

# Package ‘VanillaICE’

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**Title** A Hidden Markov Model for high throughput genotyping arrays

**Description**

Hidden Markov Models for characterizing chromosomal alteration in high throughput SNP arrays.

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ArrayViews-class      *ArrayViews class, constructor, and methods*

---

### Description

ArrayViews provides views to the low-level data – log R ratios, B allele frequencies, and genotypes that are stored in parsed files on disk, often scaled and coerced to an integer. Accessors to the low-level data are provided that extract the marker-level summaries from disk, rescaling when appropriate.

### Usage

```
ArrayViews(
  class = "ArrayViews",
  colData,
  rowRanges = GRanges(),
  sourcePaths = character(),
  scale = 1000,
  sample_ids,
  parsedPath = getwd(),
  lrrFiles = character(),
  baffFiles = character(),
  gtFiles = character()
)

## S4 method for signature 'ArrayViews,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]

colnames(x) <- value

## S4 method for signature 'ArrayViews'
colnames(x, do.NULL = TRUE, prefix = "col")

## S4 method for signature 'ArrayViews'
x$name

## S4 replacement method for signature 'ArrayViews'
x$name <- value

## S4 method for signature 'ArrayViews'
show(object)

## S4 method for signature 'ArrayViews'
sapply(X, FUN, ..., simplify = TRUE, USE.NAMES = TRUE)

## S4 method for signature 'ArrayViews'
ncol(x)
```

```
## S4 method for signature 'ArrayViews'
nrow(x)
```

```
## S4 method for signature 'ArrayViews'
dim(x)
```

```
## S4 method for signature 'ArrayViews'
start(x)
```

### Arguments

class	character string
colData	DataFrame
rowRanges	GRanges object
sourcePaths	character string provide complete path to plain text source files (one file per sample) containing log R ratios and B allele frequencies
scale	log R ratios and B allele frequencies can be stored as integers on disk to increase IO speed. If scale =1, the raw data is not transformed. If scale = 1000 (default), the log R ratios and BAFs are multiplied by 1000 and coerced to an integer.
sample_ids	character vector indicating how to name samples. Ignored if colData is specified.
parsedPath	character vector indicating where parsed files should be saved
lrrFiles	character vector of file names for storing log R ratios
bafFiles	character vector of file names for storing BAFs
gtFiles	character vector of file names for storing genotypes
x	a ArrayViews object
i	numeric vector or missing
j	numeric vector or missing
...	additional arguments to FUN
drop	ignored
value	a character-string vector
do.NULL	ignored
prefix	ignored
name	character string indicating name in colData slot of ArrayViews object
object	a ArrayViews object
X	a ArrayViews object
FUN	a function to apply to each column of X
simplify	logical indicating whether result should be simplified
USE.NAMES	whether the output should be a named vector

**Slots**

colData A character string

rowRanges A DataFrame. **WARNING:** The accessor for this slot is rowRanges, not rowRanges!

index A GRanges object

sourcePaths A character string providing complete path to source files (one file per sample) containing low-level summaries (Log R ratios, B allele frequencies, genotypes)

scale A length-one numeric vector

parsedPath A character string providing full path to where parsed files should be saved

lrrFiles character vector of filenames for log R ratios

bafFiles character vector of filenames for BAFs

gtFiles character vector of filenames for genotypes

**See Also**

[CopyNumScanParams](#) [parseSourceFile](#)

**Examples**

```

ArrayViews()
## From unit test
require(BSgenome.Hsapiens.UCSC.hg18)
require(data.table)
extdir <- system.file("extdata", package="VanillaICE", mustWork=TRUE)
features <- suppressWarnings(fread(file.path(extdir, "SNP_info.csv")))
fgr <- GRanges(paste0("chr", features$Chr), IRanges(features$Position, width=1),
              isSnp=features[["Intensity Only"]]==0)
fgr <- SnpGRanges(fgr)
names(fgr) <- features[["Name"]]
bsgenome <- BSgenome.Hsapiens.UCSC.hg18
seqlevels(fgr, pruning.mode="coarse") <- seqlevels(bsgenome)[seqlevels(bsgenome) %in% seqlevels(fgr)]
seqinfo(fgr) <- seqinfo(bsgenome)[seqlevels(fgr),]
fgr <- sort(fgr)
files <- list.files(extdir, full.names=TRUE, recursive=TRUE, pattern="FinalReport")
ids <- gsub(".rds", "", gsub("FinalReport", "", basename(files)))
views <- ArrayViews(rowRanges=fgr,
                   sourcePaths=files,
                   sample_ids=ids)

lrrFile(views)
## view of first 10 markers and samples 3 and 5
views <- views[1:10, c(3,5)]

```

---

baumWelchUpdate	<i>Function for updating parameters for emission probabilities</i>
-----------------	--

---

**Description**

This function is not meant to be called directly by the user. It is exported in the package NAMESPACE for internal use by other BioC packages.

**Usage**

```
baumWelchUpdate(param, assay_list)
```

**Arguments**

param	A container for the HMM parameters
assay_list	list of log R ratios and B allele frequencies

---

calculateEmission	<i>Calculate the emission probabilities for the 6-state HMM</i>
-------------------	---

---

**Description**

Given the data and an object containing parameters for the HMM, this function computes emission probabilities. This function is not intended to be called by the user and is exported for internal use by other BioC packages.

**Usage**

```
calculateEmission(x, param = EmissionParam())
```

**Arguments**

x	list of low-level data with two elements: a numeric vector of log R ratios and a numeric vector of B allele frequencies
param	parameters for the 6-state HMM

**Value**

A matrix of emission probabilities. Column correspond to the HMM states and rows correspond to markers on the array (SNPs and nonpolymorphic markers)

**See Also**

baumWelchUpdate

---

`cnvFilter`*Filter the HMM-derived genomic ranges for copy number variants*

---

## Description

The HMM-derived genomic ranges are represented as a GRanges-derived object. `cnvFilter` returns a GRanges object using the filters stipulated in the `filters` argument.

