

CNSet

*Create a CNSet object*

---

**Description**

This function is the preferred method for creating a new CNSet object. Users are generally discouraged from calling "new" directly. This CNSet function enforces the requirement for a "cn" matrix. This and any other "..." arguments will become part of the assayData slot of the resulting object. "..." can be matrices or DataFrame objects (from the IRanges package). This function passes control to the "initGenoSet" method which performs argument checking including dimname matching among relevant slots and sets everything to genome order. Genome order can be disrupted by "[" or "[[" calls and will be checked by methods that require it.

**Usage**

```
CNSet(locData, cn = NULL, pData = NULL, annotation = "",
      universe, assayData = NULL, ...)
```

**Arguments**

locData	A GRanges or RangedData object specifying feature chromosome locations. featureNames (names or rownames) are required to match featureNames of matrices.
cn	numeric matrix of copy number data with rownames matching featureNames and colnames matching sampleNames
pData	A data frame with rownames matching all data matrices
annotation	character, string to specify chip/platform type
universe	character, string to specify genome universe for locData. Overrides any universe/genome data in locData.
assayData	assayData, usually an environment
...	More matrix or DataFrame objects to include in assayData

**Details**

The CNSet class is deprecated. Please use GenoSet. CNSet only added the cn getter/setter functions, which are redundant with x[, , 'cn'] now.

**Value**

A CNSet object

**Author(s)**

Peter M. Haverty

**Examples**

```
test.sample.names = LETTERS[11:13]
probe.names = letters[1:10]
joe = CNSet(
  locData=RangedData(ranges=IRanges(start=1:10,width=1,names=probe.names),space=c(rep("chr1",4),rep("chr3",2)),
    cn=matrix(31:60,nrow=10,ncol=3,dimnames=list(probe.names,test.sample.names)),
  pData=data.frame(matrix(LETTERS[1:15],nrow=3,ncol=5,dimnames=list(test.sample.names,letters[1:5]))),
  annotation="SNP6"
)
```

---

CNSet-class

*Class "CNSet"*

---

**Description**

A CNSet is an extension of GenoSet that requires a 'cn' assayData element.

**Objects from the Class**

Objects can be created by calls of the form `new("CNSet", assayData, phenoData, featureData, experimentData, ...)`. However, as per BioConductor standard practice the object creation function `CNSet` is recommended.

**Slots**

**locData:** Object of class "RangedDataOrGRanges" Feature locations on the genome.

**assayData:** Object of class "AssayData" From eSet

**phenoData:** Object of class "AnnotatedDataFrame" From eSet

**featureData:** Object of class "AnnotatedDataFrame" From eSet

**experimentData:** Object of class "MIAXE" From eSet

**annotation:** Object of class "character" From eSet

**protocolData:** Object of class "AnnotatedDataFrame" From eSet

**.\_\_classVersion\_\_:** Object of class "Versions" From eSet

**Extends**

Class "[GenoSet](#)", directly. Class "[eSet](#)", by class "[GenoSet](#)", distance 2.

**Methods**

**show** signature(object = "CNSet"): ...

**cn** signature(object = "CNSet"): Getter for cn assayDataElement

**cn<-** signature(object = "CNSet", value = "matrix"): Setter for 'cn' assayDataElement

**genoPlot** signature(x = "CNSet", y = "ANY"): Plot data along the genome. Defaults to 'cn' assayDataElement

**Author(s)**

Peter M. Haverty <phaverty@gene.com>

**See Also**

[CNSet](#), [GenoSet](#), [BAFSet](#)

**Examples**

```
showClass("CNSet")
test.sample.names = LETTERS[11:13]
probe.names = letters[1:10]
cn.ds = CNSet(
  locData=GRanges(ranges=IRanges(start=1:10,width=1,names=probe.names),seqnames=c(rep("chr1",4),rep("chr3",2)),
  cn=matrix(31:60,nrow=10,ncol=3,dimnames=list(probe.names,test.sample.names)),
  pData=data.frame(matrix(LETTERS[1:15],nrow=3,ncol=5,dimnames=list(test.sample.names,letters[1:5]))),
  annotation="SNP6"
)
```

---

colMeans

*Means of columns*

---

**Description**

Calculate means of columns of a DataFrame as if it were a matrix. Allow colmeans in rangeSampleMeans for DataTable just like a real matrix. I'm sure there is much more clever way to do this using aggregate.

**Arguments**

x	DataFrame
na.rm	logical
dims	integer

**Author(s)**

Peter M. Haverty

**Examples**

```
df.ds = DataFrame( a = Rle(c(5,4,3),c(2,2,2)), b = Rle(c(3,6,9),c(1,1,4)) )
mat.ds = matrix( c(5,5,4,4,3,3,3,6,9,9,9,9), ncol=2, dimnames=list(NULL,c("a","b")))
## Not run: identical( colMeans(df.ds), colMeans(mat.ds) )
```

---

featureNames	<i>Get rownames from RangedData, GRanges, or GenoSet</i>
--------------	--

---

**Description**

Get rownames from RangedData, GRanges, or GenoSet

**Arguments**

object GRanges, RangedData, or GenoSet

**Value**

character vector with names rows/features

**Author(s)**

Peter M. Haverty

**Examples**

```
data(genoset)
head(featureNames(locData.rd))
head(featureNames(as(locData.rd,"GRanges")))
head(featureNames(cn.ds))
```

---

featureNames<-	<i>Set featureNames</i>
----------------	-------------------------

---

**Description**

Set featureNames

**Arguments**

object GenoSet, RangedData, or GRanges  
value ANY

**Details**

Set featureNames of a GenoSet, GRanges, or RangedData (rownames, names, or rownames respectively).

