# Package 'AllelicImbalance'

August 3, 2025

**Type** Package

**Title** Investigates Allele Specific Expression

**Version** 1.46.1

**Date** 2021-11-17

**Encoding** UTF-8

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**Description** Provides a framework for allelic specific expression investigation using RNA-seq data.

**License** GPL-3

**URL** https://github.com/pappewaio/AllelicImbalance

**BugReports** https://github.com/pappewaio/AllelicImbalance/issues

**Suggests** testthat, org.Hs.eg.db, TxDb.Hsapiens.UCSC.hg19.knownGene, SNPlocs.Hsapiens.dbSNP144.GRCh37, BiocStyle, knitr, rmarkdown

**Depends** R (>= 4.0.0), grid, GenomicRanges (>= 1.31.8), SummarizedExperiment (>= 0.2.0), GenomicAlignments (>= 1.15.6)

**Imports** methods, BiocGenerics, AnnotationDbi, BSgenome (>= 1.47.3), VariantAnnotation (>= 1.25.11), Biostrings (>= 2.47.6), S4Vectors (>= 0.17.25), IRanges (>= 2.13.12), Rsamtools (>= 1.99.3), GenomicFeatures (>= 1.31.3), Gviz, lattice, latticeExtra, gridExtra, seqinr, GenomeInfoDb, nlme

**LazyData** TRUE

**biocViews** Genetics, Infrastructure, Sequencing

**VignetteBuilder** knitr

**Collate** 'AllelicImbalance-package.R' 'initialize-methods.R' 'ASEset-class.R' 'DetectedAI-class.R' 'GlobalAnalysis-class.R' 'barplot-methods.R' 'locationplot-methods.R' 'GvizTrack-methods.R' 'LinkVariantAlmlof-class.R' 'RegionSummary-class.R' 'RiskVariant-class.R' 'auxillary-functions-annotation.R'

'auxillary-functions-visuals.R'
'auxillary-methods-annotation.R'
'auxillary-methods-summaries.R' 'auxillary-methods.R'
'chisq.test-methods.R' 'binom.test-methods.R'
'boxplot-methods.R' 'deprecations.R' 'detect-methods.R'
'filter-methods.R' 'histplot-methods.R' 'inference-methods.R'
'linkage-methods.R' 'list-methods.R' 'mapbias-methods.R'
'plot-methods.R' 'show-methods.R' 'simulation-methods.R'
'summary-methods.R' 'utils.R'

**RoxygenNote** 7.1.1

**git_url** https://git.bioconductor.org/packages/AllelicImbalance

**git_branch** RELEASE_3_21

**git_last_commit** 96ed018

**git_last_commit_date** 2025-05-08

**Repository** Bioconductor 3.21

**Date/Publication** 2025-08-03

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AllelicImbalance-package

*A package meant to provide all basic functions for high-throughput allele specific expression analysis*

## Description

Package AllelicImbalance has functions for importing, filtering and plotting high-throughput data to make an allele specific expression analysis. A major aim of this package is to provide functions to collect as much information as possible from regions of choice, and to be able to explore the allelic expression of that region in detail.

## Details

| | |
|---|---|
| Package: | AllelicImbalance |
| Type: | Package |
| Version: | 1.2.0 |
| Date: | 2014-08-24 |
| License: | GPL-3 |

## Overview - standard procedure

Start out creating a GRange object defining the region of interest. This can also be done using getAreaFromGeneNames providing gene names as arguments. Then use BamImpGAList to import reads from that reagion and find potential SNPs using scanForHeterozygotes. Then retrieve the allele counts of heterozygote sites by the function getAlleleCount. With this data create an ASEset. At this point all pre-requisites for a 'basic' allele specific expression analysis is available. Two ways to go on could be to apply chisq.test or barplot on this ASEset object.

## Author(s)

Author: Jesper Robert Gadin Author: Lasse Folkersen

Maintainer: Jesper Robert Gadin <j.r.gadin@gmail.com>

## References

Reference to published application note (work in progress)

## See Also

- code?ASEset

annotation-wrappers *AnnotationDb wrappers*

## Description

These functions acts as wrappers to retrieve information from annotation database objects (annotationDb objects) or (transcriptDb objects)

## Usage

```
getGenesFromAnnotation(
  OrgDb,
  GR,
  leftFlank = 0,
  rightFlank = 0,
  getUCSC = FALSE,
  verbose = FALSE
)

getGenesVector(OrgDb, GR, leftFlank = 0, rightFlank = 0, verbose = FALSE)

getExonsFromAnnotation(
  TxDb,
  GR,
  leftFlank = 0,
  rightFlank = 0,
  verbose = FALSE
)

getExonsVector(TxDb, GR, leftFlank = 0, rightFlank = 0, verbose = FALSE)

getTranscriptsFromAnnotation(
  TxDb,
  GR,
  leftFlank = 0,
  rightFlank = 0,
  verbose = FALSE
)

getTranscriptsVector(TxDb, GR, leftFlank = 0, rightFlank = 0, verbose = FALSE)

getCDSFromAnnotation(TxDb, GR, leftFlank = 0, rightFlank = 0, verbose = FALSE)

getCDSVector(TxDb, GR, leftFlank = 0, rightFlank = 0, verbose = FALSE)

getAnnotationDataFrame(
  GR,
```

```
  strand = "+",
  annotationType = NULL,
  OrgDb = NULL,
  TxDb = NULL,
  verbose = FALSE
)
```

## Arguments

| | |
|---|---|
| OrgDb | An OrgDb object |
| GR | A GenomicRanges object with sample area |
| leftFlank | An integer specifying number of additional nucleotides around the SNPs for the leftFlank |
| rightFlank | An integer specifying number of additional nucleotides around the SNPs for the rightFlank |
| getUCSC | A logical indicating if UCSC transcript IDs should also be retrieved |
| verbose | A logical making the functions more talkative |
| TxDb | A transcriptDb object |
| strand | Two options,'+' or '-' |
| annotationType | select one or more from 'gene', 'exon', 'transcript', 'cds'. |

## Details

These functions retrieve regional annotation from OrgDb or TxDb objects, when given GRanges objects.

## Value

GRanges object with ranges over the genes in the region.

The getGenesVector function will return a character vector where each element are gene symbols separated by comma

GRanges object with ranges over the exons in the region.

The getTranscriptsFromAnnotation function will return a GRanges object with ranges over the transcripts in the region.

The getCDSFromAnnotation function will return a GRanges object with ranges over the CDSFs in the region.

The getExonsVector function will return a character vector where each element are exons separated by comma

The getTranscriptsVector function will return a character vector where each element are transcripts separated by comma

The getCDSVector function will return a character vector where each element are CDSs separated by comma

The getAnnotationDataFrame function will return a data.frame with annotations. This function is used internally by i.e. the barplot-function

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
data(ASEset)
require(org.Hs.eg.db)
require(TxDb.Hsapiens.UCSC.hg19.knownGene)
OrgDb <- org.Hs.eg.db
TxDb <- TxDb.Hsapiens.UCSC.hg19.knownGene

#use for example BcfFiles as the source for SNPs of interest
GR <- rowRanges(ASEset)
#get annotation
g <- getGenesFromAnnotation(OrgDb,GR)
e <- getExonsFromAnnotation(TxDb,GR)
t <- getTranscriptsFromAnnotation(TxDb,GR)
c <- getCDSFromAnnotation(TxDb,GR)
```

---

# annotationBarplot *add annotation to AllelicImbalance barplot*

---

## Description

adds a customizable annotation functionality for AllelicImbalance barplots.

## Usage

```
annotationBarplot(
  strand,
  snp,
  lowerLeftCorner,
  annDfPlus,
  annDfMinus,
  cex = 0.7,
  ypos = 0,
  interspace = 1
)
```

## Arguments

| | |
|---|---|
| strand | strand, "+", "-", "*" or "both" |
| snp | integer for the described snp |
| lowerLeftCorner | position of the plot to add legend to (default c(0,0)) |

| | |
|---|---|
| annDfPlus | annotation dataframe plus strand |
| annDfMinus | annotation dataframe minus strand |
| cex | size of annotation text |
| ypos | relative y-axis position for the annotation text |
| interspace | space between each annotation block |

## Details

the function is preferably called from within the AllelicImbalance barplot method.

## Author(s)

Jesper R. Gadin

## Examples

```
#code placeholders
#< create a barplot without annotation >
#< add annotation >
```

---

# ASEset-barplot *barplot ASEset objects*

---

## Description

Generates barplots for ASEset objects. Two levels of plotting detail are provided: a detailed barplot of read counts by allele useful for fewer samples and SNPs, and a less detailed barplot of the fraction of imbalance, useful for more samples and SNPs.

## Usage

```
barplot(height, ...)

## S4 method for signature 'ASEset'
barplot(
  height,
  type = "count",
  sampleColour.top = NULL,
  sampleColour.bot = NULL,
  legend = TRUE,
  pValue = TRUE,
  strand = "*",
  testValue = NULL,
  testValue2 = NULL,
  OrgDb = NULL,
  TxDb = NULL,
```

```
  annotationType = c("gene", "exon", "transcript"),
  main = NULL,
  ylim = NULL,
  yaxis = TRUE,
  xaxis = FALSE,
  ylab = TRUE,
  ylab.text = NULL,
  xlab.text = "samples",
  xlab = TRUE,
  legend.colnames = "",
  las.ylab = 1,
  las.xlab = 2,
  cex.main = 1,
  cex.pValue = 0.7,
  cex.ylab = 0.7,
  cex.xlab = 0.7,
  cex.legend = 0.6,
  add = FALSE,
  lowerLeftCorner = c(0, 0),
  size = c(1, 1),
  addHorizontalLine = 0.5,
  add.frame = TRUE,
  filter.pValue.fraction = 0.99,
  legend.fill.size = 1,
  legend.interspace = 1,
  verbose = FALSE,
  top.fraction.criteria = "maxcount",
  cex.annotation = 0.7,
  ypos.annotation = 0,
  annotation.interspace = 1,
  ...
)
```

## Arguments

| | |
|---|---|
| height | An ASEset object |
| ... | for simpler generics when extending function |
| type | 'count' or 'fraction' |
| sampleColour.top | User specified colours for top fraction |
| sampleColour.bot | User specified colours for bottom fraction |
| legend | Display legend |
| pValue | Display p-value |
| strand | four options, '+', '-', 'both' or '*' |
| testValue | if set, a matrix or vector with user p-values |

| | |
|---|---|
| testValue2 | if set, a matrix or vector with user p-values |
| OrgDb | an OrgDb object which provides annotation |
| TxDb | a TxDb object which provides annotation |
| annotationType | select one or more from 'gene','exon','transcript','cds'. |
| main | text to use as main label |
| ylim | set plot y-axis limit |
| yaxis | wheter the y-axis is to be displayed or not |
| xaxis | wheter the x-axis is to be displayed or not |
| ylab | showing labels for the tic marks |
| ylab.text | ylab text |
| xlab.text | xlab text |
| xlab | showing labels for the tic marks |
| legend.colnames | gives colnames to the legend matrix |
| las.ylab | orientation of ylab text |
| las.xlab | orientation of xlab text |
| cex.main | set main label size (max 2) |
| cex.pValue | set pValue label size |
| cex.ylab | set ylab label size |
| cex.xlab | set xlab label size |
| cex.legend | set legend label size |
| add | boolean indicates if a new device should be started |
| lowerLeftCorner | integer that is only useful when add=TRUE |
| size | Used internally by locationplot. Rescales each small barplot window |
| addHorizontalLine | adds a horizontal line that marks the default fraction of 0.5 - 0.5 |
| add.frame | boolean to give the new plot a frame or not |
| filter.pValue.fraction | numeric between 0 and 1 that filter away pValues where the main allele has this frequency. |
| legend.fill.size | size of the fill/boxes in the legend (default:NULL) |
| legend.interspace | set legend space between fills and text |
| verbose | Makes function more talkative |
| top.fraction.criteria | 'maxcount', 'ref' or 'phase' |
| cex.annotation | size of annotation text |
| ypos.annotation | relative ypos for annotation text |
| annotation.interspace | space between annotation text |

### Details

filter.pValue.fraction is intended to remove p-value annotation with very large difference in frequency, which could just be a sequencing mistake. This is to avoid p-values like 1e-235 or similar.

sampleColourUser specified colours, either given as named colours ('red', 'blue', etc) or as hexadecimal code. Can be either length 1 for all samples, or else of a length corresponding to the number of samples for individual colouring.

### Author(s)

Jesper R. Gadin, Lasse Folkersen

### See Also

- The ASEset class which the barplot function can be called up on.

### Examples

```
data(ASEset)
barplot(ASEset[1])
```

---

## ASEset-class *ASEset objects*

---

### Description

Object that holds allele counts, genomic positions and map-bias for a set of SNPs

### Usage

```
alleleCounts(x, strand = "*", return.class = "list")

## S4 method for signature 'ASEset'
alleleCounts(x, strand = "*", return.class = "list")

alleleCounts(x, ...) <- value

## S4 replacement method for signature 'ASEset'
alleleCounts(x, strand = "*", return.class = "array", ...) <- value

mapBias(x, ...)