## Usage

```
cnvFilter(object, filters = FilterParam())

cnvSegs(object, filters = FilterParam(state = c("1", "2", "5", "6")))

duplication(object, filters = FilterParam(state = c("5", "6")))

deletion(object, filters = FilterParam(state = c("1", "2")))

hemizygous(object, filters = FilterParam(state = "2"))

homozygous(object, filters = FilterParam(state = "1"))

## S4 method for signature 'HMM'
cnvSegs(object, filters = FilterParam(state = as.character(c(1, 2, 5, 6))))

## S4 method for signature 'HMMList'
segs(object)

## S4 method for signature 'HMMList'
hemizygous(object)

## S4 method for signature 'HMMList'
homozygous(object)

## S4 method for signature 'HMMList'
duplication(object)

## S4 method for signature 'HMMList'
cnvSegs(object, filters = FilterParam(state = as.character(c(1, 2, 5, 6))))

## S4 method for signature 'HMMList'
cnvFilter(object, filters = FilterParam())

## S4 method for signature 'HmmGRanges'
cnvSegs(object, filters = FilterParam(state = as.character(c(1, 2, 5, 6))))
```



**Arguments**

object            see showMethods(cnvFilter)  
 filters           a [FilterParam](#) object

**See Also**

[FilterParam](#)

**Examples**

```
data(snp_exp)
fit <- hmm2(snp_exp)
segs(fit) ## all intervals
cnvSegs(fit)
filter_param <- FilterParam(probability=0.95, numberFeatures=10, state=c("1", "2"))
cnvSegs(fit, filter_param)
filter_param <- FilterParam(probability=0.5, numberFeatures=2, state=c("1", "2"))
cnvSegs(fit, filter_param)
hemizygous(fit)
homozygous(fit)
duplication(fit)
```

---

 cn\_means

*A parameter class for computing Emission probabilities*

---

**Description**

Parameters for computing emission probabilities for a 6-state HMM, including starting values for the mean and standard deviations for log R ratios (assumed to be Gaussian) and B allele frequencies (truncated Gaussian), and initial state probabilities.

This function is exported primarily for internal use by other BioC packages.

**Usage**

```
cn_means(object)

cn_sds(object)

baf_means(object)

baf_sds(object)

baf_means(object) <- value

baf_sds(object) <- value

cn_sds(object) <- value
```

```

cn_means(object) <- value

EmissionParam(
  cn_means = CN_MEANS(),
  cn_sds = CN_SDS(),
  baf_means = BAF_MEANS(),
  baf_sds = BAF_SDS(),
  initial = rep(1/6, 6),
  EMupdates = 5L,
  CN_range = c(-5, 3),
  temper = 1,
  p_outlier = 1/100,
  modelHomozygousRegions = FALSE
)

EMupdates(object)

## S4 method for signature 'EmissionParam'
show(object)

```

### Arguments

object	see showMethods("EMupdates")
value	numeric vector
cn_means	numeric vector of starting values for log R ratio means (order is by copy number state)
cn_sds	numeric vector of starting values for log R ratio standard deviations (order is by copy number state)
baf_means	numeric vector of starting values for BAF means ordered. See example for details on how these are ordered.
baf_sds	numeric vector of starting values for BAF means ordered. See example for details on how these are ordered.
initial	numeric vector of initial state probabilities
EMupdates	number of EM updates
CN_range	the allowable range of log R ratios. Log R ratios outside this range are thresholded.
temper	Emission probabilities can be tempered by $\text{emit}^{\text{temper}}$ . This is highly experimental.
p_outlier	probability that an observation is an outlier (assumed to be the same for all markers)
modelHomozygousRegions	logical. If FALSE (default), the emission probabilities for BAFs are modeled from a mixture of truncated normals and a Unif(0,1) where the mixture probabilities are given by the probability that the SNP is heterozygous. See Details below for a discussion of the implications.

**Details**

The log R ratios are assumed to be emitted from a normal distribution with a mean and standard deviation that depend on the latent copy number. Similarly, the BAFs are assumed to be emitted from a truncated normal distribution with a mean and standard deviation that depends on the latent number of B alleles relative to the total number of alleles (A+B).

**Value**

numeric vector

**Details**

When `modelHomozygousRegions` is FALSE (the default in versions  $\geq 1.28.0$ ), emission probabilities for B allele frequencies are calculated from a mixture of a truncated normal densities and a `Unif(0,1)` density with the mixture probabilities given by the probability that a SNP is homozygous. In particular, let  $p$  denote a 6 dimensional vector of density estimates from a truncated normal distribution for the latent genotypes 'A', 'B', 'AB', 'AAB', 'ABB', 'AAAB', and 'ABBB'. The probability that a genotype is homozygous is estimated as

$$prHom = (p["A"] + p["B"])/sum(p)$$

and the probability that the genotype is heterozygous (any latent genotype that is not 'A' or 'B') is given by

$$prHet = 1 - prHom$$

Since the density of a `Unif(0,1)` is 1, the 6-dimensional vector of emission probability at a SNP is given by

$$emit = prHet * p + (1 - prHet)$$

The above has the effect of minimizing the influence of BAFs near 0 and 1 on the state path estimated by the Viterbi algorithm. In particular, the emission probability at homozygous SNPs will be virtually the same for states 3 and 4, but at heterozygous SNPs the emission probability for state 3 will be an order of magnitude greater for state 3 (diploid) compared to state 4 (diploid region of homozygosity). The advantage of this parameterization are fewer false positive hemizygous deletion calls. [ Log R ratios tend to be more sensitive to technical sources of variation than the corresponding BAFs/genotypes. Regions in which the log R ratios are low due to technical sources of variation will be less likely to be interpreted as evidence of copy number loss if heterozygous genotypes have more 'weight' in the emission estimates than homozygous genotypes. ] The trade-off is that only states estimated by the HMM are those with copy number alterations. In particular, copy-neutral regions of homozygosity will not be called.