**Value**

A new object of the class of supplied object

**Author(s)**

Peter M. Haverty

---

fixSegNAs

*Fix NA runs in a Rle*

---

**Description**

Fix NA runs in a Rle when the adjacent runs have equal values

**Usage**

```
fixSegNAs(x, max.na.run = 3)
```

**Arguments**

x	Rle to be fixed
max.na.run	integer, longest run of NAs that will be fixed

**Value**

Rle

**Author(s)**

Peter M. Haverty

---

gcCorrect

*Correct copy number for GC content*

---

**Description**

Copy number estimates from various platforms show "Genomic Waves" (Diskin et al., Nucleic Acids Research, 2008) where copy number trends with local GC content. This function regresses copy number on GC percentage and removes the effect (returns residuals). GC content should be smoothed along the genome in wide windows  $\geq 100$ kb.

**Usage**

```
gcCorrect(ds, gc, retain.mean = TRUE)
```

**Arguments**

ds                    numeric matrix of copynumber or log2ratio values, samples in columns  
gc                    numeric vector, GC percentage for each row of ds, must not have NAs  
retain.mean        logical, center on zero or keep same mean?

**Value**

numeric matrix, residuals of ds regressed on gc

**Author(s)**

Peter M. Haverty

**Examples**

```
gc = runif(n=100, min=1, max=100)
ds = rnorm(100) + (0.1 * gc)
gcCorrect(ds, gc)
```

---

genomeAxis

*Label axis with base pair units*

---

**Description**

Label an axis with base positions

**Usage**

```
genomeAxis(locs = NULL, side = 1, log = FALSE,
do.other.side = TRUE)
```

**Arguments**

locs                RangedData to be used to draw chromosome boundaries, if necessary. Usually locData slot from a GenoSet.  
side                integer side of plot to put axis  
log                 logical Is axis logged?  
do.other.side     logical, label non-genome side with data values at tick marks?

**Details**

Label a plot with Mb, kb, bp as appropriate, using tick locations from axTicks

**Value**

nothing

**Author(s)**

Peter M. Haverty

**See Also**Other "genome plots": [genoPlot](#), [genoPlot](#), [genoPlot](#), [genoPlot](#)**Examples**

```

data(genoset)
  genoPlot(genoPos(baf.ds), baf(baf.ds)[,1])
  genomeAxis( locs=locData(baf.ds) ) # Add chromosome names and boundaries to a plot assuming genome along x-axis
  genomeAxis( locs=locData(baf.ds), do.other.side=FALSE ) # As above, but do not label y-axis with data values at ti
  genomeAxis() # Add nucleotide position in sensible units assuming genome along x-axis

```

---

 genoPlot

*Plot data along the genome*


---

**Description**

Plot location data and chromosome boundaries from a `GenoSet`, `RangedData`, or `GRanges` object against data from a numeric or `Rle`. Specifying a chromosome name and optionally a 'xlim' will zoom into one chromosome region. If more than one chromosome is present, the chromosome boundaries will be marked. Alternatively, for a numeric x and a numeric or `Rle` y, data in y can be plotted at genome positions x. In this case, chromosome boundaries can be taken from the argument `locs`. If data for y-axis comes from a `Rle` lines are plotted representing segments. X-axis tickmarks will be labeled with genome positions in the most appropriate units.

**Arguments**

x	<code>GenoSet</code> (or descendant), <code>RangedData</code> , or <code>GRanges</code>
y	numeric or <code>Rle</code>
element	character, <code>Deprecated</code> . when x is a <code>GenoSet</code> , the y-th column of this assay- <code>DataElement</code> is used for the y-axis data.
locs	<code>RangedData</code> , like <code>locData</code> slot of <code>GenoSet</code>
chr	Chromosome to plot, <code>NULL</code> by default for full genome
add	Add plot to existing plot
xlab	character, label for x-axis of plot
ylab	character, label for y-axis of plot
col	character, color to plot lines or points
lwd	numeric, line width for segment plots from an <code>Rle</code>
pch	character or numeric, printing character, see points
xlim	integer, length two, bounds for genome positions. Used in conjunction with "chr" to subset data for plotting.
...	Additional plotting args

**Value**

nothing

**Methods**

signature(x = "RangedDataOrGenoSetOrGRanges", y = "ANY") Plot feature locations and data from one sample.

signature(x = "numeric", y = "numeric") Plot numeric location and a vector of numeric data.

signature(x = "numeric", y = "Rle") Plot numeric location and a vector of Rle data. Uses lines for Rle runs.