## S4 method for signature 'ASEset'
mapBias(x, return.class = "list")

fraction(x, ...)
```

```
## S4 method for signature 'ASEset'
fraction(
  x,
  strand = "*",
  top.fraction.criteria = "maxcount",
  verbose = FALSE,
  ...
)

arank(x, return.type = "names", return.class = "list", strand = "*", ...)

frequency(x, ...)

genotype(x, ...)

## S4 method for signature 'ASEset'
genotype(x, return.class = "matrix")

genotype(x) <- value

## S4 replacement method for signature 'ASEset'
genotype(x) <- value

countsPerSnp(x, ...)

## S4 method for signature 'ASEset'
countsPerSnp(x, return.class = "matrix", return.type = "mean", strand = "*")

countsPerSample(x, ...)

## S4 method for signature 'ASEset'
countsPerSample(x, return.class = "matrix", return.type = "mean", strand = "*")

phase(x, ...)

## S4 method for signature 'ASEset'
phase(x, return.class = "matrix")

phase(x) <- value

## S4 replacement method for signature 'ASEset'
phase(x) <- value

mapBias(x) <- value

## S4 replacement method for signature 'ASEset'
mapBias(x) <- value
```

```
refExist(x)

## S4 method for signature 'ASEset'
refExist(x)

ref(x)

## S4 method for signature 'ASEset'
ref(x)

ref(x) <- value

## S4 replacement method for signature 'ASEset,ANY'
ref(x) <- value

altExist(x)

## S4 method for signature 'ASEset'
altExist(x)

alt(x)

## S4 method for signature 'ASEset'
alt(x)

alt(x) <- value

## S4 replacement method for signature 'ASEset,ANY'
alt(x) <- value

aquals(x, ...)

## S4 method for signature 'ASEset'
aquals(x)

aquals(x) <- value

## S4 replacement method for signature 'ASEset'
aquals(x) <- value

maternalAllele(x, ...)

## S4 method for signature 'ASEset'
maternalAllele(x)

paternalAllele(x, ...)
```

```
## S4 method for signature 'ASEset'
paternalAllele(x)
```

## Arguments

| | |
|---|---|
| x | ASEset object |
| strand | which strand of '+', '-' or '*' |
| return.class | return 'list' or 'array' |
| ... | additional arguments |
| value | replacement variable |
| top.fraction.criteria | 'maxcount', 'ref' or 'phase' |
| verbose | makes function more talkative |
| return.type | return 'names', rank or 'counts' |

## Details

An ASEset object differs from a regular RangedSummarizedExperiment object in that the assays contains an array instead of matrix. This array has ranges on the rows, sampleNames on the columns and variants in the third dimension.

It is possible to use the commands barplot and locationplot on an ASEset object see more details in barplot and locationplot.

Three different alleleCount options are available. The simples one is the * option, and is for experiments where the strand information is not known e.g. non-stranded data. The unknown strand could also be for strand specific data when the aligner could not find any strand associated with the read, but this should normally not happen, and if it does probably having an extremely low mapping quality. Then there are an option too add plus and minus stranded data. When using this, it is essential to make sure that the RNA-seq experiment under analysis has in fact been created so that correct strand information was obtained. The most functions will by default have their strand argument set to '*'.

The phase information is stored by the convention of 'maternal chromosome|paternal chromosome', with 0 as reference allele and 1 as alternative allele. '|' when the phase is known and '/' when the phase is unknown. Internally the information will be stored as an three dimensional array, dim 1 for SNPs, dim 2 for Samples and dim 3 which is fixed and stores maternal chromosome, paternal chromosome and phased (1 equals TRUE).

## Value

An object of class ASEset containing location information and allele counts for a number of SNPs measured in a number of samples on various strand, as well as mapBias information. All data is stored in a manner similar to the SummarizedExperiment class.

## Table

table(...)

Arguments:

**...** An `ASEset` `object` that contains the variants of interest

The generics for table does not easily allow more than one argument so in respect to the different strand options, `table` will return a SimpleList with length 3, one element for each strand.

## Frequency

frequency(x, return.class = "list", strand = "*", threshold.count.sample = 15)

Arguments:

**x** An `ASEset` `object` that contains the variants of interest

**x** threshold.count.samplesif sample has fewer counts the function return NA.

## Constructor

ASEsetFromCountList(rowRanges, countListNonStranded = NULL, countListPlus = NULL, countListMinus = NULL, countListUnknown = NULL, colData = NULL, mapBiasExpMean = array(), verbose=FALSE, ...)

Arguments:

**rowRanges** A `GenomicRanges` `object` that contains the variants of interest

**countListNonStranded** A `list` where each entry is a matrix with allele counts as columns and sample counts as rows

**countListPlus** A `list` where each entry is a matrix with allele counts as columns and sample counts as rows

**countListMinus** A `list` where each entry is a matrix with allele counts as columns and sample counts as rows

**countListUnknown** A `list` where each entry is a matrix with allele counts as columns and sample counts as rows

**colData** A `DataFrame` object containing sample specific data

**mapBiasExpMean** A 3D `array` describing mapping bias. The SNPs are in the 1st dimension, samples in the 2nd dimension and variants in the 3rd dimension.

**verbose** Makes function more talkative

**...** arguments passed on to SummarizedExperiment constructor

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#make example countList
set.seed(42)
countListPlus <- list()
snps <- c('snp1','snp2','snp3','snp4','snp5')
for(snp in snps){
  count<-matrix(rep(0,16),ncol=4,dimnames=list(
```

```
c('sample1','sample2','sample3','sample4'),
c('A','T','G','C')))
  #insert random counts in two of the alleles
  for(allele in sample(c('A','T','G','C'),2)){
count[,allele]<-as.integer(rnorm(4,mean=50,sd=10))
  }
  countListPlus[[snp]] <- count
}

#make example rowRanges
rowRanges <- GRanges(
  seqnames = Rle(c('chr1', 'chr2', 'chr1', 'chr3', 'chr1')),
  ranges = IRanges(1:5, width = 1, names = head(letters,5)),
  snp = paste('snp',1:5,sep='')
)

#make example colData
colData <- DataFrame(Treatment=c('ChIP', 'Input','Input','ChIP'),
 row.names=c('ind1','ind2','ind3','ind4'))

#make ASEset
a <- ASEsetFromCountList(rowRanges, countListPlus=countListPlus,
colData=colData)


#example phase matrix (simple form)
p1 <- matrix(sample(c(1,0),replace=TRUE, size=nrow(a)*ncol(a)),nrow=nrow(a), ncol(a))
p2 <- matrix(sample(c(1,0),replace=TRUE, size=nrow(a)*ncol(a)),nrow=nrow(a), ncol(a))
p <- matrix(paste(p1,sample(c("|","|","/"), size=nrow(a)*ncol(a), replace=TRUE), p2, sep=""),
 nrow=nrow(a), ncol(a))

phase(a) <- p


#generate ASEset from array
snps <- 999
samples <-5
ar <-array(rep(unlist(lapply(1:snps,
   function(x){(sample(c(TRUE,FALSE,TRUE,FALSE), size = 4))})), samples),
   dim=c(4,snps,samples))
ar2 <- array(sample(50:300, 4*snps*samples,replace=TRUE), dim=c(4,snps,samples))
ar2[ar] <- 0
ar2 <- aperm(ar2, c(2, 3, 1))
dimnames(ar2) <- list(paste("snp",1:snps,sep=""),paste("sample",1:samples,sep=""),
      c("A","C","G","T"))
gr <- GRanges(seqnames=c("chr2"), ranges=IRanges(start=1:dim(ar2)[1], width=1), strand="*")
a <- ASEsetFromArrays(gr, countsUnknown=ar2)
```

ASEset-filters *genotype filter methods*

## Description

useful genotype filters

## Usage

```
hetFilt(x, ...)

## S4 method for signature 'ASEset'
hetFilt(x, source = "genotype", ...)
```

## Arguments

| | |
|---|---|
| x | ASEset object |
| ... | internal param |
| source | 'genotype' or 'alleleCounts' |

## Details

hetFilt returns TRUE if the samples is heterozygote, based on stored genotype information present in the phase data.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#load example data
data(ASEset)
a <- ASEset

genotype(a) <- inferGenotypes(a)
hets <- hetFilt(a)
```

ASEset-gbarplot *gbarplot ASEset objects*

## Description

Generates gbarplots for ASEset objects. Two levels of plotting detail are provided: a detailed gbarplot of read counts by allele useful for fewer samples and SNPs, and a less detailed gbarplot of the fraction of imbalance, useful for more samples and SNPs.

## Usage

```
gbarplot(x, type = "count", strand = "*", verbose = FALSE, ...)
```

## Arguments

| | |
|---|---|
| x | An ASEset object |
| type | 'count' or 'fraction' |
| strand | four options, '+', '-', 'both' or '*' |
| verbose | Makes function more talkative |
| ... | for simpler generics when extending function |

## Details

This function serves the same purpose as the normal barplot, but with trellis graphics using lattice, to be able to integrate well with Gviz track functionality.

## Author(s)

Jesper R. Gadin

## See Also

- The ASEset class which the gbarplot function can be called up on.
- The barplot non trellis barplot.

## Examples

```
data(ASEset)
gbarplot(ASEset[1])
```

ASEset-glocationplot *glocationplot ASEset objects*

## Description

plotting ASE effects over a specific genomic region using Gviz functionality

## Usage

```
glocationplot(
  x,
  type = "fraction",
  strand = "*",
  BamGAL = NULL,
  GenomeAxisTrack = FALSE,
  trackNameDeAn = paste("deTrack", type),
  TxDb = NULL,
  sizes = NULL,
  add = FALSE,
  verbose = FALSE,
  ...
)
```

## Arguments

| | |
|---|---|
| x | an ASEset object. |
| type | 'fraction' or 'count' |
| strand | '+','-','*' or 'both'. This argument determines which strand is plotted. See getAlleleCounts for more information of choice of strand. |
| BamGAL | GAlignmentsList covering the same genomic region as the ASEset |
| GenomeAxisTrack | include an genomic axis track |
| trackNameDeAn | trackname for deAnnotation track |
| TxDb | a TxDb object which provides annotation |
| sizes | vector with the sum 1. Describes the size of the tracks |
| add | add to existing plot |
| verbose | if set to TRUE it makes function more talkative |
| ... | arguments passed on to barplot function |

## Details

The glocationplot methods visualises the distribution of ASE over a larger region on one chromosome. It takes and ASEset object as well as additional information on plot type (see gbarplot), strand type (see getAlleleCounts), Annotation tracks are created from the Gviz packageh. It is obviously important to make sure that the genome build used is set correctly, e.g. 'hg19'.

sizes has to be of the same length as the number of tracks used.

### Author(s)

Jesper R. Gadin

### See Also

- The ASEset class which the glocationplot function can be called up on.

### Examples

```
data(ASEset)
genome(ASEset) <- 'hg19'

glocationplot(ASEset,strand='+')

#for ASEsets with fewer SNPs the 'count' type plot is useful
glocationplot(ASEset,type='count',strand='+')
```

---

## ASEset-gviztrack *ASEset-gviztrack ASEset objects*

---

### Description

plotting ASE effects over a specific genomic region

### Usage

```
ASEDAnnotationTrack(
  x,
  GR = rowRanges(x),
  type = "fraction",
  strand = "*",
  trackName = paste("deTrack", type),
  verbose = TRUE,
  ...
)

## S4 method for signature 'ASEset'
ASEDAnnotationTrack(
  x,
  GR = rowRanges(x),
  type = "fraction",
  strand = "*",
  trackName = paste("deTrack", type),
  verbose = TRUE,
  ...
)
```