By setting `modelHomozygousRegions = TRUE`, the emission probabilities at a SNP are given simply by the  $p$  vector described above and copy-neutral regions of homozygosity will be called.#'

**Examples**

```

ep <- EmissionParam()
cn_means(ep)
ep <- EmissionParam()
cn_sds(ep)
ep <- EmissionParam()
baf_means(ep)
ep <- EmissionParam()
baf_sds(ep)
ep <- EmissionParam()
baf_means(ep) <- baf_means(ep)
ep <- EmissionParam()
baf_sds(ep) <- baf_sds(ep)
ep <- EmissionParam()
cn_sds(ep) <- cn_sds(ep)
ep <- EmissionParam()
cn_means(ep) <- cn_means(ep)
ep <- EmissionParam()
show(ep)
cn_means(ep)
cn_sds(ep)
baf_means(ep)
baf_sds(ep)

```

---

CopyNumScanParams-class

*Parameters for parsing source files containing SNP-array processed data, such as GenomeStudio files for the Illumina platform*

---

**Description**

Raw SNP array processed files have headers and variable labels that may depend the software, how the output files was saved, the software version, and other factors. The purpose of this container is to collect the parameters relevant for reading in the source files for a particular project in a single container. This may require some experimentation as the example illustrates. The function `fread` in the `data.table` package greatly simplifies this process.

**Usage**

```

CopyNumScanParams(
  cnvar = "Log R Ratio",
  bafvar = "B Allele Freq",
  gtvar = c("Allele1 - AB", "Allele2 - AB"),
  index_genome = integer(),
  select = integer(),
  scale = 1000,
  row.names = 1L
)

```

```
## S4 method for signature 'CopyNumScanParams'
show(object)
```

### Arguments

cnvar	length-one character vector providing name of variable for log R ratios
bafvar	length-one character vector providing name of variable for B allele frequencies
gtvar	length-one character vector providing name of variable for genotype calls
index_genome	integer vector indicating which rows of the of the source files (e.g., GenomeStudio) to keep. By matching on a sorted GRanges object containing the feature annotation (see example), the information on the markers will also be sorted.
select	integer vector specifying indicating which columns of the source files to import (see examples)
scale	length-one numeric vector for rescaling the raw data and coercing to class integer. By default, the low-level data will be scaled and saved on disk as integers.
row.names	length-one numeric vector indicating which column the SNP names are in
object	a CopyNumScanParams object

### Slots

index\_genome an integer vector

cnvar the column label for the log R ratios

bafvar the column label for the B allele frequencies

gtvar the column label(s) for the genotypes

scale length-one numeric vector indicating how the low-level data should be scaled prior to saving on disk

select numeric vector indicating which columns to read

row.names length-one numeric vector indicating which column the SNP names are in

### See Also

[ArrayViews parseSourceFile](#)

### Examples

```
CopyNumScanParams() ## empty container
```

---

doUpdate	<i>Helper function to determine whether to update the HMM parameters via the Baum-Welch algorithm</i>
----------	---

---

### Description

This function is not intended to be called directly by the user, and is exported only for internal use by other BioC packages.

### Usage

```
doUpdate(param)
```

### Arguments

param            An object containing parameters for the HMM

### See Also

[HmmParam](#)

---

dropDuplicatedMapLocs	<i>Drop markers on the same chromosome having the same genomic coordinates</i>
-----------------------	--

---

### Description

If there are multiple markers on the same chromosome with the same annotated position, only the first is kept.

### Usage

```
dropDuplicatedMapLocs(object)
```

### Arguments

object            a container for which the methods seqnames and start are defined

### Value

an object of the same class with duplicated genomic positions removed

**Examples**

```

data(snp_exp)
g <- rowRanges(snp_exp)
## duplicate the first row
g[length(g)] <- g[1]
rowRanges(snp_exp) <- g
snp_exp2 <- dropDuplicatedMapLocs(snp_exp)

```

---

dropSexChrom                      *Filter sex chromosomes*

---

**Description**

Removes markers on chromosomes X and Y.

**Usage**

```
dropSexChrom(object)
```

**Arguments**

object                      an object for which the methods seqnames and rowRanges are defined.

**Value**

an object of the same class as the input

---

emission                      *Methods to set and get emission probabilities*

---

**Description**

Get or set a matrix of emission probabilities. This function is exported primarily for internal use by other BioC packages.

**Usage**

```
emission(object)
```

```
emission(object) <- value
```

**Arguments**

object                      see showMethods(emission)  
value                      a matrix of emission probabilities

**Value**

matrix

---

emissionParam	<i>Accessor for parameters used to compute emission probabilities</i>
---------------	---

---

### Description

Parameters for computing emission probabilities include the starting values for the Baum Welch update and initial state probabilities.

### Usage

```
emissionParam(object)

emissionParam(object) <- value
```

### Arguments

object	an object of class EmissionParam
value	an object of class EmissionParam

### Value

[EmissionParam](#) instance

### Examples

```
hparam <- HmmParam()
emissionParam(hparam)
ep <- EmissionParam()
cn_means(ep) <- log2(c(.1/2, 1/2, 2/2, 2/2, 3/2, 4/2))
emissionParam(hparam) <- ep
```

---

FilterParam-class	<i>Container for the common criteria used to filtering genomic ranges</i>
-------------------	---

---

### Description

The maximum a posteriori estimate of the trio copy number state for each genomic range is represented in a [GRanges](#)-derived class. Ultimately, these ranges will be filtered based on the trio copy number state (e.g., denovo deletions), size, number of features (SNPs), or chromosome. FilterParam is a container for the parameters commonly used to filter the genomic ranges.



**Usage**

```

FilterParam(
  probability = 0.99,
  numberFeatures = 10,
  seqnames = paste0("chr", c(1:22, "X", "Y")),
  state = as.character(1:6),
  width = 1L
)

## S4 method for signature 'FilterParam'
probability(object)

## S4 method for signature 'FilterParam'
state(object)

## S4 method for signature 'FilterParam'
show(object)

```

**Arguments**

probability	mininum probability for the call
numberFeatures	mininum number of SNPs/nonpolymorphic features in a region
seqnames	the seqnames (character string or R1e to keep)
state	character: the HMM states to keep
width	the minimum widht of a region
object	a FilterParam object

**Slots**

probability a length-one numeric vector indicating the minimum posterior probability for the called state. Genomic intervals with posterior probabilities below probability will be filtered.

numberFeatures a positive integer indicating the minimum number of features in a segment

seqnames a character vector of seqnames to select (i.e., 'chr1' for only those intervals on chromosome 1)

width positive integer indicating the minimal width of genomic intervals

state character string indicating which hidden Markov model states to select

**See Also**

[cnvFilter](#) [cnvSegs](#) [hmm2](#)