**Author(s)**

Peter M. Haverty

**See Also**

Other "genome plots": [genomeAxis](#)

**Examples**

```
data(genoset)
genoPlot( x=baf.ds,y=baf.ds[,1,"lrr"] )
genoPlot( genoPos(baf.ds), baf.ds[,1,"lrr"], locs=locData(baf.ds) ) # The same
genoPlot( 1:10, Rle(c(rep(0,5),rep(3,4),rep(1,1))) )
```

---

genoPos

*Convert chromosome positions to positions from start of genome*

---

**Description**

Get base positions of features in genome-scale units

**Arguments**

object            A `GenoSet` object or a `RangedData` object

**Details**

Get base positions of array features in bases counting from the start of the genome. Chromosomes are ordered numerically, when possible, then lexically.

**Value**

numeric position of each feature in whole genome units, in original order



**Author(s)**

Peter M. Haverty

**Examples**

```
data(genoset)
  head(genoPos(genoset.ds))
  head(genoPos(locData(genoset.ds))) # The same
```

---

GenoSet

*Create a GenoSet object*

---

**Description**

This function is the preferred method for creating a new GenoSet object. Users are generally discouraged from calling "new" directly. Any "..." arguments will become part of the assayData slot of the resulting object. "..." can be matrices or DataFrame objects (from IRanges). This function passes control to the "initGenoSet" method which performs argument checking including dimname matching among relevant slots and sets everything to genome order. Genome order can be disrupted by "[" calls and will be checked by methods that require it.

**Usage**

```
GenoSet(locData, pData = NULL, annotation = "", universe,
        assayData = NULL, ...)
```

**Arguments**

locData	A RangedData object specifying feature chromosome locations. Rownames are required to match featureNames.
pData	A data frame with rownames matching all data matrices
annotation	character, string to specify chip/platform type
universe	character, a string to specify the genome universe for locData
assayData	assayData, usually an environment
...	More matrix or DataFrame objects to include in assayData

**Value**

A GenoSet object

**Author(s)**

Peter M. Haverty

**Examples**

```

test.sample.names = LETTERS[11:13]
probe.names = letters[1:10]
gs = GenoSet(
  locData=RangedData(ranges=IRanges(start=1:10,width=1,names=probe.names),space=c(rep("chr1",4),rep("chr3",2)),
    cn=matrix(31:60,nrow=10,ncol=3,dimnames=list(probe.names,test.sample.names)),
  pData=data.frame(matrix(LETTERS[1:15],nrow=3,ncol=5,dimnames=list(test.sample.names,letters[1:5]))),
  annotation="SNP6"
)

```

---

GenoSet-class

*Class "GenoSet"*


---

**Description**

GenoSet extends eSet by adding genome location information in the form of the locData slot. GenoSet uses this location information to allow quick subsetting and summarization by a set of genome locations (RangedData or GRanges). GenoSet implements and extends the RangedData/GRanges API for access to the underlying location information.

**Objects from the Class**

Objects can be created by calls of the form `new("GenoSet", assayData, phenoData, featureData, experimentData, ...)`. However, as per BioConductor standard practice the object creation function `GenoSet` is recommended.

**Slots**

**locData:** Object of class "RangedDataOrGRanges" Locations of features on the genome

**assayData:** Object of class "AssayData" From eSet

**phenoData:** Object of class "AnnotatedDataFrame" From eSet

**featureData:** Object of class "AnnotatedDataFrame" From eSet

**experimentData:** Object of class "MIAXE" From eSet

**annotation:** Object of class "character" From eSet

**protocolData:** Object of class "AnnotatedDataFrame" From eSet

**.\_\_classVersion\_\_:** Object of class "Versions" From eSet

**Extends**

Class "eSet", directly.

**Methods**

```

[ signature(x = "GenoSet", i = "ANY", j = "ANY", drop = "ANY"): ...
[ signature(x = "GenoSet", i = "character", j = "ANY", drop = "ANY"): ...
[ signature(x = "GenoSet", i = "RangedData", j = "ANY", drop = "ANY"): ...
[<- signature(x = "GenoSet", i = "ANY", j = "ANY", value = "ANY"): ...
chr signature(object = "GenoSet"): ...
chrNames signature(object = "GenoSet"): ...
elementLengths signature(x = "GenoSet"): ...
featureNames signature(object = "GenoSet"): ...
featureNames<- signature(object = "GenoSet"): ...
sampleNames signature(object = "GenoSet"): ...
dim signature(object = "GenoSet"): ...
genoPlot signature(x = "GenoSet", y = "ANY"): ...
locData signature(object = "GenoSet"): ...
locData<- signature(object = "GenoSet", value = "RangedData"): ...
names signature(x = "GenoSet"): ...
ranges signature(x = "GenoSet"): ...
show signature(object = "GenoSet"): ...
toGenomeOrder signature(ds = "GenoSet"): ...