```
CoverageDataTrack(
  x,
  GR = rowRanges(x),
  BamList = NULL,
  strand = NULL,
  start = NULL,
  end = NULL,
  trackNameVec = NULL,
  meanCoverage = FALSE,
  verbose = TRUE,
  ...
)
```

## Arguments

| | |
|---|---|
| `x` | an ASEset object. |
| `GR` | genomic range of plotting |
| `type` | 'fraction' or 'count' |
| `strand` | '+','-'. This argument determines which strand is plotted. |
| `trackName` | name of track (ASEDAnnotationTrack) |
| `verbose` | Setting `verbose=TRUE` gives details of procedure during function run |
| `...` | arguments passed on to barplot function |
| `BamList` | GAlignmnentsList object of reads from the same genomic region as the ASEset |
| `start` | start position of reads to be plotted |
| `end` | end position of reads to be plotted |
| `trackNameVec` | names of tracks (CoverageDataTrack) |
| `meanCoverage` | mean of coverage over samples (CoverageGataTrack) |

## Details

For information of how to use these tracks in more ways, visit the Gviz package manual.

## Author(s)

Jesper R. Gadin

## See Also

- The `ASEset` class which the functions can be called up on.

## Examples

```
data(ASEset)
x <- ASEset[,1:2]
r <- reads[1:2]
genome(x) <- 'hg19'
seqlevels(r) <- seqlevels(x)

GR <- GRanges(seqnames=seqlevels(x),
  ranges=IRanges(start=min(start(x)),end=max(end(x))),
  strand='+', genome=genome(x))

deTrack <- ASEDAnnotationTrack(x, GR=GR, type='fraction',strand='+')
covTracks <- CoverageDataTrack(x,BamList=r,strand='+')

lst <- c(deTrack,covTracks)

sizes <- c(0.5,rep(0.5/length(covTracks),length(covTracks)))
#temporarily do not run this function
#plotTracks(lst, from=min(start(x)), to=max(end(x)),
#sizes=sizes, col.line = NULL, showId = FALSE, main='mainText',
#cex.main=1, title.width=1, type='histogram')
```

---

# ASEset-locationplot *locationplot ASEset objects*

---

## Description

plotting ASE effects over a specific genomic region

## Usage

```
locationplot(x, ...)

## S4 method for signature 'ASEset'
locationplot(
  x,
  type = "fraction",
  strand = "*",
  yaxis = TRUE,
  xaxis = FALSE,
  xlab = FALSE,
  ylab = TRUE,
  xlab.text = "",
  ylab.text = "",
  legend.colnames = "",
  size = c(0.8, 1),
```

```
  main = NULL,
  pValue = FALSE,
  cex.main = 0.7,
  cex.ylab = 0.6,
  cex.legend = 0.5,
  OrgDb = NULL,
  TxDb = NULL,
  verbose = TRUE,
  top.fraction.criteria = "maxcount",
  allow.whole.chromosome = FALSE,
  ...
)
```

## Arguments

| | |
|---|---|
| x | an ASEset object. |
| ... | arguments passed on to barplot function |
| type | 'fraction' or 'count' |
| strand | '+','-','*' or 'both'. This argument determines which strand is plotted. See `getAlleleCounts` for more information on strand. |
| yaxis | wheter the y-axis is to be displayed or not |
| xaxis | wheter the x-axis is to be displayed or not |
| xlab | showing labels for the tic marks |
| ylab | showing labels for the tic marks |
| xlab.text | xlab text |
| ylab.text | ylab text |
| legend.colnames | gives colnames to the legend matrix |
| size | will give extra space in the margins of the inner plots |
| main | text to use as main label |
| pValue | Display p-value |
| cex.main | set main label size |
| cex.ylab | set ylab label size |
| cex.legend | set legend label size |
| OrgDb | an OrgDb object from which to plot a gene map. If given together with argument TxDb this will only be used to extract genesymbols. |
| TxDb | a TxDb object from which to plot an exon map. |
| verbose | Setting `verbose=TRUE` gives details of procedure during function run |
| top.fraction.criteria | 'maxcount', 'ref' or 'phase' |
| allow.whole.chromosome | logical, overrides 200kb region limit, defaults to FALSE |

## Details

The locationplot methods visualises how fractions are distributed over a larger region of genes on one chromosome. It takes and ASEset object as well as additional information on plot type (see barplot), strand type (see getAlleleCounts), colouring, as well as annotation. The annotation is taken either from the bioconductor OrgDb-sets, the TxDb sets or both. It is obviously important to make sure that the genome build used is the same as used in aligning the RNA-seq data.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## See Also

- The ASEset class which the locationplot function can be called up on.

## Examples

```
data(ASEset)
locationplot(ASEset)

#SNPs are plotted in the order in which they are found.
#This can be sorted according to location as follows:
locationplot(ASEset[order(start(rowRanges(ASEset))),])

#for ASEsets with fewer SNPs the 'count' type plot is
# useful for detailed visualization.
locationplot(ASEset,type='count',strand='*')
```

---

# ASEset-scanForHeterozygotes *scanForHeterozygotes*

---

## Description

Identifies the positions of SNPs found in BamGR reads.

## Usage

```
scanForHeterozygotes(BamList, ...)

## S4 method for signature 'GAlignmentsList'
scanForHeterozygotes(
  BamList,
  minimumReadsAtPos = 20,
  maximumMajorAlleleFrequency = 0.9,
  minimumMinorAlleleFrequency = 0.1,
```

```
  minimumBiAllelicFrequency = 0.9,
  verbose = TRUE,
  ...
)
```

## Arguments

| | |
|---|---|
| BamList | A GAlignmentsList object |
| ... | argument to pass on |
| minimumReadsAtPos | minimum number of reads required to call a SNP at a given position |
| maximumMajorAlleleFrequency | maximum frequency allowed for the most common allele. Setting this parameter lower will minimise the SNP calls resulting from technical read errors, at the cost of missing loci with potential strong ASE |
| minimumMinorAlleleFrequency | minimum frequency allowed for the second most common allele. Setting this parameter higher will minimise the SNP calls resulting from technical read errors, at the cost of missing loci with potential strong ASE |
| minimumBiAllelicFrequency | minimum frequency allowed for the first and second most common allele. Setting a Lower value for this parameter will minimise the identification of loci with three or more alleles in one sample. This is useful if sequencing errors are suspected to be common. |
| verbose | logical indicating if process information should be displayed |

## Details

This function scans all reads stored in a GAlignmentsList for possible heterozygote positions. The user can balance the sensitivity of the search by modifying the minimumReadsAtPos, maximumMajorAlleleFrequency and minimumBiAllelicFrequency arguments.

## Value

scanForHeterozygotes returns a GRanges object with the SNPs for the BamList object that was used as input.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## See Also

- The getAlleleCounts which is a function that count the number of reads overlapping a site.

## Examples

```
data(reads)
s <- scanForHeterozygotes(reads,verbose=FALSE)
```

---

ASEset.old *ASEset.old object*

---

## Description

old version of an ASEset which needs to be updated

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
##load eample data (Not Run)
#data(ASEset.old)
```

---

ASEset.sim *ASEset.sim object*

---

## Description

ASEset with simulated data with SNPs within the first 200bp of chromosome 17, which is required to have example data for the refAllele function.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
##load eample data (Not Run)
#data(ASEset.sim)
```

ASEsetFromBam *ASEset from bam file*

## Description

count alleles and create an ASEset direct from bam file instead of reading into R first.

## Usage

```
ASEsetFromBam(gr, ...)

## S4 method for signature 'GRanges'
ASEsetFromBam(
  gr,
  pathToDir,
  PE = TRUE,
  flagsMinusStrand = c(83, 163),
  flagsPlusStrand = c(99, 147),
  strandUnknown = FALSE,
  ...
)
```

## Arguments

| | |
|---|---|
| gr | GenomicRanges of SNPs to create ASEset for |
| ... | passed on to ASEsetFromBam function |
| pathToDir | Directory of bam files with index in same directory |
| PE | if paired end or not (default: TRUE) |
| flagsMinusStrand | flags that mark reads coming from minus strand |
| flagsPlusStrand | flags that mark reads coming from plus strand |
| strandUnknown | default: FALSE |

## Details

counts the alleles in a bam file based on GRanges positions.

## Author(s)

Jesper R. Gadin

## Examples

```
data(GRvariants)
gr <- GRvariants

##no execution at the moment
#pathToDir <- system.file('inst/extdata/ERP000101_subset', package='AllelicImbalance')
#a <- ASEsetFromBam(gr, pathToDir)
```

---

barplot-lattice-support

*lattice barplot inner functions for ASEset objects*

---

## Description

Generates lattice barplots for ASEset objects. Two levels of plotting detail are provided: a detailed barplot of read counts by allele useful for fewer samples and SNPs, and a less detailed barplot of the fraction of imbalance, useful for more samples and SNPs.

## Usage

```
barplotLatticeFraction(identifier, ...)

barplotLatticeCounts(identifier, ...)
```

## Arguments

| | |
|---|---|
| identifier | the single snp name to plot |
| ... | used to pass on variables |

## Details

`filter.pValue.fraction` is intended to remove p-value annotation with very large difference in frequency, which could just be a sequencing mistake. This is to avoid p-values like 1e-235 or similar.

`sampleColour`User specified colours, either given as named colours ('red', 'blue', etc) or as hexadecimal code. Can be either length 1 for all samples, or else of a length corresponding to the number of samples for individual colouring.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## See Also

- The `ASEset` class which the barplot function can be called up on.

### Examples

```
a <- ASEset
name <- rownames(a)[1]

barplotLatticeFraction(identifier=name, x=a, astrand="+")
barplotLatticeCounts(identifier=name,  x=a, astrand="+")
```

---

`binom.test` *binomial test*

---

### Description

Performs a binomial test on an ASEset object.

### Usage

```
## S4 method for signature 'ASEset'
binom.test(x, n = "*")
```

### Arguments

| | |
|---|---|
| x | ASEset object |
| n | strand option |

### Details

the test can only be applied to one strand at the time.

### Value

`binom.test` returns a matrix

### Author(s)

Jesper R. Gadin, Lasse Folkersen

### See Also

- The `chisq.test` which is another test that can be applied on an ASEset object.

### Examples

```
#load example data
data(ASEset)

#make a binomial test
binom.test(ASEset,'*')
```

chisq.test *chi-square test*

## Description

Performs a chisq.test on an ASEset object.

## Usage

```
## S4 method for signature 'ASEset'
chisq.test(x, y = "*")
```

## Arguments

| | |
|---|---|
| x | ASEset object |
| y | strand option |

## Details

The test is performed on one strand in an ASEset object.

## Value

chisq.test returns a matrix with the chisq.test P-value for each SNP and sample

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## See Also

- The binom.test which is another test that can be applied on an ASEset object.

## Examples

```
#load example data
data(ASEset)

#make a chi-square test on default non-stranded strand
chisq.test(ASEset)
```

cigar-utilities *realCigarPosition*

## Description

From a GAlignments calculate the real corresponding position for each read based on its cigar.

## Usage

```
realCigarPosition.old(RleCigar, BpPos)

realCigarPositions.old(RleCigar)

realCigarPositionsList.old(RleCigarList)
```

## Arguments

| | |
|---|---|
| RleCigar | An Rle containing cigar information |
| BpPos | the absolute position on the chromosome of interest |
| RleCigarList | An RleList containing cigar information |

## Details

The main intention for these functions are to be the internal functions for scanForHeterozygotes and getAlleleCount.

## Value

realCigarPosition returns the new position realCigarPositions returns a vector with the corrected positions to be subsetted from a read. realCigarPositionsList returns a list where each element i a vector with the corrected positions to be subsetted from a read.

## Author(s)

Jesper R. Gadin

## Examples

```
RleCigarList <-  cigarToRleList('3M4I93M')
BpPos <- 5

newPos <- realCigarPosition.old(RleCigar=RleCigarList[[1]], BpPos)
newPositions <- realCigarPositions.old(RleCigar=RleCigarList[[1]])
newPositionsList <- realCigarPositionsList.old(RleCigarList=RleCigarList)
```

`countAllelesFromBam` *alleleCounts from bam file*

## Description

count alleles before creating ASEse.

## Usage

```
countAllelesFromBam(gr, ...)