**Examples**

```
fp <- FilterParam()
width(fp)
numberFeatures(fp)
seqnames(fp)
## To select CNV segments for which
## - the CNV call has a 'posterior' probability of at least 0.95
## - the number of features is at least 10
## - the HMM states are 1 (homozygous deletion) or 2 (hemizygous deletion)
FilterParam(probability=0.95, numberFeatures=10, state=c("1", "2"))
```

---

filters	<i>Accessor for HMM filter parameters</i>
---------	---

---

**Description**

Accessor for HMM filter parameters

**Usage**

```
filters(object)
```

**Arguments**

object            see showMethods(filters)

---

genotypes	<i>Accessor for SNP genotypes</i>
-----------	-----------------------------------

---

**Description**

Extract SNP genotypes. Genotypes are assumed to be represented as integers: 1=AA, 2=AB, 3=BB.

**Usage**

```
genotypes(object)

## S4 method for signature 'ArrayViews'
lrr(object)

## S4 method for signature 'ArrayViews'
baf(object)

## S4 method for signature 'ArrayViews'
genotypes(object)
```

```
## S4 method for signature 'SnpArrayExperiment'  
baf(object)  
  
## S4 method for signature 'SnpArrayExperiment'  
copyNumber(object)  
  
## S4 method for signature 'SnpArrayExperiment'  
lrr(object)  
  
## S4 method for signature 'SnpArrayExperiment'  
genotypes(object)
```

**Arguments**

object            see showMethods("genotypes")

**See Also**

copyNumber

---

getExampleSnpExperiment

*Create an example SnpArrayExperiment from source files containing marker-level genomic data that are provided in this package*

---

**Description**

Create an example SnpArrayExperiment from source files containing marker-level genomic data that are provided in this package

**Usage**

```
getExampleSnpExperiment(bsgenome)
```

**Arguments**

bsgenome            a BSgenome object

**Value**

A [SnpArrayExperiment](#)

**Examples**

```
## Not run:
  if(require("BSgenome.Hsapiens.UCSC.hg18")){
    genome <- BSgenome.Hsapiens.UCSC.hg18
    snp_exp <- getExampleSnpExperiment(genome)
  }

## End(Not run)
```

---

getHmmParams	<i>Accessor for HMM model parameters</i>
--------------	--

---

**Description**

Accessor for HMM model parameters

**Usage**

```
getHmmParams(object)
```

**Arguments**

object            see showMethods(HmmParam)

**Examples**

```
hmm_object <- HMM()
getHmmParams(hmm_object)
```

---

HMM-class	<i>Container for the segmented data and the 6-state HMM model parameters</i>
-----------	--

---

**Description**

The constructor HMM creates and object of class HMM. Not typically called directly by the user.

**Usage**

```
HMM(
  granges = GRanges(),
  param = HmmParam(),
  posterior = matrix(),
  filters = FilterParam()
)
```

```
## S4 method for signature 'HMM'  
state(object)
```

```
## S4 method for signature 'HMM'  
show(object)
```

### Arguments

granges	a GRanges object
param	a HmmParam object
posterior	matrix of posterior probabilities
filters	an object of class FilterParam
object	a HMM object

### Slots

granges	a GRanges object
param	a HmmParam object
posterior	a matrix of posterior probabilities
filters	a FilterParam object

### See Also

[hmm2](#)

### Examples

```
data(snp_exp)  
hmm_list <- hmm2(snp_exp[,1])  
resultsFirstSample <- hmm_list[[1]]  
resultsFirstSample  
HMM()
```

---

hmm2

*Fit a 6-state HMM to log R ratios and B allele frequencies estimated from SNP arrays*

---

### Description

This function is intended for estimating the integer copy number from germline or DNA of clonal origin using a 6-state HMM. The states are homozygous deletion, hemizygous deletion, diploid copy number, diploid region of homozygosity, single copy gain, and two+ copy gain. Because heterozygous markers are more informative for copy number than homozygous markers and regions of homozygosity are common in normal genomes, we currently computed a weighted average of the BAF emission matrix with a uniform 0,1 distribution by the probability that the marker is heterozygous, thereby downweighting the contribution of homozygous SNPs to the likelihood. In addition

to making the detection of copy-neutral regions of homozygosity less likely, it also helps prevent confusing hemizygous deletions with copy neutral regions of homozygosity – the former would be driven mostly by the log R ratios. This is experimental and subject to change.

### Usage

```
hmm2(
  object,
  emission_param = EmissionParam(),
  transition_param = TransitionParam(),
  ...
)

## S4 method for signature 'SnpArrayExperiment'
hmm2(
  object,
  emission_param = EmissionParam(),
  transition_param = TransitionParam(),
  ...
)

## S4 method for signature 'oligoSnpSet'
hmm2(
  object,
  emission_param = EmissionParam(),
  transition_param = TransitionParam(),
  ...
)

## S4 method for signature 'ArrayViews'
hmm2(
  object,
  emission_param = EmissionParam(),
  transition_param = TransitionParam(),
  tolerance = 2,
  verbose = FALSE,
  ...
)
```

### Arguments

object	A <a href="#">SnpArrayExperiment</a>
emission_param	A <a href="#">EmissionParam</a> object
transition_param	A <a href="#">TransitionParam</a> object
...	currently ignored
tolerance	length-one numeric vector. When the difference in the log-likelihood of the Viterbi state path between successive models (updated by Baum Welch) is less

than the tolerance, no additional model updates are performed.  
 verbose            logical. Whether to display messages indicating progress.

### Details

The `hmm2` method allows parallelization across samples using the `foreach` paradigm. Parallelization is automatic when enabled via packages such as `snow/doSNOW`.