```

**Author(s)**

Peter M. Haverly <phaverly@gene.com>

**See Also**

[GenoSet](#), [CNSet](#), [BAFSet](#)

**Examples**

```

showClass("GenoSet")
test.sample.names = LETTERS[11:13]
probe.names = letters[1:10]
gs = GenoSet(
  locData=GRanges(ranges=IRanges(start=1:10,width=1,names=probe.names),seqnames=c(rep("chr1",4),rep("chr3",2)),
  cn=matrix(31:60,nrow=10,ncol=3,dimnames=list(probe.names,test.sample.names)),
  pData=data.frame(matrix(LETTERS[1:15],nrow=3,ncol=5,dimnames=list(test.sample.names,letters[1:5]))),
  annotation="SNP6"
)

```

---

genoset-datasets      *Example GenoSet, BAFSet, and CNSet objects and the data to create them.*

---

### Description

Fake LRR, BAF, pData and location data were generated and saved as fake.lrr, fake.cn, fake.baf, fake.pData and locData.rd. These were used to construct the objects genoset.ds, baf.ds, and cn.ds

### Usage

```
data(genoset)
```

### Format

**fake.lrr** A matrix with some randomly generated LRR (log2ratio copynumber) data

**fake.cn** A matrix with some randomly generated LRR (log2ratio copynumber) data

**fake.baf** A matrix with some randomly generated BAF (B-Allele Frequency) data

**fake.pData** A data.frame of sample annotation to go with fake.lrr and fake.baf

**locData.rd** A RangedData object describing the genomic locations of the probes in fake.baf and fake.lrr

**locData.gr** A GRanges object describing the genomic locations of the probes in fake.baf and fake.lrr

**genoset.ds** A GenoSet object created with fake.lrr as the "lrr" element, locData.rd as the locData, and fake.pData as the phenoData

**baf.ds** A BAFSet object created with fake.lrr as the "lrr" element, fake.baf as the "baf" element, locData.rd as the locData, and fake.pData as the phenoData

**cn.ds** A CNSet object created with fake.lrr as the "cn" element, locData.rd as the locData, and fake.pData as the phenoData

### Source

Fake data generated using rnorm and the like.

---

genoset-deprecated      *Deprecated genoset features*

---

### Description

The CNSet and BAFSet classes have been deprecated. They only really added getter/setter methods for specific assayDataElements, so they are now redundant with the preferred method of using the assayDataElement name as the third argument to bracket, e.g. `x[i, j, "lrr"]`. Accordingly `BAFSet.to.ExpressionSets` is also deprecated.

**Details**

Additionally, names, ranges, and space on a GenoSet are also deprecated. In an effort to make a consistent API for either RangedData or GRanges in the locData slot, we recommend using chrNames for names and chr for space.

---

initGenoSet	<i>Create a GenoSet or derivative object</i>
-------------	--

---

**Description**

This function is the preferred method for creating a new GenoSet object. Users are generally discouraged from calling "new" directly. The "..." argument is for any number of matrices of matching size that will become part of the assayData slot of the resulting object. This function passes control to the "genoSet" object which performs argument checking including dimname matching among relevant slots and sets everything to genome order. Genome order can be disrupted by "[" calls and will be checked by methods that require it.

**Usage**

```
initGenoSet(type, locData, pData = NULL, annotation = "",
            universe, assayData = NULL, ...)
```

**Arguments**

type	character, the type of object (e.g. GenoSet, BAFSet, CNSet) to be created
locData	A GRanges or RangedData object specifying feature chromosome locations. featureNames (names or rownames) are required to match featureNames.
pData	A data frame with rownames matching sampleNames (colnames of all assay-DataElements)
annotation	character, string to specify chip/platform type
universe	character, a string to specify the genome universe for locData, overrides universe/genome data in locData
assayData	assayData, usually an environment
...	More matrix or DataFrame objects to include in assayData

**Value**

A GenoSet object or derivative as specified by "type" arg

**Author(s)**

Peter M. Haverty

**Examples**

```

test.sample.names = LETTERS[11:13]
probe.names = letters[1:10]
gs = GenoSet(
  locData=RangedData(ranges=IRanges(start=1:10,width=1,names=probe.names),space=c(rep("chr1",4),rep("chr3",2)),
    cn=matrix(31:60,nrow=10,ncol=3,dimnames=list(probe.names,test.sample.names)),
  pData=data.frame(matrix(LETTERS[1:15],nrow=3,ncol=5,dimnames=list(test.sample.names,letters[1:5]))),
  annotation="SNP6"
)

```

---

isGenomeOrder

---

*Check if a GRanges, GenoSet or RangedData is in genome order*


---

**Description**

Checks that rows in each chr are ordered by start. If strict=TRUE, then chromosomes must be in order specified by chrOrder. isGenomeOrder for GRanges differs from order in that it orders by chromosome and start position only, rather than chromosome, strand, start, and width.

**Arguments**

ds                   GenoSet, GRanges, or RangedData  
strict               logical, should space/chromosome order be identical to that from chrOrder?

**Value**

logical

**Author(s)**

Peter M. Haverty

**See Also**

Other "genome ordering": [chrOrder](#), [toGenomeOrder](#), [toGenomeOrder](#), [toGenomeOrder](#), [toGenomeOrder](#)

**Examples**

```

data(genoset)
isGenomeOrder( locData(genoset.ds) )

```

---

locData	<i>Access the feature genome position info</i>
---------	--

---

**Description**

The position information for each probe/feature is stored as an IRanges RangedData object. The locData functions allow this data to be accessed or re-set.