## S4 method for signature 'GRanges'
countAllelesFromBam(
  gr,
  pathToDir,
  flag = NULL,
  scanBamFlag = NULL,
  return.class = "array",
  verbose = TRUE,
  ...
)
```

## Arguments

| | |
|---|---|
| `gr` | GRanges that contains SNPs of interest |
| `...` | arguments to pass on |
| `pathToDir` | path to directory of bam files |
| `flag` | specify one flag to use as filter, default is no filtering. allowed flags are 99, 147, 83 and 163 |
| `scanBamFlag` | set a custom flag to use as filter |
| `return.class` | type of class for the returned object |
| `verbose` | makes funciton more talkative |

## Details

counts the alleles in a bam file based on GRanges positions.

Important excerpt from the details section of the internal applyPileups function: Regardless of 'param' values, the algorithm follows samtools by excluding reads flagged as unmapped, secondary, duplicate, or failing quality control.

## Author(s)

Jesper R. Gadin

## Examples

```
data(GRvariants)
gr <- GRvariants

##not run at the moment
#pathToDir <- system.file('inst/extdata/ERP000101_subset', package='AllelicImbalance')
#ar <- countAllelesFromBam(gr, pathToDir)
```

---

coverageMatrixListFromGAL

*coverage matrix of GAlignmentsList*

---

## Description

Get coverage per nucleotide for reads covering a region

## Usage

```
coverageMatrixListFromGAL(BamList, ...)

## S4 method for signature 'GAlignmentsList'
coverageMatrixListFromGAL(BamList, strand = "*", ignore.empty.bam.row = TRUE)
```

## Arguments

| | |
|---|---|
| BamList | GAlignmentsList containing reads over the region to calculate coverage |
| ... | arguments to pass on |
| strand | strand has to be '+' or '-' |
| ignore.empty.bam.row | argument not in use atm |

## Details

a convenience function to get the coverage from a list of reads stored in GAlignmnetsList, and returns by default a list with one matrix, and information about the genomic start and stop positions.

## Author(s)

Jesper R. Gadin

## Examples

```
r <- reads
seqlevels(r) <- '17'
covMatList <- coverageMatrixListFromGAL(BamList=r, strand='+')
```

decorateWithExons *decorateWithExons*

## Description

Internal function that can draw gene regions on pre-specified surfaces. Necessary for the genomic-location plots.

## Usage

```
decorateWithExons(x, exonsInRegion, xlim, ylim, chromosome)
```

## Arguments

| | |
|---|---|
| x | ASEset object |
| exonsInRegion | GRanges object with generegions. Can be obtained using getExonsFromAnnotation. Must contain a column 'tx_name' |
| xlim | xlim values for the pre-specified surface |
| ylim | ylim values for the pre-specified surface |
| chromosome | character |

## Details

The main intention of this function is to be used when plotting several bar plots in the same window. This function add gene regions under the bars.

## Value

decorateWithExons returns nothing, but draws genes

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## See Also

- The locationplot which is uses this function internally.
- The decorateWithGenes which is another similar function that locationplot uses internally.

## Examples

```
data(ASEset)
```

decorateWithGenes *decorateWithGenes*

## Description

Internal function that can draw gene regions on pre-specified surfaces. Necessary for the genomic-location plots.

## Usage

```
decorateWithGenes(x, genesInRegion, xlim, ylim, chromosome)
```

## Arguments

| | |
|---|---|
| x | ASEset object |
| genesInRegion | GRanges object with gene regions. Can be obtained using getGenesFromAnnotation |
| xlim | xlim values for the pre-specified surface |
| ylim | ylim values for the pre-specified surface |
| chromosome | character |

## Details

The main intention of this function is to be used when plotting several bar plots in the same window. This function add gene regions under the bars.

## Value

decorateWithGenes returns nothing, but draws genes

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## See Also

- The locationplot which is uses this function internally.
- The decorateWithExons which is another similar function that locationplot uses internally.

## Examples

```
data(ASEset)
```

`defaultMapBias` *Generate default mapbias from genotype*

## Description

Create mapbias array from genotype matrix requires genotype information

## Usage

```
defaultMapBias(x, ...)

## S4 method for signature 'ASEset'
defaultMapBias(x, return.class = "array")
```

## Arguments

| | |
|---|---|
| `x` | `ASEset` object |
| `...` | internal arguments |
| `return.class` | "array" or "ASEset" |

## Details

Default mapbias will be 0.5 for bi-allelic snps and 1 for homozygots. For genotypes with NA, 0.5 will be placed on all four alleles. Therefore tri-allelic can not be used atm. Genotype information has to be placed in the genotype(x) assay.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#load example data
data(ASEset.sim)

fasta <- system.file('extdata/hg19.chr17.subset.fa', package='AllelicImbalance')
refAllele(ASEset.sim,fasta=fasta)
a <- refAllele(ASEset.sim,fasta=fasta)
```

defaultPhase *defaultPhase*

## Description

used to populate the phase slot in an ASEset object

## Usage

```
defaultPhase(i, ...)

## S4 method for signature 'numeric'
defaultPhase(i, j, ...)
```

## Arguments

| | |
|---|---|
| i | number of rows |
| ... | arguments to forward to internal functions |
| j | number of columns |

## Details

will set everything to 0

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
i <- 5
j <- 10
defaultPhase(i,j)
```

detectAI *detectAI*

## Description

detection of AllelicImbalance

## Usage

```
detectAI(x, ...)

## S4 method for signature 'ASEset'
detectAI(
  x,
  return.class = "DetectedAI",
  strand = "*",
  threshold.frequency = 0,
  threshold.count.sample = 1,
  threshold.delta.frequency = 0,
  threshold.pvalue = 0.05,
  inferGenotype = FALSE,
  random.ref = FALSE,
  function.test = "binom.test",
  verbose = TRUE,
  gc = FALSE,
  biasMatrix = FALSE
)
```

## Arguments

| | |
|---|---|
| x | ASEset |
| ... | internal arguments |
| return.class | class to return (atm only class 'logical') |
| strand | strand to infer from |
| threshold.frequency | least fraction to classify (see details) |
| threshold.count.sample | least amount of counts to try to infer allele |
| threshold.delta.frequency | minimum of frequency difference from 0.5 (or mapbias adjusted value) |
| threshold.pvalue | pvalue over this number will be filtered out |
| inferGenotype | infer genotypes based on count data in ASEset object |
| random.ref | set the reference as random if you dont know. Affects interpretation of results. |
| function.test | At the moment the only available option is 'binomial.test' |
| verbose | makes function more talkative |
| gc | use garbage collection when possible to save space |
| biasMatrix | use biasMatrix in ASEset, or use default expected frequency of 0.5 for all sites |

## Details

threshold.frequency is the least fraction needed to classify as bi tri or quad allelic SNPs. If 'all' then all of bi tri and quad allelic SNPs will use the same threshold. Everything under the treshold

will be regarded as noise. 'all' will return a matrix with snps as rows and uni bi tri and quad will be columns. For this function Anything that will return TRUE for tri-allelicwill also return TRUE for uni and bi-allelic for the same SNP an Sample.

return.type 'ref' return only AI when reference allele is more expressed. 'alt' return only AI when alternative allele is more expressed or 'all' for both 'ref' and 'alt' alleles. Reference allele is the one present in the reference genome on the forward strand.

threshold.delta.frequency and function.test will use the value in mapBias(x) as expected value.

function.test will use the two most expressed alleles for testing. Make therefore sure there are no tri-allelic SNPs or somatic mutations among the SNPs in the ASEset.

inferGenotype(), set TRUE it should be used with as much samples as possible. If you split up the samples and run detectAI() on each sample separately, please make sure you have inferred the genotypes in before hand, alternatively used the genotypes detected by another variantCaller or chip-genotypes. Use ONLY biallelic genotypes.

## Author(s)

Jesper R. Gadin

## Examples

```
#load example data
data(ASEset)
a <- ASEset

dai <- detectAI(a)
```

---

# DetectedAI-class *DetectedAI class*

---

## Description

Object that holds results from AI detection.

## Usage

```
referenceFrequency(x, ...)

## S4 method for signature 'DetectedAI'
referenceFrequency(x, return.class = "array")

thresholdFrequency(x, ...)

## S4 method for signature 'DetectedAI'
thresholdFrequency(x, return.class = "array")
```

```
thresholdCountSample(x, ...)

## S4 method for signature 'DetectedAI'
thresholdCountSample(x, return.class = "array")

thresholdDeltaFrequency(x, ...)

## S4 method for signature 'DetectedAI'
thresholdDeltaFrequency(x, return.class = "array")

thresholdPvalue(x, ...)

## S4 method for signature 'DetectedAI'
thresholdPvalue(x, return.class = "array")
```

## Arguments

| | |
|---|---|
| x | ASEset object or list of ASEsets |
| ... | pass arguments to internal functions |
| return.class | type of class returned eg. "list or ""array". |

## Details

The DetectedAI-class contains

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
data(ASEset)
a <- ASEset
dai <- detectAI(a)

#summary(gba)
#write.tables(dai)
```

---

# DetectedAI-plot *DetectedAI plot*

---

## Description

plot functions for the DetectedAI-class

## Usage

```
frequency_vs_threshold_variable_plot(x, ...)

## S4 method for signature 'DetectedAI'
frequency_vs_threshold_variable_plot(
  x,
  var = "threshold.count.sample",
  hetOverlay = TRUE,
  smoothscatter = FALSE
)

detectedAI_vs_threshold_variable_plot(x, ...)

## S4 method for signature 'DetectedAI'
detectedAI_vs_threshold_variable_plot(
  x,
  var = "threshold.count.sample",
  summaryOverSamples = "sum",
  hetOverlay = TRUE,
  smoothscatter = FALSE
)

reference_frequency_density_vs_threshold_variable_plot(x, ...)

## S4 method for signature 'DetectedAI'
reference_frequency_density_vs_threshold_variable_plot(
  x,
  var = "threshold.count.sample"
)

detectedAI_vs_threshold_variable_multigraph_plot(x, ...)

## S4 method for signature 'DetectedAI'
detectedAI_vs_threshold_variable_multigraph_plot(x, ncol = 2, ...)

frequency_vs_threshold_variable_multigraph_plot(x, ...)

## S4 method for signature 'DetectedAI'
frequency_vs_threshold_variable_multigraph_plot(x, ncol = 2, ...)

reference_frequency_density_vs_threshold_variable_multigraph_plot(x, ...)

## S4 method for signature 'DetectedAI'
reference_frequency_density_vs_threshold_variable_multigraph_plot(
  x,
  ncol = 2,
  ...
)
```

### Arguments

| | |
|---|---|
| x | detectedAI object |
| ... | pass on variables internally |
| var | string, see details for available options |
| hetOverlay | logical, if TRUE show nr of het SNPs used to calculate the reference allele frequency mean |
| smoothscatter | boolean, smoothscatter over the means |
| summaryOverSamples | 'mean' or 'sum' |
| ncol | nr of columns for multiplots |

### Details

plot helper functions. The documentation will be improved before next release.

### Author(s)

Jesper R. Gadin, Lasse Folkersen

### Examples

```
#some example code here
#generate example
data(ASEset)
a <- ASEset
dai <- detectAI(a,
   threshold.count.sample=1:50,
   threshold.frequency=seq(0,0.5,by=0.01),
   threshold.delta.frequency=seq(0,0.5,by=0.01),
   threshold.pvalue=rev(seq(0.001,0.05, by=0.005))
)

frequency_vs_threshold_variable_plot(dai)
detectedAI_vs_threshold_variable_plot(dai)
detectedAI_vs_threshold_variable_multigraph_plot(dai)
frequency_vs_threshold_variable_multigraph_plot(dai)
```

---

## DetectedAI-summary *DetectedAI summary*

---

### Description

Summary helper functions for the DetectedAI-class

## Usage

```
frequency_vs_threshold_variable_summary(x, ...)

## S4 method for signature 'DetectedAI'
frequency_vs_threshold_variable_summary(
  x,
  var = "threshold.count.sample",
  return.class = "matrix",
  ...
)

detectedAI_vs_threshold_variable_summary(x, ...)

## S4 method for signature 'DetectedAI'
detectedAI_vs_threshold_variable_summary(x, var = "threshold.count.sample")

usedSNPs_vs_threshold_variable_summary(x, ...)

## S4 method for signature 'DetectedAI'
usedSNPs_vs_threshold_variable_summary(x, var = "threshold.count.sample")
```

## Arguments

| | |
|---|---|
| x | detectedAI object |
| ... | pass on variables internally |
| var | string, see details for available options |
| return.class | 'matrix' or 'array' |

## Details

Summary helper functions. The documentation will be improved before next release.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#some example code here
#generate example
data(ASEset)
a <- ASEset
dai <- detectAI(a,
   threshold.count.sample=1:50,
   threshold.frequency=seq(0,0.5,by=0.01),
   threshold.delta.frequency=seq(0,0.5,by=0.01),
   threshold.pvalue=rev(seq(0.001,0.05, by=0.005))
)
```

```
frequency_vs_threshold_variable_summary(dai)
```

---

`fractionPlotDf` *Plot Dataframe*

---

## Description

Summarizes information to ease creating plots

## Usage

```
fractionPlotDf(x, snp, strand = "*", top.fraction.criteria = "maxcount", ...)