### Examples

```
tp <- TransitionParam()
TransitionParam(taup=1e12)
data(snp_exp)
emission_param <- EmissionParam(temper=1/2)
fit <- hmm2(snp_exp, emission_param)
unlist(fit)
cnvSegs(fit)
## There is too little data to infer cnv reliably in this trivial example.
## To illustrate filtering options on the results, we select
## CNVs for which
## - the CNV call has a posterior probability of at least 0.5
## - the number of features is 2 or more
## - the HMM states are 1 (homozygous deletion) or 2 (hemizygous deletion)
fp <- FilterParam(probability=0.5, numberFeatures=2, state=c("1", "2"))
cnvSegs(fit, fp)
## for parallelization
## Not run:
  library(snow)
  library(doSNOW)
  cl <- makeCluster(2, type = "SOCK")
  registerDoSNOW(cl)
  fit <- hmm2(snp_exp, emission_param)

## End(Not run)
```

---

HMMList

*Constructor for HMMList class*

---

### Description

The constructor function for the `HMMList` class. The constructor is useful for representing a list of HMM objects.

### Usage

```
HMMList(object)
```

### Arguments

`object`            a list. Each element of the list is in instance of the HMM class.

**See Also**[HMMList HMM hmm2](#)

---

HMMList-class	<i>Class, constructor, and methods for representing HMM results from multiple samples</i>
---------------	---

---

**Description**

Each element of the HMMList contains the genomic intervals of the HMM segmentation (GRanges-derived object), parameters from the Baum-Welch, and a FilterParam object.

**Usage**

```
## S4 method for signature 'HMMList'
show(object)

## S4 method for signature 'HMMList'
unlist(x, recursive = TRUE, use.names = TRUE)
```

**Arguments**

object	a HMMList object
x	a HMMList object
recursive	logical; currently ignored
use.names	logical; currently ignored

**Slots**

.Data a list. Each element of the list should be a HMM object.

**See Also**[HMM](#)**Examples**

```
data(snp_exp)
fit <- hmm2(snp_exp)
class(fit)
identical(length(fit), ncol(snp_exp))
unlist(fit)
```



---

HmParam                      *Constructor for HmParam class*

---

### Description

Contains emission probabilities, parameters for emission probabilities, and transition probabilities required for computing the most likely state path via the Viterbi algorithm

### Usage

```
HmParam(
  emission = matrix(0, 0, 0),
  emission_param = EmissionParam(),
  transition = rep(0.99, nrow(emission)),
  chromosome = character(nrow(emission)),
  loglik = LogLik(),
  viterbi = Viterbi(),
  compute_posteriors = TRUE,
  verbose = FALSE
)

## S4 method for signature 'HmParam'
show(object)

## S4 method for signature 'HmParam'
nrow(x)

## S4 method for signature 'HmParam'
ncol(x)
```

### Arguments

emission	A matrix of emission probabilities
emission_param	an object of class EmissionParam
transition	vector of transition probabilities whose length is N-1, where N is the number of markers. User should provide the probability that the state at marker j is the same as the state at marker j-1. It is assumed that the probability of transitioning to state_j from state_j-1 is the same for all states != state_j-1.
chromosome	character vector
loglik	an object of class LogLik
viterbi	an object of class Viterbi
compute_posteriors	logical
verbose	logical
object	a HmParam object
x	a HmParam object

**Examples**

```
HmmParam()
```

---

```
hmmResults
```

*Example output from the hidden markov model*

---

**Description**

The results of a 6-state HMM fit to simulated copy number and genotype data.

**Format**

a GRanges object

---

```
HmmTrellisParam
```

*Constructor for HmmTrellisParam class*

---

**Description**

Constructor for HmmTrellisParam class

**Usage**

```
HmmTrellisParam(
  ylimits = list(c(0, 1), c(-3, 1)),
  expandfun = function(g) { width(g) * 50 }
)
```

**Arguments**

ylimits	length-two list of the y-axis limits for B allele frequencies and log R ratios, respectively
expandfun	a function that takes a length-one GRanges object as an argument and computes a width relative to the width of the GRanges object

---

IdiogramParams	<i>Constructor for IdiogramParam objects</i>
----------------	--

---

**Description**

Parameters for plotting idiograms

**Usage**

```
IdiogramParams(  
  seqnames = character(),  
  seqlengths = numeric(),  
  unit = "kb",  
  genome = "hg19",  
  box = list(color = "blue", lwd = 1)  
)  
  
## S4 method for signature 'IdiogramParams,ANY'  
plot(x, y, ...)
```

**Arguments**

seqnames	length-one character vector providing chromosome name
seqlengths	length-one numeric vector indicating size of chromosome
unit	character string indicating unit for genomic position
genome	character string indicating genome build
box	a list of parameters for plotting the box around the part of the idiogram that is plotted
x	an IdiogramParam object
y	ignored
...	ignored

**Value**

IdiogramParam object

---

IdiogramParams-class *Parameter class for plotting idiograms*

---

## Description

Parameter class for plotting idiograms

## Usage

```
## S4 method for signature 'IdiogramParams'
show(object)
```

## Arguments

object            an IdiogramParam object

## Slots

seqnames length-one character vector providing chromosome name  
 seqlengths length-one numeric vector indicating size of chromosome  
 unit character string indicating unit for genomic position (default is 'kb')  
 genome character string indicating genome build  
 box a list of parameters for plotting the box around the part of the idiogram that is plotted.

## Examples

```
if(require(BSgenome.Hsapiens.UCSC.hg18) && require(grid)){
  si <- seqinfo(BSgenome.Hsapiens.UCSC.hg18)
  iparam <- IdiogramParams(seqnames="chr1",
                           genome="hg18",
                           seqlengths=seqlengths(si)["chr1"],
                           box=list(xlim=c(20e6L, 25e6L), color="blue", lwd=2))
  iparam
  idiogram <- plot(iparam)
  vp <- viewport(x=0.05, y=0.8, width=unit(0.9, "npc"), height=unit(0.2, "npc"),
                 name="vp1", just=c("left", "bottom"))
  grid.newpage()
  pushViewport(vp)
  print(idiogram, vp=vp, newpage=FALSE)
}
```

---

isHeterozygous	<i>Assess whether genotype is heterozygous based on BAFs</i>
----------------	--

---

**Description**

Assess whether genotype is heterozygous based on BAFs

**Usage**

```
isHeterozygous(object, cutoff)

## S4 method for signature 'ArrayViews'
isHeterozygous(object, cutoff)

## S4 method for signature 'SnpArrayExperiment'
isHeterozygous(object, cutoff)

## S4 method for signature 'numeric'
isHeterozygous(object, cutoff)

## S4 method for signature 'matrix'
isHeterozygous(object, cutoff)
```