**Arguments**

object	GenoSet
value	RangedData describing features

**Value**

A GenoSet object

**Methods**

signature(object = "GenoSet") Get location data.  
signature(object = "GenoSet", value = "RangedData") Set location data.

**Author(s)**

Peter M. Haverty

**Examples**

```
data(genoset)
rd = locData(genoset.ds)
locData(genoset.ds) = rd
```

---

lr2cn	<i>Take vector or matrix of log2 ratios, convert to copynumber Utility function for converting log2ratio units (zero is normal) to copynumber units (two is normal)</i>
-------	---

---

**Description**

Take vector or matrix of log2 ratios, convert to copynumber Utility function for converting log2ratio units (zero is normal) to copynumber units (two is normal)

**Usage**

```
lr2cn(x)
```

**Arguments**

x                    numeric data in log2ratio values

**Value**

data of same type as "x" transformed into copynumber units

**Author(s)**

Peter M. Haverty <phaverty@gene.com>

**See Also**

cn2lr

---

lrr                    *Get lrr data*

---

**Description**

Get or Set the lrr assayData slot

**Arguments**

object              A BAFset object

**Details**

Get or Set the lrr assayData slot

**Value**

matrix

**Author(s)**

Peter M. Haverty

**Examples**

```
data(genoset)
lrr(baf.ds) # Returns assayDataElement called "lrr"
lrr(baf.ds) <- lrr(baf.ds) + 0.1
```



---

modeCenter	<i>Center continuous data on mode</i>
------------	---------------------------------------

---

**Description**

Copynumber data distributions are generally multi-modal. It is often assumed that the tallest peak represents "normal" and should therefore be centered on a log2ratio of zero. This function uses the density function to find the mode of the dominant peak and subtracts that value from the input data.

**Usage**

```
modeCenter(ds)
```

**Arguments**

ds	numeric matrix
----	----------------

**Value**

numeric matrix

**Author(s)**

Peter M. Haverty

**Examples**

```
modeCenter( matrix( rnorm(150, mean=0), ncol=3 ))
```

---

pos	<i>Positions for features</i>
-----	-------------------------------

---

**Description**

Chromosome position of features

**Arguments**

object	GRanges, RangedData or GenoSet
--------	--------------------------------

**Details**

Get chromosome position of features/ranges. Defined as floor of mean of start and end.

**Value**

numeric vector of feature positions within a chromosome

**Author(s)**

Peter Haverty

**Examples**

```

test.sample.names = LETTERS[11:13]
probe.names = letters[1:10]
gs = GenoSet(
  locData=RangedData(ranges=IRanges(start=1:10,width=1,names=probe.names),space=c(rep("chr1",4),rep("chr3",2),
  cn=matrix(31:60,nrow=10,ncol=3,dimnames=list(probe.names,test.sample.names)),
  pData=data.frame(matrix(LETTERS[1:15],nrow=3,ncol=5,dimnames=list(test.sample.names,letters[1:5]))),
  annotation="SNP6"
)
pos(gs) # 1:10
pos(locData(gs)) # The same

```

---

rangeColMeans

*Calculate column means for multiple ranges*


---

**Description**

Essentially colMeans with a loop, all in a .Call. Designed to take a 2-column matrix of row indices, bounds, for a matrix, x, and calculate mean for each range in each column (or along a single vector). bounds matrix need not cover all rows.

**Usage**

```
rangeColMeans(bounds, x)
```

**Arguments**

bounds            A two column integer matrix of row indices  
x                    A numeric matrix with rows corresponding to indices in bounds.

**Value**

A numeric matrix or vector, matching the form of x. One row for each row in bounds, one col for each col of x and appropriate dimnames. If x is a vector, just a vector with names from the rownames of bounds.

**Author(s)**

Peter M. Haverty &lt;phaverty@gene.com&gt;

**See Also**

Other "range summaries": [boundingIndices](#), [boundingIndices2](#), [boundingIndicesByChr](#), [rangeSampleMeans](#)

---

rangeSampleMeans	<i>Average features in ranges per sample</i>
------------------	--

---

### Description

This function takes per-feature genomic data and returns averages for each of a set of genomic ranges. The most obvious application is determining the copy number of a set of genes. The features corresponding to each gene are determined with boundingIndices such that all features with the bounds of a gene (overlaps). The features on either side of the gene unless those positions exactly match the first or last base covered by the gene. Therefore, genes falling between two features will at least cover two features. This is similar to rangeSampleMeans, but it checks the subject positions for being sorted and not being NA and also treats them as doubles, not ints. Range bounding performed by the boundingIndices function.

### Usage

```
rangeSampleMeans(query.rd, subject, assay.element)
```

### Arguments

query.rd	RangedData object representing genomic regions (genes) to be averaged.
subject	A GenoSet object or derivative
assay.element	character, name of element in assayData to use to extract data

### Value

numeric matrix of features in each range averaged by sample

### Author(s)

Peter M. Haverty

### See Also

Other "range summaries": [boundingIndices](#), [boundingIndices2](#), [boundingIndicesByChr](#), [rangeColMeans](#)

### Examples

```
data(genoset)
my.genes = RangedData( ranges=IRanges(start=c(35e6,128e6),end=c(37e6,129e6),names=c("HER2","CMYC")), space=c("
rangeSampleMeans( my.genes, baf.ds, "lrr" )
```

---

readGenoSet	<i>Load a GenoSet from a RData file</i>
-------------	---

---

**Description**

Given a rds file or a rda file with one object (a GenoSet or related object), load it, and return.