## S4 method for signature 'ASEset'
fractionPlotDf(x, snp, strand = "*", top.fraction.criteria = "maxcount", ...)
```

## Arguments

| | |
|---|---|
| `x` | ASEset |
| `snp` | rownames identifier for ASEset or row number |
| `strand` | '+', '-' or '*' |
| `top.fraction.criteria` | 'maxcount', 'ref' or 'phase' |
| `...` | arguments to forward to internal functions |

## Details

Main purpose is to reduce the amount of overall code and ease maintenance.

top.fraction.criteria can take three options, maxcount, ref and phase. The top allele will be every second row in the data frame, with start from row 2. The maxcount argument will put the allele with most reads on top of the bivariate fraction. Similarly the ref argument will put always the reference allele on top. The phase arguments puts the maternal phase always on top. The top.fraction.criteria for the ref or phase arguments requires that both ref and alt is set in mcols(ASEset).

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#test on example ASEset
data(ASEset)
a <- ASEset
df <- fractionPlotDf(a, 1, strand="+")
```

## gba *global analysis wrapper*

### Description

A wrapper to make a global analysis based on paths for BAM, VCF and GFF files

### Usage

```
gba(pathBam, ...)

## S4 method for signature 'character'
gba(pathBam, pathVcf, pathGFF = NULL, verbose)
```

### Arguments

| | |
|---|---|
| pathBam | path to bam file |
| ... | arguments to pass on |
| pathVcf | path to vcf file |
| pathGFF | path to gff file |
| verbose | makes function more talkative |

### Author(s)

Jesper R. Gadin

### Examples

```
#empty as function doesn't exist
```

## genomatrix *genomatrix object*

### Description

genomatrix is an example of a matrix with genotypes

### Author(s)

Jesper R. Gadin, Lasse Folkersen

### Examples

```
##load eample data (Not Run)
#data(genomatrix)
```

genotype2phase *genotype2phase*

## Description

used to convert the genomatrix from the visually friendly matrix to phase array.

## Usage

```
genotype2phase(x, ...)

## S4 method for signature 'matrix'
genotype2phase(
  x,
  ref = NULL,
  return.class = "array",
  levels = c("A", "C", "G", "T"),
  ...
)
```

## Arguments

| | |
|---|---|
| x | matrix see examples |
| ... | pass on additional param |
| ref | reference alleles |
| return.class | 'array' or 'list' |
| levels | vector of expected alleles |

## Details

To not introduce redundant information in the ASEset object, the genotype matrix is translated to a phase matrix, containing the same information. Does not allow tri-allelic or multi-allelic SNPs, and if present the multi-allelic SNPs will lose the least occuring genotype.

This function can handle indels, but if the reference allele is not provided, the rank matrix which is temporary created might use lots of memory, depending on the amount of indels among the genotypes. As conclusion, it is preferable to send in reference genome when converting to phase.

levels information is only important if the reference allele has to be guessed, and so if reference information is provided, the levels argument can be ignored.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#load example data
data(genomatrix)
data(ASEset)
p <- genotype2phase(genomatrix, ref(ASEset))
```

---

`getAlleleCounts` *snp count data*

---

## Description

Given the positions of known SNPs, this function returns allele counts from a BamGRL object

## Usage

```
getAlleleCounts(BamList, ...)

## S4 method for signature 'GAlignmentsList'
getAlleleCounts(
  BamList,
  GRvariants,
  strand = "*",
  return.class = "list",
  verbose = TRUE,
  ...
)
```

## Arguments

| | |
|---|---|
| `BamList` | A `GAlignmentsList` object or `GRangesList` object containing data imported from a bam file |
| `...` | parameters to pass on |
| `GRvariants` | A `GRanges` object that contains positions of SNPs to retrieve |
| `strand` | A length 1 `character` with value '+', '-', or '*'. This argument determines if `getAlleleCounts` will retrieve counts from all reads, or only from reads marked as '+', '-' or '*' (unknown), respectively. |
| `return.class` | 'list' or 'array' |
| `verbose` | Setting `verbose=TRUE` makes function more talkative |

## Details

This function is used to retrieve the allele counts from specified positions in a set of RNA-seq reads. The `BamList` argument will typically have been created using the `impBamGAL` function on bam-files. The `GRvariants` is either a GRanges with user-specified locations or else it is generated through scanning the same bam-files as in `BamList` for heterozygote locations (e.g. using `scanForHeterozygotes`). The GRvariants will currently only accept locations having width=1, corresponding to bi-allelic SNPs. In the `strand` argument, specifying '*' is the same as retrieving the sum count of '+' and '-' reads (and unknown strand reads in case these are found in the bam file). '*' is the default behaviour and can be used when the RNA-seq experiments strand information is not available.

## Value

`getAlleleCounts` returns a list of several data.frame objects, each storing the count data for one SNP.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## See Also

- The `scanForHeterozygotes` which is a function to find possible heterozygote sites in a GenomicAlignments object

## Examples

```
#load example data
data(reads)
data(GRvariants)


#get counts at the three positions specified in GRvariants
alleleCount <- getAlleleCounts(BamList=reads,GRvariants,
strand='*')

#if the reads had contained stranded data, these two calls would
#have given the correct input objects for getAlleleCounts
alleleCountPlus <- getAlleleCounts(BamList=reads,GRvariants,
strand='+')
alleleCountMinus <- getAlleleCounts(BamList=reads,GRvariants,
strand='-')
```

getAlleleQuality *snp quality data*

## Description

Given the positions of known SNPs, this function returns allele quality from a BamGRL object

## Usage

```
getAlleleQuality(BamList, ...)

## S4 method for signature 'GAlignmentsList'
getAlleleQuality(
  BamList,
  GRvariants,
  fastq.format = "illumina.1.8",
  return.class = "array",
  verbose = TRUE,
  ...
)
```

## Arguments

| | |
|---|---|
| BamList | A GAlignmentsList object or GRangesList object containing data imported from a bam file |
| ... | parameters to pass on |
| GRvariants | A GRanges object that contains positions of SNPs to retrieve. |
| fastq.format | default 'illumina.1.8' |
| return.class | 'list' or 'array' |
| verbose | Setting verbose=TRUE makes function more talkative |

## Details

This function is used to retrieve the allele quality strings from specified positions in a set of RNA-seq reads. The BamList argument will typically have been created using the impBamGAL function on bam-files. The GRvariants is either a GRanges with user-specified locations or else it is generated through scanning the same bam-files as in BamList for heterozygote locations (e.g. using scanForHeterozygotes). The GRvariants will currently only accept locations having width=1, corresponding to bi-allelic SNPs. The strand type information will be kept in the returned object. If the strand is marked as unknown "*", it will be forced to the "+" strand.

quaity information is extracted from the BamList object, and requires the presence of mcols(BamList)[["qual"]] to contain quality sequences.

## Value

getAlleleQuality returns a list of several data.frame objects, each storing the count data for one SNP.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#load example data
data(reads)
data(GRvariants)

#get counts at the three positions specified in GRvariants
alleleQualityArray <- getAlleleQuality(BamList=reads,GRvariants)

#place in ASEset object
alleleCountsArray <- getAlleleCounts(BamList=reads,GRvariants,
                     strand='*', return.class="array")

 a <- ASEsetFromArrays(GRvariants, countsUnknown = alleleCountsArray)
 aquals(a) <- alleleQualityArray
```

---

# getAreaFromGeneNames *Get Gene Area*

---

## Description

Given a character vector with genesymbols and an OrgDb object, this function returns a GRanges giving the coordinates of the genes.

## Usage

```
getAreaFromGeneNames(genesymbols, ...)

## S4 method for signature 'character'
getAreaFromGeneNames(
  genesymbols,
  OrgDb,
  leftFlank = 0,
  rightFlank = 0,
  na.rm = FALSE,
  verbose = TRUE
)
```

## Arguments

| | |
|---|---|
| genesymbols | A character vector that contains genesymbols of genes from which we wish to retrieve the coordinates |
| ... | arguments to pass on |
| OrgDb | An OrgDb object containing gene annotation |

| | |
|---|---|
| leftFlank | A integer specifying number of additional nucleotides before the genes |
| rightFlank | A integer specifying number of additional nucleotides after the genes |
| na.rm | A boolean removing genes that returned NA from the annotation |
| verbose | Setting verbose=TRUE makes function more talkative |

## Details

This function is a convenience function that can be used to determine which genomic coordinates to specify to e.g. impBamGAL when retrieving reads.

The function cannot handle genes that do not exist in the annotation. To remove these please set the na.rm=TRUE.

## Value

getAreaFromGeneNames returns a GRanges object with genomic coordinates around the specified genes

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#load example data
data(ASEset)

#get counts at the three positions specified in GRvariants
library(org.Hs.eg.db )
searchArea<-getAreaFromGeneNames(c('PAX8','TLR7'), org.Hs.eg.db)
```

---

# getDefaultMapBiasExpMean

*Map Bias*

---

## Description

an allele frequency array

## Usage

```
getDefaultMapBiasExpMean(alleleCountList, ...)

getDefaultMapBiasExpMean3D(alleleCountList, ...)

## S4 method for signature 'list'
getDefaultMapBiasExpMean(alleleCountList)
```

```
## S4 method for signature 'ANY'
getDefaultMapBiasExpMean3D(alleleCountList)
```

### Arguments

| | |
|---|---|
| alleleCountList | A GRangesList object containing read information |
| ... | parameters to pass on |

### Details

This function will assume there is no bias that comes from the mapping of reads, and therefore create a matrix with expected frequency of 0.5 for each allele.

### Value

getDefaultMapBiasExpMean returns a matrix with a default expected mean of 0.5 for every element.

### Author(s)

Jesper R. Gadin, Lasse Folkersen

### Examples

```
#load example data
data(ASEset)
#access SnpAfList
alleleCountList <- alleleCounts(ASEset)
#get default map bias exp mean
matExpMean <- getDefaultMapBiasExpMean(alleleCountList)
```

---

## getSnpIdFromLocation *Get rsIDs from locations of SNP*

---

### Description

Given a GRanges object of SNPs and a SNPlocs annotation, this function attempts to replace the names of the GRanges object entries with rs-IDs.

### Usage

```
getSnpIdFromLocation(GR, ...)

## S4 method for signature 'GRanges'
getSnpIdFromLocation(GR, SNPloc, return.vector = FALSE, verbose = TRUE)
```

### Arguments

| | |
|---|---|
| GR | A GRanges that contains positions of SNPs to look up |
| ... | arguments to pass on |
| SNPloc | A SNPlocs object containing information on SNP locations (e.g. SNPlocs.Hsapiens.dbSNP.xxxxxxxx) |
| return.vector | Setting return.vector=TRUE returns vector with rsIds |
| verbose | Setting verbose=TRUE makes function more talkative |

### Details

This function is used to try to identify the rs-IDs of SNPs in a GRanges object.

### Value

getSnpIdFromLocation returns the same GRanges object it was given with, but with updated with rs.id information.

### Author(s)

Jesper R. Gadin, Lasse Folkersen

### Examples

```
is_32bit_windows <- .Platform$OS.type == "windows" &&
                    .Platform$r_arch == "i386"
if (!is_32bit_windows && require(SNPlocs.Hsapiens.dbSNP144.GRCh37)) {
 #load example data
 data(ASEset)

  #get counts at the three positions specified in GRvariants
  updatedGRanges <- getSnpIdFromLocation(rowRanges(ASEset),
    SNPlocs.Hsapiens.dbSNP144.GRCh37)
}
```

---

## GlobalAnalysis-class *GlobalAnalysis class*

---

### Description

Object that holds results from a global AI analysis including reference bias estimations and AI detection.

### Arguments

| | |
|---|---|
| x | ASEset object or list of ASEsets |
| TxDb | A transcriptDb object |
| ... | pass arguments to internal functions |

### Details

The GlobalAnalysis-class contains summaries and "pre-configured and pre-calculated lattice plots" needed to create an AI-report

### Value

An object of class GlobalAnalysis containing all data to make report.

### Author(s)

Jesper R. Gadin, Lasse Folkersen

### Examples

```
data(ASEset)
#a <- ASEset
#gba <- gba(a)

#report(gba)
#write.tables(gba)
#graphs(gba)
#as.list(gba)
```

---

## GRvariants *GRvariants object*

---

### Description

this data is a GRanges object that contains the ranges for three example SNPs.

### Author(s)

Jesper R. Gadin, Lasse Folkersen

### See Also

- The reads which is another example object

### Examples

```
#load example data
data(GRvariants)
```

histplot *histogram plots*

## Description

uses base graphics hist plot

## Usage

```
## S4 method for signature 'ASEset'
hist(x, strand = "*", type = "mean", log = 1, ...)
```

## Arguments

| | |
|---|---|
| x | ReferenceBias object or ASEset object |
| strand | '+','-' or '*' |
| type | 'mean' (only one option atm) |
| log | an integer to log each value (integer 10 for log10) |
| ... | arguments to forward to interal boxplots function |

## Details

The histogram will show the density over frequencies for each sample

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
##load example data

#data(ASEset)
#a <- ASEset
#hist(a)
```

## implodeList.old *implode list of arguments into environment*

### Description

apply on list of variables to be put in the local environment

### Usage

```
implodeList.old(x)
```

### Arguments

| | |
|---|---|
| x | list of variables |

### Details

help the propagation of e.g. graphical paramters

### Author(s)

Jesper R. Gadin

### Examples

```
lst <- list(hungry='yes', thirsty='no')
implodeList.old(lst)
#the check ls()
 ls()
```

## import-bam *Import Bam*

### Description

Imports a specified genomic region from a bam file using a GRanges object as search area.