**Arguments**

object	a SnpArrayExperiment or ArrayViews object containing BAFs, a matrix of BAFs, or a numeric vector of BAFs. vector of BAFs
cutoff	a length-two numeric vector providing the range of BAFs consistent with allelic heterozygosity

**Examples**

```
if(require("BSgenome.Hsapiens.UCSC.hg18")){
  bsgenome <- BSgenome.Hsapiens.UCSC.hg18
  snp_exp <- getExampleSnpExperiment(bsgenome)
  is_het <- isHeterozygous(snp_exp[, 1], c(0.4, 0.6))
  table(is_het)
}
```

---

LogLik	<i>Constructor for LogLik class</i>
--------	-------------------------------------

---

**Description**

A container for the log likelihood of the Viterbi state path. Stores the log likelihood from successive updates of model parameters. When the difference between the log likelihoods at iteration  $i$  and  $i-1$  is below the tolerance, no additional updates are performed.

**Usage**

```
LogLik(loglik = numeric(), tolerance = 1L)
```

**Arguments**

loglik	length-one numeric vector for the log likelihood of the Viterbi state path
tolerance	if the difference in the log-likelihood of the Viterbi state path after the Baum-Welch update is less than the specified tolerance, no additional Baum-Welch updates are required

**See Also**

[LogLik](#)

---

LogLik-class	<i>Classes and methods for storing/getting log-likelihoods from Viterbi algorithm</i>
--------------	---

---

**Description**

Exported for internal use by other BioC packages

**Usage**

```
## S4 method for signature 'LogLik'
length(x)
```

```
## S4 method for signature 'LogLik'
show(object)
```

**Arguments**

x	object of class LogLik
object	a LogLik object

**Slots**

loglik	a numeric vector
tolerance	a numeric vector

**See Also**

[LogLik](#)

---

`IrrFile`*Accessors for objects of class ArrayViews*

---

**Description**

Accessors for objects of class ArrayViews

**Usage**

```
IrrFile(object)
```

```
IrrFile(object) <- value
```

```
bafFile(object)
```

```
gtFile(object)
```

```
## S4 method for signature 'ArrayViews'  
IrrFile(object)
```

```
## S4 replacement method for signature 'ArrayViews'  
IrrFile(object) <- value
```

```
## S4 method for signature 'ArrayViews'  
bafFile(object)
```

```
## S4 method for signature 'ArrayViews'  
gtFile(object)
```

**Arguments**

`object`            see `showMethods("IrrFile")`

`value`            a character vector of filenames for the log R ratios

**Examples**

```
views <- ArrayViews(parsedPath=tempdir())  
sourcePaths(views)  
IrrFile(views)  
bafFile(views)  
gtFile(views)
```

---

matrixOrNULL	<i>A class allowing matrix or NULL objects</i>
--------------	--

---

**Description**

Exported for internal use by other BioC packages

---

NA_filter	<i>Remove SNPs with NAs in any of the low-level estimates</i>
-----------	---

---

**Description**

Remove SNPs with NAs in any of the low-level estimates

**Usage**

```
NA_filter(x, i)
```

**Arguments**

x	a container for SNP data ( <a href="#">SnpArrayExperiment</a> )
i	integer vector to subset

**Value**

An object of the same class

---

numberFeatures	<i>The number of SNP/nonpolymorphic probes contained in a genomic interval</i>
----------------	--

---

**Description**

The number of SNP/nonpolymorphic probes contained in a genomic interval

**Usage**

```
numberFeatures(object)
```

**Arguments**

object	see <code>showMethods(numberFeatures)</code>
--------	--



---

parsedPath	<i>Complete path to directory for keeping parsed files</i>
------------	--

---

**Description**

A character string indicating the complete path for storing parsed files.

**Usage**

```
parsedPath(object)
```

```
## S4 method for signature 'ArrayViews'  
parsedPath(object)
```

**Arguments**

object            a `ArrayViews` object

**See Also**

[parseSourceFile ArrayViews](#)  
[ArrayViews](#)

---

parseSourceFile	<i>Function for parsing GenomeStudio files</i>
-----------------	--

---

**Description**

This function parses genome studio files, writing the low-level data for log R ratios, B allele frequencies, and genotypes to disk as integers (1 file per subject per data type).

**Usage**

```
parseSourceFile(object, param)
```

```
## S4 method for signature 'ArrayViews,CopyNumScanParams'  
parseSourceFile(object, param)
```

**Arguments**

object            An `ArrayViews` object  
param            An object of class `CopyNumScanParams`

**See Also**

[ArrayViews ArrayViews CopyNumScanParams](#)

**Examples**

```

require(BSgenome.Hsapiens.UCSC.hg18)
bsgenome <- BSgenome.Hsapiens.UCSC.hg18
require(data.table)
extdir <- system.file("extdata", package="VanillaICE", mustWork=TRUE)
features <- suppressWarnings(fread(file.path(extdir, "SNP_info.csv")))
fgr <- GRanges(paste0("chr", features$Chr), IRanges(features$Position, width=1),
              isSnp=features[["Intensity Only"]]==0)
fgr <- SnpGRanges(fgr)
names(fgr) <- features[["Name"]]
seqlevels(fgr) <- seqlevels(bsgenome)[seqlevels(bsgenome) %in% seqlevels(fgr)]
seqinfo(fgr) <- seqinfo(bsgenome)[seqlevels(fgr),]
fgr <- sort(fgr)
files <- list.files(extdir, full.names=TRUE, recursive=TRUE, pattern="FinalReport")
views <- ArrayViews(rowRanges=fgr, sourcePaths=files, parsedPath=tempdir())
show(views)

## read the first file
dat <- fread(files[1], skip="[Data]")
## information to store on the markers
select <- match(c("SNP Name", "Allele1 - AB", "Allele2 - AB",
                 "Log R Ratio", "B Allele Freq"), names(dat))

##
## which rows to keep in the MAP file. By matching on the sorted GRanges object
## containing the feature annotation, the low-level data for the log R ratios/
## B allele frequencies will also be sorted
##
index_genome <- match(names(fgr), dat[["SNP Name"]])
scan_params <- CopyNumScanParams(index_genome=index_genome, select=select)
##
## parse the source files
##
parseSourceFile(views, scan_params)
list.files(parsedPath(views))
##
## Inspecting source data through accessors defined on the views object
##
require(oligoClasses)
## log R ratios
r <- head(lrr(views))
## B allele frequencies
b <- head(baf(views))
g <- head(genotypes(views))