**Usage**

```
readGenoSet(path)
```

**Arguments**

path                    character, path to rds or rda file

**Value**

GenoSet or related object (only object in RData file)

**Author(s)**

Peter M. Haverty <phaverty@gene.com>

**Examples**

```
## Not run: ds = readGenoSet("/path/to/genoSet.RData")
## Not run: ds = readGenoSet("/path/to/genoSet.rda")
## Not run: ds = readGenoSet("/path/to/genoSet.rds")
```

---

runCBS	<i>Run CBS Segmentation</i>
--------	-----------------------------

---

**Description**

Utility function to run CBS's three functions on one or more samples

**Usage**

```
runCBS(data, locs, return.segs = FALSE, n.cores = 1,
        smooth.region = 2, outlier.SD.scale = 4,
        smooth.SD.scale = 2, trim = 0.025, alpha = 0.001)
```

**Arguments**

data	numeric matrix with continuous data in one or more columns
locs	RangeData, like locData slot of GenoSet
return.segs	logical, if true list of segment data.frames return, otherwise a DataFrame of Rle vectors. One Rle per sample.
n.cores	numeric, number of cores to ask mclapply to use
smooth.region	number of positions to left and right of individual positions to consider when smoothing single point outliers
outlier.SD.scale	number of SD single points must exceed smooth.region to be considered an outlier
smooth.SD.scale	floor used to reset single point outliers
trim	fraction of sample to smooth
alpha	pvalue cutoff for calling a breakpoint

**Details**

Takes care of running CBS segmentation on one or more samples. Makes appropriate input, smooths outliers, and segment

**Value**

data frame of segments from CBS

**Author(s)**

Peter M. Haverty

**See Also**

Other "segmented data": [bounds2Rle](#), [segPairTable](#), [segPairTable](#), [segPairTable](#), [segs2RangedData](#), [segs2Rle](#), [segs2RleDataFrame](#), [segTable](#), [segTable](#), [segTable](#)

**Examples**

```
sample.names = paste("a", 1:2, sep="")
probe.names = paste("p", 1:30, sep="")
ds = matrix(c(c(rep(5,20), rep(3,10)), c(rep(2,10), rep(7,10), rep(9,10))), ncol=2, dimnames=list(probe.names, sample.names))
locs = RangedData(ranges=IRanges(start=c(1:20, 1:10), width=1, names=probe.names), space=paste("chr", c(rep(1,20), rep(1,10))))

seg.rle.result = DataFrame( a1 = Rle(c(rep(5,20), rep(3,10))), a2 = Rle(c(rep(2,10), rep(7,10), rep(9,10))), row.names=sample.names)
seg.list.result = list(
  a1 = data.frame( ID=rep("a1",2), chrom=factor(c("chr1","chr2")), loc.start=c(1,1), loc.end=c(20,10), num.mark=c(5,3)),
  a2 = data.frame( ID=rep("a2",3), chrom=factor(c("chr1","chr1","chr2")), loc.start=c(1,11,1), loc.end=c(10,20,10), num.mark=c(2,1,1))
)

runCBS(ds,locs) # Should give seg.rle.result
runCBS(ds,locs,return.segs=TRUE) # Should give seg.list.result
```

---

sampleNames	<i>Get sampleNames from a GenoSet</i>
-------------	---------------------------------------

---

**Description**

Get sampleNames from a GenoSet

**Arguments**

object	GenoSet
--------	---------

**Value**

character vector with names of samples

**Examples**

```
data(genoset)
head(sampleNames(cn.ds))
```

---

segPairTable	<i>Convert Rle objects to tables of segments</i>
--------------	--

---

**Description**

Like segTable, but for two Rle objects. Takes a pair of Rle or DataFrames with Rle columns and makes one or more data.frames with bounds of each new segment. Rle objects are broken up so that each resulting segment has one value from each Rle. For a DataFrame, the argument stack combines all of the individual data.frames into one large data.frame and adds a "Sample" column of sample ids.

**Arguments**

x	Rle or list/DataFrame of Rle vectors
y	Rle or list/DataFrame of Rle vectors
locs	RangedData with rows corresponding to rows of df
chr.ind	matrix, like from chrIndices method
start	integer, vector of feature start positions
end	integer, vector of feature end positions
factor.chr	scalar logical, make 'chrom' column a factor?
stack	logical, rbind list of segment tables for each sample and add "Sample" column?

**Details**

For a Rle, the user can provide `locs` or `chr.ind`, `start` and `stop`. The latter is surprisingly much faster and this is used in the `DataFrame` version.