### Usage

```
impBamGAL(UserDir, ...)

## S4 method for signature 'character'
impBamGAL(
  UserDir,
  searchArea,
  files = NULL,
```

```
  XStag = FALSE,
  verbose = TRUE,
  ...
)
```

## Arguments

| | |
|---|---|
| UserDir | The relative or full path of folder containing bam files. |
| ... | arguments to pass on |
| searchArea | A GenomicRanges object that contains the regions of interest |
| files | use character vector to specify one or more files to import. The default imports all bam files from the directory. |
| XStag | Setting XStag=TRUE stores the strand specific information in the mcols slot 'XS' |
| verbose | makes the function more talkative. |

## Details

If the sequence data is strand-specific you may want to set XStag=TRUE. The strand specific information has then to be stored in the meta columns with column name 'XS'. If the aligner did not set the XS-tag and the data is strand- specific it is still be possible to infer the strand from the bit flags after importing the reads to R. Depending on the strand-specific protocol different combinations of the flags will have to be used. For illumina fr-secondstrand, 83 and 163 are minus strand reads and 99 and 147 are plus strand reads.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#Declare searchArea
searchArea <- GRanges(seqnames=c('17'), ranges=IRanges(79478301,79478361))

#Relative or full path
pathToFiles <- system.file('extdata/ERP000101_subset', package='AllelicImbalance')

#all files in directory
reads <- impBamGAL(pathToFiles,searchArea,verbose=FALSE)
#specified files in directory
reads <- impBamGAL(pathToFiles,searchArea,
   files=c("ERR009160.bam", "ERR009167.bam"),verbose=FALSE)
```

`import-bam-2` *Import Bam-2*

## Description

Imports bla bal bal a specified genomic region from a bam file using a GenomicRanges object as search area.

## Usage

```
impBamGRL.old(UserDir, searchArea, verbose = TRUE)
```

## Arguments

| | |
|---|---|
| `UserDir` | The relative or full path of folder containing bam files. |
| `searchArea` | A `GenomicRanges object` that contains the regions of interest |
| `verbose` | Setting `verbose=TRUE` gives details of procedure during function run. |

## Details

These functions are right on tahea wrappers to import bam files into R and store them into either GRanges, GAlignments or GappedAlignmentpairs objects.

It is recommended to use the impBamGAL() which takes information of gaps into account. It is also possible to use the other variants as well, but then pre-filtering becomes important keps to understand because gapped, intron-spanning reads will cause problems. This is because the GRanges objects can not handle if gaps are present and will then give a wrong result when calculating the allele (SNP) count table.

## Value

`impBamGRL` returns a GRangesList object containing the RNA-seq reads in the region defined by the `searchArea` argument. `impBamGAL` returns a list with GAlignments objects containing the RNA-seq reads in the region defined by the `searchArea` argument. `funImpBamGAPL` returns a list with GappedAlignmentPairs object containing the RNA-seq reads in the region defined by the `searchArea` argument.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#Declare searchArea
searchArea <- GRanges(seqnames=c('17'), ranges=IRanges(79478301,79478361))

#Relative or full path
pathToFiles <- system.file('extdata/ERP000101_subset', package='AllelicImbalance')
```

import-bcf *Import Bcf Selection*

## Description

Imports a selection of a bcf file or files specified by a GenomicRanges object as search area.

## Usage

```
impBcfGRL(UserDir, ...)

## S4 method for signature 'character'
impBcfGRL(UserDir, searchArea = NULL, verbose = TRUE, ...)

impBcfGR(UserDir, ...)

## S4 method for signature 'character'
impBcfGR(UserDir, searchArea = NULL, verbose = TRUE, ...)
```

## Arguments

| | |
|---|---|
| UserDir | The relative or full path of folder containing bam files. |
| ... | parameters to pass on |
| searchArea | A GenomicRanges object that contains the regions of interest |
| verbose | Setting verbose=TRUE gives details of the procedure during function run. |

## Details

A wrapper to import bcf files into R in the form of GenomicRanges objects.

## Value

BcfImpGRList returns a GRangesList object. BcfImpGR returns one GRanges object of all unique entries from one or more bcf files.

## Note

Make sure there is a complementary index file *.bcf.csi for each bcf file in UserDir. If there is not, then the functions impBcfGRL and impBcfGR will try to create them.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## See Also

- The impBamGRL for importing bam files
- The getAlleleCounts for how to get allele(SNP) counts
- The scanForHeterozygotes for how to find possible heterozygote positions

## Examples

```
#Declare searchArea
searchArea <- GRanges(seqnames=c('17'), ranges=IRanges(79478301,79478361))

#Relative or full path
pathToFiles <- system.file('extdata/ERP000101_subset', package='AllelicImbalance')

#import
reads <- impBcfGRL(pathToFiles, searchArea, verbose=FALSE)
```

---

# inferAlleles *inference of SNPs of ASEset*

---

## Description

inference of SNPs

## Usage

```
inferAlleles(
  x,
  strand = "*",
  return.type = "bi",
  threshold.frequency = 0,
  threshold.count.sample = 1,
  inferOver = "eachSample",
  allow.NA = FALSE
)
```

## Arguments

| | |
|---|---|
| x | ASEset |
| strand | strand to infer from |
| return.type | 'uni' 'bi' 'tri' 'quad' 'all' |
| threshold.frequency | least fraction to classify (see details) |
| threshold.count.sample | least amount of counts to try to infer allele |
| inferOver | 'eachSample' or 'allSamples' |
| allow.NA | treat NA as zero when TRUE |

### Details

threshold.frequency is the least fraction needed to classify as bi tri or quad allelic SNPs. If 'all' then all of bi tri and quad allelic SNPs will use the same threshold. Everything under the treshold will be regarded as noise. 'all' will return a matrix with snps as rows and uni bi tri and quad will be columns. For this function Anything that will return TRUE for tri-allelicwill also return TRUE for uni and bi-allelic for the same SNP an Sample.

### Author(s)

Jesper R. Gadin

### Examples

```
data(ASEset)
i <- inferAlleles(ASEset)
```

---

## inferAltAllele *inferAltAllele*

---

### Description

inference of the alternate allele based on count data

### Arguments

| | |
|---|---|
| x | matrix see examples |
| return.class | class of returned object |
| allele.source | 'arank' |
| verbose | make function more talkative |
| ... | arguments to forward to internal functions |

### Details

The inference essentially ranks all alleles and the most expressed allele not declared as reference will be inferred as the alternative allele. At the moment only inference of bi-allelic alternative alleles are available.

### Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#load data
data(ASEset)

alt <- inferAltAllele(ASEset)
```

---

`inferGenotypes` *infererence of genotypes from ASEset count data*

---

## Description

inference of genotypes

## Usage

```
inferGenotypes(
  x,
  strand = "*",
  return.class = "matrix",
  return.allele.allowed = "bi",
  threshold.frequency = 0,
  threshold.count.sample = 1
)
```

## Arguments

| | |
|---|---|
| `x` | ASEset |
| `strand` | strand to infer from |
| `return.class` | 'matrix' or 'vector' |
| `return.allele.allowed` | vector with 'bi' 'tri' or 'quad'. 'uni' Always gets returned |
| `threshold.frequency` | least fraction to classify (see details) |
| `threshold.count.sample` | least amount of counts to try to infer allele |

## Details

Oftern necessary information to link AI to SNPs outside coding region

## Author(s)

Jesper R. Gadin

## Examples

```
data(ASEset)
g <- inferGenotypes(ASEset)
```

---

`initialize-ASEset` *Initialize ASEset*

---

## Description

Functions to construct ASEset objects

## Usage

```
ASEsetFromCountList(
  rowRanges,
  countListUnknown = NULL,
  countListPlus = NULL,
  countListMinus = NULL,
  colData = NULL,
  mapBiasExpMean = NULL,
  phase = NULL,
  aquals = NULL,
  verbose = FALSE,
  ...
)

ASEsetFromArrays(
  rowRanges,
  countsUnknown = NULL,
  countsPlus = NULL,
  countsMinus = NULL,
  colData = NULL,
  mapBiasExpMean = NULL,
  phase = NULL,
  genotype = NULL,
  aquals = NULL,
  verbose = FALSE,
  ...
)
```

## Arguments

| | |
|---|---|
| `rowRanges` | A `GenomicRanges object` that contains the variants of interest |
| `countListUnknown` | A `list` where each entry is a matrix with allele counts as columns and sample counts as rows |

| | |
|---|---|
| countListPlus | A list where each entry is a matrix with allele counts as columns and sample counts as rows |
| countListMinus | A list where each entry is a matrix with allele counts as columns and sample counts as rows |
| colData | A DataFrame object containing sample specific data |
| mapBiasExpMean | A 3D array where the SNPs are in the 1st dimension, samples in the 2nd dimension and variants in the 3rd dimension. |
| phase | A matrix or an array containing phase information. |
| aquals | A 4-D array containing the countinformation, see details |
| verbose | Makes function more talkative |
| ... | arguments passed on to SummarizedExperiment constructor |
| countsUnknown | An array containing the countinformation |
| countsPlus | An array containing the countinformation |
| countsMinus | An array containing the countinformation |
| genotype | matrix |

## Details

The resulting ASEset object is based on the RangedSummarizedExperiment class, and will therefore inherit the same accessors and ranges operations.

If both countListPlus and countListMinus are given they will be used to calculate countListUnknown, which is the sum of the plus and minus strands.

countListPlus, countListMinus and countListUnknown are i.e. the outputs from the getAlleleCounts function.

aquals is new for the devel branch and will be changed slighly before the relase to include better granularity.

## Value

ASEsetFromCountList returns an ASEset object.

## Note

ASEsetFromCountList requires the same input data as a RangedSummarizedExperiment, but with minimum one assay for the allele counts.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#make example alleleCountListPlus
set.seed(42)
countListPlus <- list()
snps <- c('snp1','snp2','snp3','snp4','snp5')
for(snp in snps){
count<-matrix(rep(0,16),ncol=4,dimnames=list(
c('sample1','sample2','sample3','sample4'),
c('A','T','G','C')))
#insert random counts in two of the alleles
for(allele in sample(c('A','T','G','C'),2)){
count[,allele]<-as.integer(rnorm(4,mean=50,sd=10))
}
countListPlus[[snp]] <- count
}

#make example alleleCountListMinus
countListMinus <- list()
snps <- c('snp1','snp2','snp3','snp4','snp5')
for(snp in snps){
count<-matrix(rep(0,16),ncol=4,dimnames=list(
c('sample1','sample2','sample3','sample4'),
c('A','T','G','C')))
#insert random counts in two of the alleles
for(allele in sample(c('A','T','G','C'),2)){
count[,allele]<-as.integer(rnorm(4,mean=50,sd=10))
}
countListMinus[[snp]] <- count
}


#make example rowRanges
rowRanges <- GRanges(
seqnames = Rle(c('chr1', 'chr2', 'chr1', 'chr3', 'chr1')),
         ranges = IRanges(1:5, width = 1, names = head(letters,5)),
         snp = paste('snp',1:5,sep='')
         )
#make example colData
colData <- DataFrame(Treatment=c('ChIP', 'Input','Input','ChIP'),
 row.names=c('ind1','ind2','ind3','ind4'))

#make ASEset
a <- ASEsetFromCountList(rowRanges, countListPlus=countListPlus,
countListMinus=countListMinus, colData=colData)
```