```

---

probability

*Accessor for probability filter*


---

**Description**

Accessor for probability filter

**Usage**

```
probability(object)
```

**Arguments**

```
object          a FilterParam object
```

---

```
rescale          Rescale a numeric vector
```

---

**Description**

Rescale a numeric vector

**Usage**

```
rescale(x, l, u)
```

**Arguments**

```
x              numeric vector
l              lower limit of rescaled x
u              upper limit of rescaled x
```

---

```
rowModes       Robust statistics for matrices
```

---

**Description**

Compute the column-wide or row-wise mode of numeric matrices

**Usage**

```
rowModes(x)
```

```
colModes(x)
```

```
rowMAD(x, ...)
```

**Arguments**

```
x              matrix
...           additional arguments to rowMedians
```

**Value**

numeric vector

**See Also**

[mad](#)

[mad rowMedians](#)

**Examples**

```
X <- matrix(rnorm(100), 10, 10)
rowMAD(X)
```

---

segs	<i>Accessor for the HMM segments</i>
------	--------------------------------------

---

**Description**

Accessor to obtain all segments from the HMM.

**Usage**

```
segs(object)
```

**Arguments**

object            see `showMethods(segs)`

**Value**

a GRanges-derived object

---

show, Viterbi-method	<i>Show method for objects of class Viterbi</i>
----------------------	---

---

**Description**

Show method for objects of class Viterbi

**Usage**

```
## S4 method for signature 'Viterbi'
show(object)
```

**Arguments**

object            a Viterbi object

---

snpArrayAssays      *Create an assays object from log R ratios and B allele frequencies*

---

### Description

This function is exported primarily for internal use by other BioC packages.

### Usage

```
snpArrayAssays(cn = new("matrix"), baf = new("matrix"), ...)
```

### Arguments

cn	matrix of log R ratios
baf	matrix of B allele frequencies
...	additional matrices of the same dimension, such as SNP genotypes.

### Examples

```
data(snp_exp, package="VanillaICE")
r <- lrr(snp_exp)
b <- baf(snp_exp)
s1 <- snpArrayAssays(cn=r, baf=b)
```

---

SnpArrayExperiment-class

*A RangedSummarizedExperiment-derived class of marker-level SNP array data for copy number inference*

---

### Description

Constructor for SnpArrayExperiment

### Usage

```
SnpArrayExperiment(
  cn,
  baf,
  rowRanges = GRanges(),
  colData = DataFrame(),
  isSnp = logical(),
  ...
)

## S4 method for signature 'missing'
```

```

SnpArrayExperiment(
  cn,
  baf,
  rowRanges = GRanges(),
  colData = DataFrame(),
  isSnp = logical(),
  ...
)

## S4 method for signature 'matrix'
SnpArrayExperiment(
  cn,
  baf,
  rowRanges = GRanges(),
  colData = DataFrame(row.names = colnames(cn)),
  isSnp = logical(),
  ...
)

```

### Arguments

cn	matrix of copy number estimates (e.g., log R ratios)
baf	matrix of B allele frequencies
rowRanges	GRanges object for SNPs/nonpolymorphic markers
colData	DataFrame containing sample-level covariates
isSnp	logical vector indicating whether marker is a SNP
...	additional arguments passed to SummarizedExperiment() constructor function

### Examples

```

## empty container
library(VanillaICE)
data(snp_exp, package="VanillaICE") # example

se <- SnpArrayExperiment(cn=lrr(snp_exp), baf=baf(snp_exp),
  rowRanges=rowRanges(snp_exp))

```

---

SnpExperiment

*Constructor for SnpArrayExperiment*

---

### Description

A single-argument generic function to construct a SnpArrayExperiment.

**Usage**

```
SnpExperiment(object)

## S4 method for signature 'ArrayViews'
SnpExperiment(object)
```

**Arguments**

object            see showMethods('SnpExperiment') for a list of supported objects

**Examples**

```
view <- ArrayViews()
SnpExperiment(view)
```

---

SnpGRanges-class            *An extension to GRanges for representing SNPs*

---

**Description**

An extension to GRanges for representing SNPs  
 Constructor for SnpGRanges class

**Usage**

```
SnpGRanges(object = GRanges(), isSnp, ...)
```

```
## S4 method for signature 'missing'
SnpGRanges(object, isSnp)
```

```
## S4 method for signature 'GRanges'
SnpGRanges(object, isSnp)
```

**Arguments**

object            A GRanges object

isSnp            A logical vector. Each genomic interval in the GRanges container corresponds to a marker on the genotyping array. isSnp is FALSE for nonpolymorphic markers such as those included on the Affymetrix 6.0 chips.

...            ignored

**Slots**

elementMetadata a SnpDataFrame

**Examples**

```
SnpGRanges()  
g <- GRanges("chr1", IRanges(15L, 15L))  
SnpGRanges(g, isSnp=TRUE)
```

---

snp_exp	<i>An example SnpArrayExperiment</i>
---------	--------------------------------------

---

**Description**

A container for low-level summaries used for downstream copy number estimation, including log R ratios, B allele frequencies, and genotypes

**Format**

a SnpArrayExperiment object

---

sourcePaths	<i>Accessor for file paths containing SNP-level summaries</i>
-------------	---

---

**Description**

Files containing SNP-level summaries for log R ratios, B allele frequencies, and genotypes – one sample per subject – are required.

**Usage**

```
sourcePaths(object)
```

**Arguments**

object            an ArrayViews object

**Examples**

```
sourcePaths(ArrayViews())
```



---

start,oligoSnpSet-method

*Retrieve genomic location of SNPs*

---

### **Description**

Retrieve genomic location of SNPs

### **Usage**

```
## S4 method for signature 'oligoSnpSet'  
start(x)
```

### **Arguments**

x                    a oligoSnpSet object

---

state,HmmGRanges-method

*Accessor for copy number state*

---

### **Description**

Extract the copy number state for each genomic interval.