**Value**

one or a list of `data.frames` with columns `chrom`, `loc.start`, `loc.end`, `num.mark`, `seg.mean`

**Author(s)**

Peter M. Haverty

**See Also**

Other "segmented data": [bounds2Rle](#), [runCBS](#), [segs2RangedData](#), [segs2Rle](#), [segs2RleDataFrame](#), [segTable](#), [segTable](#), [segTable](#)

**Examples**

```
cn = Rle(c(3,4,5,6),rep(3,4))
loh = Rle(c(2,4,6,8,10,12),rep(2,6))
start = c(9:11,4:9,15:17)
end = start
locs = RangedData(IRanges(start=start,end=end),space=c(rep("chr1",3),rep("chr2",6),rep("chr3",3)))
segPairTable(cn,loh,locs)
```

---

segs2RangedData

*Make a RangedData from segments*

---

**Description**

Starting from a `data.frame` of segments, like from `CBS` and `segTable`, organize as a `RangedData`. Label data "score", so it can easily be made into various genome browser formats using `rtracklayer`.

**Usage**

```
segs2RangedData(segs)
```

**Arguments**

`segs` `data.frame`, like from segment in `DNAcopy` or `segTable`

**Value**

`RangedData`

**Author(s)**

Peter M. Haverty <phaverty@gene.com>

**See Also**

Other "segmented data": [bounds2Rle](#), [runCBS](#), [segPairTable](#), [segPairTable](#), [segPairTable](#), [segs2Rle](#), [segs2RleDataFrame](#), [segTable](#), [segTable](#), [segTable](#)

---

 segs2Rle

*Make Rle from segments for one sample*


---

**Description**

Take output of CBS, make Rle representing all features in 'locs' ranges. CBS output contains run length and run values for genomic segments, which could very directly be converted into a Rle. However, as NA values are often removed, especially for mBAF data, these run lengths do not necessarily cover all features in every sample. Using the start and top positions of each segment and the location of each feature, we can make a Rle that represents all features.

**Usage**

```
segs2Rle(segs, locs)
```

**Arguments**

segs	data.frame of segments, formatted as output of segment function from DNACopy package
locs	RangedData, like locData slot of a GenoSet

**Value**

Rle with run lengths and run values covering all features in the data set.

**Author(s)**

Peter M. Haverty <phaverty@gene.com>

**See Also**

Other "segmented data": [bounds2Rle](#), [runCBS](#), [segPairTable](#), [segPairTable](#), [segPairTable](#), [segs2RangedData](#), [segs2RleDataFrame](#), [segTable](#), [segTable](#), [segTable](#)

**Examples**

```
data(genoset)
segs = runCBS( lrr(baf.ds), locData(baf.ds), return.segs=TRUE )
segs2Rle( segs[[1]], locData(baf.ds) ) # Take a data.frame of segments, say from DNACopy's segment function, and r
```



---

segs2RleDataFrame	<i>CBS segments to probe matrix</i>
-------------------	-------------------------------------

---

**Description**

Given segments, make a DataFrame of Rle objects for each sample

**Usage**

```
segs2RleDataFrame(seg.list, locs)
```

**Arguments**

seg.list	list, list of data frames, one per sample, each is result from CBS
locs	locData from a GenoSet object

**Details**

Take table of segments from CBS, convert DataTable of Rle objects for each sample.

**Value**

DataFrame of Rle objects with nrows same as locs and one column for each sample

**Author(s)**

Peter Haverty

**See Also**

Other "segmented data": [bounds2Rle](#), [runCBS](#), [segPairTable](#), [segPairTable](#), [segPairTable](#), [segs2RangedData](#), [segs2Rle](#), [segTable](#), [segTable](#), [segTable](#)

**Examples**

```
data(genoset)
seg.list = runCBS( lrr(baf.ds), locData(baf.ds), return.segs=TRUE )
segs2RleDataFrame( seg.list, locData(baf.ds) ) # Loop segs2Rle on list of data.frames in seg.list
```

---

segTable	<i>Convert Rle objects to tables of segments</i>
----------	--

---

### Description

Like the inverse of `segs2Rle` and `segs2RleDataFrame`. Takes a `Rle` or a `DataFrame` with `Rle` columns and the `locData` `RangedData` both from a `GenoSet` object and makes a list of `data.frames` each like the result of `CBS`'s `segment`. Note the `loc.start` and `loc.stop` will correspond exactly to probe locations in `locData` and the input to `segs2RleDataFrame` are not necessarily so. For a `DataFrame`, the argument `stack` combines all of the individual `data.frames` into one large `data.frame` and adds a "Sample" column of sample ids.

### Arguments

<code>object</code>	<code>Rle</code> or <code>list/DataFrame</code> of <code>Rle</code> vectors
<code>locs</code>	<code>RangedData</code> with rows corresponding to rows of <code>df</code>
<code>chr.ind</code>	matrix, like from <code>chrIndices</code> method
<code>start</code>	integer, vector of feature start positions
<code>end</code>	integer, vector of feature end positions
<code>factor.chr</code>	scalar logical, make 'chrom' column a factor?
<code>stack</code>	logical, <code>rbind</code> list of segment tables for each sample and add "Sample" column?

### Details

For a `Rle`, the user can provide `locs` or `chr.ind`, `start` and `stop`. The latter is surprisingly much faster and this is used in the `DataFrame` version.