---

`initialize-DetectedAI` *Initialize DetectedAI*

---

## Description

Functions to construct DetectedAI objects

## Usage

```
DetectedAIFromArray(
  x = "ASEset",
  strand = "*",
  reference.frequency = NULL,
  threshold.frequency = NULL,
  threshold.count.sample = NULL,
  threshold.delta.frequency = NULL,
  threshold.pvalue = NULL,
  threshold.frequency.names = NULL,
  threshold.count.sample.names = NULL,
  threshold.delta.frequency.names = NULL,
  threshold.pvalue.names = NULL,
  ...
)
```

## Arguments

| | |
|---|---|
| x | ASEset |
| strand | set strand to detectAI over "+","-","*" |
| reference.frequency | frequencies of reference alleles based allele counts |
| threshold.frequency | logical array for frequency thresholds |
| threshold.count.sample | logical array for per sample allele count thresholds |
| threshold.delta.frequency | logical array for delta frequency thresholds. |
| threshold.pvalue | logical array for pvalue thresholds (max 1, min 0) |
| threshold.frequency.names | character vector |
| threshold.count.sample.names | character vector |
| threshold.delta.frequency.names | character vector |
| threshold.pvalue.names | character vector |
| ... | internal arguments |

## Details

produces a class container for reference bias calculations

### Author(s)

Jesper R. Gadin, Lasse Folkersen

### Examples

```
data(ASEset)
a <- ASEset
dai <- detectAI(a)
```

---

## initialize-GlobalAnalysis
*Initialize GlobalAnalysis*

---

### Description

Functions to construct GlobalAnalysis objects

### Usage

```
GAnalysis(x = "ASEset", ...)
```

### Arguments

| | |
|---|---|
| x | ASEset |
| ... | internal arguments |

### Details

produces a class container for a global analysis

### Author(s)

Jesper R. Gadin, Lasse Folkersen

### Examples

```
data(ASEset)
a <- ASEset
# gba <- gba(a)
```

initialize-RiskVariant *Initialize RiskVariant*

## Description

Functions to construct RiskVariant objects

## Usage

```
RiskVariantFromGRangesAndPhaseArray(x, phase, ...)
```

## Arguments

| | |
|---|---|
| x | GRanges object for the SNPs |
| phase | array with phaseinfo |
| ... | internal arguments |

## Details

produces a class container for reference bias calculations

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
data(ASEset)
#p <- getPhaseFromSomewhere
#rv <- RiskVariantFromGRangesAndPhaseArray(x=GRvariants, phase=p)
```

legendBarplot *add legend to AllelicImbalance barplot*

## Description

adds a very customizable legend function for AllelicImbalance barplots.

## Usage

```
legendBarplot(
  lowerLeftCorner,
  size,
  rownames,
  colnames,
  boxsize = 1,
  boxspace = 1,
  fgCol,
  bgCol,
  ylegendPos = 1,
  xlegendPos = 0.96,
  cex = 1
)
```

## Arguments

| | |
|---|---|
| lowerLeftCorner | position of the plot to add legend to (default c(0,0)) |
| size | scale the plot, default is 1 |
| rownames | rownames in legend |
| colnames | colnames in legend |
| boxsize | size of each box fill |
| boxspace | space inbetween the box fill |
| fgCol | color for allele1 |
| bgCol | color for allele2 |
| ylegendPos | placement of the legend within the plot for y |
| xlegendPos | placement of the legend within the plot for x |
| cex | size of legend text |

## Details

the function is preferably called from within the AllelicImbalance barplot method.

## Author(s)

Jesper R. Gadin

## Examples

```
#code placeholders
#< create a barplot with legend >
#< add legend >
```

LinkVariantAlmlof-class *LinkVariantAlmlof class*

## Description

Object that holds results from AI detection.

## Usage

```
pvalue(x, ...)

## S4 method for signature 'LinkVariantAlmlof'
pvalue(x)
```

## Arguments

| | |
|---|---|
| x | LinkVariantAlmlof object |
| ... | pass arguments to internal functions |

## Details

The LinkVariantAlmlof-class contains

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#some code
```

LinkVariantAlmlof-plot *plot LinkVariantAlmlof objects*

## Description

plot an object of type LinkVariantAlmlof

## Usage

```
plot(x, y, ...)

## S4 method for signature 'LinkVariantAlmlof,ANY'
plot(x, y, ...)
```

## Arguments

| | |
|---|---|
| x | LinkVariantAlmlof object |
| y | not used |
| ... | pass on arguments to internal methods |

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
data(ASEset)
a <- ASEset
# Add phase
set.seed(1)
p1 <- matrix(sample(c(1,0),replace=TRUE, size=nrow(a)*ncol(a)),nrow=nrow(a), ncol(a))
p2 <- matrix(sample(c(1,0),replace=TRUE, size=nrow(a)*ncol(a)),nrow=nrow(a), ncol(a))
p <- matrix(paste(p1,sample(c("|","|","/"), size=nrow(a)*ncol(a), replace=TRUE), p2, sep=""),
 nrow=nrow(a), ncol(a))

phase(a) <- p

#add alternative allele information
mcols(a)[["alt"]] <- inferAltAllele(a)

#init risk variants
p.ar <- phaseMatrix2Array(p)
rv <- RiskVariantFromGRangesAndPhaseArray(x=GRvariants, phase=p.ar)

#colnames has to be samea and same order in ASEset and RiskVariant
colnames(a) <- colnames(rv)

# in this example each and every snp in the ASEset defines a region
r1 <- granges(a)

# in this example two overlapping subsets of snps in the ASEset defines the region
r2 <- split(granges(a)[c(1,2,2,3)],c(1,1,2,2))

# link variant almlof (lva)
lv1 <- lva(a, rv, r1)
lv2 <- lva(a, rv, r2)
plot(lv2[1])
```

---

`lva` *lva*

---

## Description

make an almlof regression for arrays

## Usage

```
lva(x, ...)

## S4 method for signature 'ASEset'
lva(
  x,
  rv,
  region,
  settings = list(),
  return.class = "LinkVariantAlmlof",
  type = "lm",
  verbose = FALSE,
  covariates = matrix(),
  ...
)
```

## Arguments

| | |
|---|---|
| x | ASEset object with phase and 'ref'/'alt' allele information |
| ... | arguments to forward to internal functions |
| rv | RiskVariant object with phase and 'ref'/'alt' allele information |
| region | RiskVariant object with phase and alternative allele information |
| settings | RiskVariant object with phase and alternative allele information |
| return.class | 'LinkVariantAlmlof' (more options in future) |
| type | "lm" or "nlme", "nlme" needs subject information |
| verbose | logical, if set TRUE, then function will be more talkative |
| covariates | add data.frame with covariates (only integers and numeric) |

## Details

internal method that takes one array with results from regionSummary and one matrix with group information for each risk SNP (based on phase)

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
data(ASEset)
a <- ASEset
# Add phase
set.seed(1)
p1 <- matrix(sample(c(1,0),replace=TRUE, size=nrow(a)*ncol(a)),nrow=nrow(a), ncol(a))
p2 <- matrix(sample(c(1,0),replace=TRUE, size=nrow(a)*ncol(a)),nrow=nrow(a), ncol(a))
p <- matrix(paste(p1,sample(c("|","|","/"), size=nrow(a)*ncol(a), replace=TRUE), p2, sep=""),
 nrow=nrow(a), ncol(a))
```

```
phase(a) <- p

#add alternative allele information
mcols(a)[["alt"]] <- inferAltAllele(a)

#init risk variants
p.ar <- phaseMatrix2Array(p)
rv <- RiskVariantFromGRangesAndPhaseArray(x=GRvariants, phase=p.ar)

#colnames has to be samea and same order in ASEset and RiskVariant
colnames(a) <- colnames(rv)

# in this example each and every snp in the ASEset defines a region
r1 <- granges(a)

#use GRangesList to merge and use regions defined by each element of the
#GRangesList
r1b <- GRangesList(r1)
r1c <- GRangesList(r1, r1)

# in this example two overlapping subsets of snps in the ASEset defines the region
r2 <- split(granges(a)[c(1,2,2,3)],c(1,1,2,2))

# link variant almlof (lva)
lva(a, rv, r1)
lva(a, rv, r1b)
lva(a, rv, r1c)
lva(a, rv, r2)

# Use covariates (integers or nuemric)
cov <- data.frame(age=sample(20:70, ncol(a)), sex=rep(c(1,2), each=ncol(a)/2),
row.names=colnames(a))
lva(a, rv, r1, covariates=cov)
lva(a, rv, r1b, covariates=cov)
lva(a, rv, r1c, covariates=cov)
lva(a, rv, r2, covariates=cov)

# link variant almlof (lva), using nlme
a2 <- a
ac <- assays(a2)[["countsPlus"]]
jit <- sample(c(seq(-0.10,0,length=5), seq(0,0.10,length=5)), size=length(ac) , replace=TRUE)
assays(a2, withDimnames=FALSE)[["countsPlus"]] <- round(ac * (1+jit),0)
ab <- cbind(a, a2)
colData(ab)[["subject.group"]] <- c(1:ncol(a),1:ncol(a))
rv2 <- rv[,c(1:ncol(a),1:ncol(a))]
colnames(ab) <- colnames(rv2)

lva(ab, rv2, r1, type="nlme")
lva(ab, rv2, r1b, type="nlme")
lva(ab, rv2, r1c, type="nlme")
lva(ab, rv2, r2, type="nlme")
```

lva.internal *lva.internal*

## Description

make an almlof regression for arrays (internal function)

## Usage

```
lva.internal(x, ...)

## S4 method for signature 'array'
lva.internal(
  x,
  grp,
  element = 3,
  type = "lm",
  subject = NULL,
  covariates = matrix(),
  ...
)
```

## Arguments

| | |
|---|---|
| x | regionSummary array phased for maternal allele |
| ... | arguments to forward to internal functions |
| grp | group 1-3 (1 for 0:0, 2 for 1:0 or 0:1, and 3 for 1:1) |
| element | which column in x contains the values to use with lm. |
| type | which column in x contains the values to use with lm. |
| subject | which samples belongs to the same individual |
| covariates | add data.frame with covariates (only integers and numeric) |

## Details

internal method that takes one array with results from regionSummary and one matrix with group information for each risk SNP (based on phase). Input and output objects can change format slightly in future.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
data(ASEset)
a <- ASEset
# Add phase
set.seed(1)
p1 <- matrix(sample(c(1,0),replace=TRUE, size=nrow(a)*ncol(a)),nrow=nrow(a), ncol(a))
p2 <- matrix(sample(c(1,0),replace=TRUE, size=nrow(a)*ncol(a)),nrow=nrow(a), ncol(a))
p <- matrix(paste(p1,sample(c("|","|","/"), size=nrow(a)*ncol(a), replace=TRUE), p2, sep=""),
 nrow=nrow(a), ncol(a))

phase(a) <- p

#add alternative allele information
mcols(a)[["alt"]] <- inferAltAllele(a)

# in this example two overlapping subsets of snps in the ASEset defines the region
region <- split(granges(a)[c(1,2,2,3)], c(1,1,2,2))
rs <- regionSummary(a, region, return.class="array", return.meta=FALSE)

# use  (change to generated riskSNP phase later)
phs <- array(c(phase(a,return.class="array")[1,,c(1, 2)],
    phase(a,return.class="array")[2,,c(1, 2)]), dim=c(20,2,2))
grp <- matrix(2, nrow=dim(phs)[1], ncol=dim(phs)[2])
grp[(phs[,,1] == 0) & (phs[,,2] == 0)] <- 1
grp[(phs[,,1] == 1) & (phs[,,2] == 1)] <- 3
#only use mean.fr at the moment, which is col 3
lva.internal(x=assays(rs)[["rs1"]],grp=grp, element=3)
```

---

# makeMaskedFasta *makes masked fasta reference*

---

## Description

Replaces all selected positions in a fasta file with the character N

## Usage

```
makeMaskedFasta(fastaIn, ...)