### **Usage**

```
## S4 method for signature 'HmmGRanges'  
state(object)
```

### **Arguments**

object                a HmmGRanges object

---

state-methods	<i>Accessor for the Viterbi state path</i>
---------------	--

---

### Description

The states are represented as integers: 1=homozygous deletion, 2=hemizygous deletion, 3=diploid normal heterozygosity, 4=diploid region of homozygosity, 5=single copy gain, 6=two or more copy gain.

### Usage

```
## S4 method for signature 'Viterbi'
state(object)
```

### Arguments

object	a Viterbi object
--------	------------------

---

sweepMode	<i>Sweep the modal log R ratio (by row or column) from a matrix of log R ratios</i>
-----------	---

---

### Description

This function simplifies the process of sweeping the modal log R ratio from the rows or columns of a `SnpArrayExperiment` object. It is most useful when a large number of samples (more than 10) are available and the dataset is a collection of germline samples. We assume that the samples are from a single batch and that the modal value will be a robust estimate of the mean log R ratio for diploid copy number. Variation in the modal estimates between markers is presumed to be attributable to probe effects (e.g., differences hybridization efficiency/PCR do to sequence composition). For sex chromosomes, one should apply this function separately to men and women and then recenter the resulting matrix according to the expected copy number.

### Usage

```
sweepMode(x, MARGIN)
```

```
## S4 method for signature 'SnpArrayExperiment'
sweepMode(x, MARGIN)
```

### Arguments

x	see <code>showMethods(sweepMode)</code>
MARGIN	integer indicating which margin (1=rows, 2=columns) to sweep the mode

**Value**

an object of the same class as x

**Examples**

```
data(snp_exp)
snp_exp_rowcentered <- sweepMode(snp_exp, 1)
snp_exp_colcentered <- sweepMode(snp_exp, 2)
x <- lrr(snp_exp)
x_rowcentered <- sweep(x, 1, rowModes(x))
all.equal(lrr(snp_exp_rowcentered), x_rowcentered)
```

---

threshold	<i>Threshold numeric values</i>
-----------	---------------------------------

---

**Description**

Threshold numeric values according to user-specific limits. The thresholded values can also be jittered near the limits.

**Usage**

```
threshold(x, lim = c(-Inf, Inf), amount = 0)
```

**Arguments**

x	numeric matrix or vector
lim	limit at which to threshold entries in x
amount	see <a href="#">jitter</a>

**See Also**

[jitter](#)

**Examples**

```
x <- rnorm(1000, 0, 3)
y <- threshold(x, c(-5,5))
range(y)
```

---

TransitionParam      *Constructor for TransitionParam class*

---

### Description

Contains parameters for computing transition probabilities

### Usage

```
TransitionParam(taup = 1e+10, taumax = 1 - 5e+06)
```

```
## S4 method for signature 'TransitionParam'
show(object)
```

### Arguments

taup	length-one numeric vector
taumax	The maximum probability that the current state is the same as the preceding state. See details
object	a TransitionParam object

### Details

Diagonal elements of the transition probability matrix are computed as  $e^{-2*d/taup}$ , where  $d$  is the distance between markers  $i$  and  $i-1$  and  $taup$  is typically in the range of  $1e10$ . This probability is constrained to be no larger than  $taumax$ . The probabilities on the off-diagonal elements are the same and are subject to the constraint that the rows of the transition probability matrix sum to 1.

### Examples

```
TransitionParam()
## higher values of taup make transitions between states less likely
TransitionParam(taup=1e12)
```

---

updateHmmParams      *Run the Baum-Welch algorithm to update HMM parameters*

---

### Description

This function is not intended to be called directly by the user. It is exported in the package NAMESPACE for internal use by other BioC packages.

**Usage**

```
updateHmmParams(
  object,
  emission_param = EmissionParam(),
  transition_param = TransitionParam()
)
```

**Arguments**

object            a [SnpArrayExperiment](#) object  
 emission\_param a [EmissionParam](#) object  
 transition\_param            a [TransitionParam](#) object

---

VanillaICE	<i>A hidden markov model for detection of germline copy number variants from arrays</i>
------------	---

---



---

viewports	<i>Default viewports for plotting CNV data with lattice-style graphics</i>
-----------	--

---

**Description**

Default viewports for plotting CNV data with lattice-style graphics

**Usage**

```
viewports()
```

**Value**

list

**See Also**

[xyplotList](#) [xygrid](#)

**Examples**

```
vps <- viewports()
```

xyplotList

*Lattice-style plots for granges and SnpArrayExperiment objects***Description**

Data for the graphic is generated by a call to `grangesData`.

**Usage**

```
xyplotList(granges, se, param = HmmTrellisParam())

## S4 method for signature 'HmmGRanges,SnpArrayExperiment'
xyplotList(granges, se, param = HmmTrellisParam())

## S4 method for signature 'GRangesList,SnpArrayExperiment'
xyplotList(granges, se, param = HmmTrellisParam())

xygrid(trellis_plot, viewports, granges)
```

**Arguments**

<code>granges</code>	a <code>HmmGRanges</code> object
<code>se</code>	a <code>SnpArrayExperiment</code>
<code>param</code>	trellis parameters for plotting HMM
<code>trellis_plot</code>	an object of class <code>trellis</code>
<code>viewports</code>	a list of viewports as provided by the <code>viewports</code> function

**See Also**

[viewports](#)

**Examples**

```
if(require("BSgenome.Hsapiens.UCSC.hg18")){
  bsgenome <- BSgenome.Hsapiens.UCSC.hg18
  snp_exp <- getExampleSnpExperiment(bsgenome)
  seqlevels(snp_exp, pruning.mode="coarse") <- "chr22"
  fit <- hmm2(snp_exp)
  g <- reduce(hemizygous(fit), min.gapwidth=500e3)
  trellis_param <- HmmTrellisParam()
  fig <- xyplotList(g, snp_exp, trellis_param)
  vps <- viewports()
  xygrid(fig[[1]], vps, g)
}
```

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