### Value

one or a list of `data.frames` with columns `chrom`, `loc.start`, `loc.end`, `num.mark`, `seg.mean`

### Author(s)

Peter M. Haverty

### See Also

Other "segmented data": [bounds2Rle](#), [runCBS](#), [segPairTable](#), [segPairTable](#), [segPairTable](#), [segs2RangedData](#), [segs2Rle](#), [segs2RleDataFrame](#)

**Examples**

```

data(genoset)
seg.list = runCBS( lrr(baf.ds), locData(baf.ds), return.segs=TRUE )
df = segs2RleDataFrame( seg.list, locData(baf.ds) ) # Loop segs2Rle on list of data.frames in seg.list
assayDataElement( baf.ds, "lrr.segs" ) = df
segTable( df, locData(baf.ds) )
segTable( assayDataElement(baf.ds,"lrr.segs"), locData(baf.ds) )
segTable( assayDataElement(baf.ds,"lrr.segs")[,1], locData(baf.ds), sampleNames(baf.ds)[1] )

```

---

subsetAssayData	<i>Subset assayData</i>
-----------------	-------------------------

---

**Description**

Subset or re-order assayData

**Usage**

```
subsetAssayData(orig, i, j, ..., drop = FALSE)
```

**Arguments**

orig	assayData environment
i	row indices
j	col indices
...	Additional args to give to subset operator
drop	logical, drop dimensions when subsetting with single value?

**Details**

Subset or re-order assayData locked environment, environment, or list. Shamelessly stolen from "[" method in Biobase version 2.8 along with guts of assayDataStorageMode()

**Value**

assayData data structure

**Author(s)**

Peter M. Haverty

**Examples**

```

data(genoset)
ad = assayData(genoset.ds)
small.ad = subsetAssayData(ad,1:5,2:3)

```

---

toGenomeOrder	<i>Set a GRanges, GenoSet, or RangedData to genome order</i>
---------------	--

---

### Description

Returns a re-ordered object sorted by chromosome and start position. If `strict=TRUE`, then chromosomes must be in order specified by `chrOrder`. If `ds` is already ordered, no re-ordering is done. Therefore, checking order with `isGenomeOrder`, is unnecessary if order will be corrected if `isGenomeOrder` is `FALSE`.

### Arguments

<code>ds</code>	GenoSet, GRanges, or RangedData
<code>strict</code>	logical, should chromosomes be in order specified by <code>chrOrder</code> ?

### Details

`toGenomeOrder` for `GRanges` differs from `sort` in that it orders by chromosome and start position only, rather than chromosome, strand, start, and width.

### Value

re-ordered `ds`

### Author(s)

Peter M. Haverty

### See Also

Other "genome ordering": [chrOrder](#), [isGenomeOrder](#), [isGenomeOrder](#), [isGenomeOrder](#)

### Examples

```
data(genoset)
toGenomeOrder( baf.ds, strict=TRUE )
toGenomeOrder( baf.ds, strict=FALSE )
toGenomeOrder( locData(baf.ds) )
```

---

universe

*Get and set the genome universe annotation.*


---

### Description

Genome universe for locData

Set genome universe

Get start of location for each feature

Get end of location for each feature

Get width of location for each feature

Get chromosome names

Get ranges from locData slot

locData slot holds a RangedData, which keeps the chromosome of each feature in a factor names 'space'. The ranges method on a GenoSet is deprecated. Please use space(locData(x)) or seq-names(locData(x)) as appropriate for RangedData or GRanges.

Get elementLengths from locData slot

### Arguments

x	GenoSet or GRanges
x	GenoSet or GRanges
value	character, new universe string, e.g. hg19
x	GenoSet
x	GenoSet
x	GenoSet
x	GenoSet
x	GenoSet
x	GenoSet
x	GenoSet
x	GenoSet
i	character, RangedData, logical, integer
j	character, RangedData, logical, integer
k	character or integer
drop	logical drop levels of space factor?
...	additional subsetting args

**Details**

The genome positions of the features in `locData`. The UCSC notation (e.g. hg18, hg19, etc.) should be used. For a `GRanges`, the first value is returned if there are multiple.

Get chromosome names, which are the names of the `locData` slot. The `names` method on a `GenoSet` is deprecated. Please use `chrNames`.

Get ranges from `locData` slot. The `ranges` method on a `GenoSet` is deprecated. Please use `ranges(locData(x))`.

Get `elementLengths` from `locData` slot

**Value**

character, e.g. hg19

updated copy of x

integer

integer

integer

character

character

factor

character

**Author(s)**

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Peter M. Haverty

Peter Haverty

**Examples**

```
data(genoset)
  universe(locData.rd)
  universe(locData.rd) = "hg19"
data(genoset)
chr(genoset.ds)
start(genoset.ds)
end(genoset.ds)
chrNames(genoset.ds)
elementLengths(genoset.ds) # Returns the number of probes per chromosome
```

```
data(genoset)
  genoset.ds[1:5,2:3] # first five probes and samples 2 and 3
  genoset.ds[ , "K"] # Sample called K
rd = RangedData(ranges=IRanges(start=seq(from=15e6,by=1e6,length=7),width=1),names=letters[8:14],space=rep("c",7))
genoset.ds[ rd, "K" ] # sample K and probes overlapping those in rd, which overlap specified ranges on chr17
```

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