## S4 method for signature 'character'
makeMaskedFasta(
  fastaIn,
  fastaOut,
  posToReplace,
  splitOnSeqlevels = TRUE,
  verbose = TRUE
)
```

### Arguments

| | |
|---|---|
| fastaIn | character string of the path for the fasta file to be used |
| ... | arguments to pass on |
| fastaOut | character string of the path for the masked fasta file (no extension) |
| posToReplace | GRanges object with the genomic ranges to replace |
| splitOnSeqlevels | write on file for each seqlevel to save memory |
| verbose | makes function more talkative |

### Author(s)

Jesper R. Gadin

### Examples

```
data(ASEset.sim)
gr <- rowRanges(ASEset.sim)
fastaIn <- system.file('extdata/hg19.chr17.subset.fa', package='AllelicImbalance')
makeMaskedFasta(fastaIn=fastaIn, fastaOut="fastaOut",posToReplace=gr)
```

---

## mapBiasRef *mapBias for reference allele*

---

### Description

Create a matrix of bias for the reference allele

### Usage

```
mapBiasRef(x, ...)

## S4 method for signature 'ASEset'
mapBiasRef(x)
```

### Arguments

| | |
|---|---|
| x | ASEset object |
| ... | internal arguments |

### Details

select the expected frequency for the reference allele

### Author(s)

Jesper R. Gadin, Lasse Folkersen

### Examples

```
#load example data
data(ASEset)
a <- ASEset

mat <- mapBiasRef(a)
```

---

`minCountFilt` *minCountFilt methods*

---

### Description

filter on minCountFilt snps

### Usage

```
minCountFilt(x, ...)

## S4 method for signature 'ASEset'
minCountFilt(
  x,
  strand = "*",
  threshold.counts = 1,
  sum = "all",
  replace.with = "zero",
  return.class = "ASEset"
)
```

### Arguments

| | |
|---|---|
| `x` | `ASEset` object |
| `...` | internal param |
| `strand` | strand to infer from |
| `threshold.counts` | cutoff for read counts (see details) |
| `sum` | 'each' or 'all' |
| `replace.with` | only option 'zero' |
| `return.class` | 'ASEset', 'array' or 'matrix' |

### Details

Description info here

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#load example data
data(ASEset)
a <- ASEset

minCountFilt(a)
```

---

`minFreqFilt` *minFreqFilt methods*

---

## Description

filter on minFreqFilt snps

## Usage

```
minFreqFilt(x, ...)

## S4 method for signature 'ASEset'
minFreqFilt(
  x,
  strand = "*",
  threshold.frequency = 0.1,
  replace.with = "zero",
  return.class = "ASEset",
  sum = "all"
)
```

## Arguments

| | |
|---|---|
| `x` | `ASEset` object |
| `...` | internal param |
| `strand` | strand to infer from |
| `threshold.frequency` | least fraction to classify (see details) |
| `replace.with` | only option 'zero' |
| `return.class` | 'ASEset', 'array' or 'matrix' |
| `sum` | 'each' or 'all' |

## Details

Description info here

### Author(s)

Jesper R. Gadin, Lasse Folkersen

### Examples

```
#load example data
data(ASEset)
a <- ASEset

minFreqFilt(a)
```

---

## multiAllelicFilt *multi-allelic filter methods*

---

### Description

filter on multiallelic snps

### Usage

```
multiAllelicFilt(x, ...)

## S4 method for signature 'ASEset'
multiAllelicFilt(
  x,
  strand = "*",
  threshold.count.sample = 10,
  threshold.frequency = 0.1,
  filterOver = "eachSample"
)
```

### Arguments

| | |
|---|---|
| x | ASEset object |
| ... | internal param |
| strand | strand to infer from |
| threshold.count.sample | least amount of counts to try to infer allele |
| threshold.frequency | least fraction to classify (see details) |
| filterOver | 'eachSample' or 'allSamples' |

### Details

based on the allele counts for all four variants A, T, G and C and returns true if there is counts enough suggesting a third or more alleles. The sensitivity can be specified using 'threshold.count.sample' and 'threshold.frequency'.

### Author(s)

Jesper R. Gadin, Lasse Folkersen

### Examples

```
#load example data
data(ASEset)
a <- ASEset

multiAllelicFilt(a)
```

---

`phase2genotype` *phase2genotype*

---

### Description

Convert the phase from the internally stored phase, ref and alt information

### Usage

```
phase2genotype(x, ...)

## S4 method for signature 'array'
phase2genotype(x, ref, alt, return.class = "matrix", ...)
```

### Arguments

| | |
|---|---|
| `x` | array see examples |
| `...` | pass on additional param |
| `ref` | reference allele vector |
| `alt` | alternative allele vector |
| `return.class` | 'matrix' or 'array' |

### Details

To not introduce redundant information in the ASEset object, the genotype matrix is accessed from the phase matrix, which together with ref and alt allele information contains the same information(not taken into account three-allelic or more SNPs).

The genotype matrix retrieved from an ASEset object can differ from the genotype matrix stored in the object if reference and alternative alleles were not used or has changed since the phase genotype matrix was stored. Basically, it is preferable to provide reference and alternative information when storing the genotype matrix.

If possible, it is better to not use a genotype matrix, but instead relying completely on storing a phase matrix(or array) together with reference and alternative allele information.

### Author(s)

Jesper R. Gadin, Lasse Folkersen

### Examples

```
#load example data
data(ASEset)
data(genomatrix)
p <- genotype2phase(genomatrix, ref(ASEset), return.class="array")
ref <- ref(ASEset)
alt <- inferAltAllele(ASEset)

gt <- phase2genotype(p, ref, alt, return.class="matrix")
```

---

## phaseArray2phaseMatrix

*phaseArray2phaseMatrix*

---

### Description

used to convert the phase from the visually friendly matrix to array.

### Usage

```
phaseArray2phaseMatrix(x, ...)

## S4 method for signature 'array'
phaseArray2phaseMatrix(x, ...)
```

### Arguments

| | |
|---|---|
| x | array see examples |
| ... | arguments to forward to internal functions |

### Details

A more effectice way of store the phase data in the ASEset object

### Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#load data
data(ASEset)
a <- ASEset

#example phase matrix
p1 <- matrix(sample(c(1,0),replace=TRUE, size=nrow(a)*ncol(a)),nrow=nrow(a), ncol(a))
p2 <- matrix(sample(c(1,0),replace=TRUE, size=nrow(a)*ncol(a)),nrow=nrow(a), ncol(a))
p <- matrix(paste(p1,sample(c("|","|","/"), size=nrow(a)*ncol(a), replace=TRUE), p2, sep=""),
 nrow=nrow(a), ncol(a))

ar <- phaseMatrix2Array(p)

#Convert back
mat <- phaseArray2phaseMatrix(ar)
```

---

# phaseMatrix2Array *phaseMatrix2Array*

---

## Description

used to convert the phase from the visually friendly matrix to array.

## Usage

```
phaseMatrix2Array(x, ...)

## S4 method for signature 'matrix'
phaseMatrix2Array(x, dimnames = NULL, ...)
```

## Arguments

| | |
|---|---|
| x | matrix see examples |
| ... | arguments to forward to internal functions |
| dimnames | list with dimnames |

## Details

A more effectice way of store the phase data in the ASEset object

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#load data
data(ASEset)
a <- ASEset

#example phase matrix
p1 <- matrix(sample(c(1,0),replace=TRUE, size=nrow(a)*ncol(a)),nrow=nrow(a), ncol(a))
p2 <- matrix(sample(c(1,0),replace=TRUE, size=nrow(a)*ncol(a)),nrow=nrow(a), ncol(a))
p <- matrix(paste(p1,sample(c("|","|","/"), size=nrow(a)*ncol(a), replace=TRUE), p2, sep=""),
 nrow=nrow(a), ncol(a))

ar <- phaseMatrix2Array(p)
```

---

# randomRef *Random ref allele from genotype*

---

## Description

Create a vector of random reference alleles

## Usage

```
randomRef(x, ...)

## S4 method for signature 'ASEset'
randomRef(x, source = "alleleCounts", ...)
```

## Arguments

| | |
|---|---|
| x | ASEset object |
| ... | internal arguments |
| source | 'alleleCounts' |

## Details

Randomly shuffles which of the two alleles for each genotype that is indicated as reference allele, based on either allele count information or previous ref and alt alleles.

When the source is 'alleleCounts', the two most expressed alleles are taken as reference and alternative allele.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#load example data
data(ASEset.sim)
a <- ASEset.sim

ref(a) <- randomRef(a, source = 'alleleCounts')
```

---

`reads` *reads object*

---

## Description

This data set corresponds to the BAM-file data import illustrated in the vignette. The data set consists of a chromosome 17 region from 20 RNA-seq experiments of HapMap samples.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## References

Montgomery SB et al. Transcriptome genetics using second generation sequencing in a Caucasian population. Nature. 2010 Apr 1;464(7289):773-7.

## See Also

- The `GRvariants` which is another example object

## Examples

```
##load eample data (Not Run)
#data(reads)
```

---

`refAllele` *Reference allele*

---

## Description

Extract the allele based on SNP location from the reference fasta file

## Usage

```
refAllele(x, fasta)
```

### Arguments

| | |
|---|---|
| x | ASEset object |
| fasta | path to fasta file, index should be located in the same folder |

### Details

The alleles will be placed in the rowRanges() meta column 'ref'

### Author(s)

Jesper R. Gadin, Lasse Folkersen

### Examples

```
#load example data
data(ASEset.sim)

fasta <- system.file('extdata/hg19.chr17.subset.fa', package='AllelicImbalance')
a <- refAllele(ASEset.sim,fasta=fasta)
```

---

## regionSummary *regionSummary*

---

### Description

Gives a summary of AI-consistency for a transcript

### Usage

```
regionSummary(x, ...)

## S4 method for signature 'ASEset'
regionSummary(x, region, strand = "*", return.class = "RegionSummary", ...)
```

### Arguments

| | |
|---|---|
| x | ASEset object |
| ... | arguments to forward to internal functions |
| region | to summmarize over, the object can be a GRanges, GRangesList |
| strand | can be "+", "-" or "*" |
| return.class | "array" or "list". |

## Details

From a given set of e.g. transcripts exon ranges the function will return a summary for the sum of all exons. Phase information, reference and alternative allele is required.

A limitation comes to the strand-specificness. At the moment it is not possible to call over more than one strand type using the strands in region. This will be improved before going to release.

to calculate the direction and binomial p-values of AI the mapbias stored in the ASEset is used. see '?mapBias'.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
data(ASEset)
a <- ASEset
# Add phase
set.seed(1)
p1 <- matrix(sample(c(1,0),replace=TRUE, size=nrow(a)*ncol(a)),nrow=nrow(a), ncol(a))
p2 <- matrix(sample(c(1,0),replace=TRUE, size=nrow(a)*ncol(a)),nrow=nrow(a), ncol(a))
p <- matrix(paste(p1,sample(c("|","|","/"), size=nrow(a)*ncol(a), replace=TRUE), p2, sep=""),
 nrow=nrow(a), ncol(a))

phase(a) <- p

#add alternative allele information
mcols(a)[["alt"]] <- inferAltAllele(a)

# in this example each and all snps in the ASEset defines the region
region <- granges(a)
t <- regionSummary(a, region)

# in this example two overlapping subsets of snps in the ASEset defines the region
region <- split(granges(a)[c(1,2,2,3)],c(1,1,2,2))
t <- regionSummary(a, region)
```

---

# RegionSummary-class *RegionSummary class*

---

## Description

Object that holds results from the regionSummary method

## Usage

```
sumnames(x, ...)

## S4 method for signature 'RegionSummary'
sumnames(x)

basic(x, ...)

## S4 method for signature 'RegionSummary'
basic(x)
```

## Arguments

| | |
|---|---|
| x | RegionSummary object |
| ... | pass arguments to internal functions |

## Details

The RegionSummary-class objects contains summaries for specified regions

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#some code
```

---

# RiskVariant-class *RiskVariant class*

---

## Description

Object that holds results from AI detection.

## Usage

```
## S4 method for signature 'RiskVariant'
ref(x)

## S4 replacement method for signature 'RiskVariant,ANY'
ref(x) <- value

## S4 method for signature 'RiskVariant'
alt(x)
```

```
## S4 replacement method for signature 'RiskVariant,ANY'
alt(x) <- value

## S4 method for signature 'RiskVariant'
phase(x, return.class = "matrix")

## S4 replacement method for signature 'RiskVariant'
phase(x) <- value
```

## Arguments

| | |
|---|---|
| x | RiskVariant object or list of RiskVariants |
| value | argument used for replacement |
| return.class | type of class returned eg. "list or ""array". |

## Details

The RiskVariant-class contains

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## Examples

```
#some code
```

---

# scanForHeterozygotes.old

*scanForHeterozygotes-old*

---

## Description

Identifies the positions of SNPs found in BamGR reads.

## Usage

```
scanForHeterozygotes.old(
  BamList,
  minimumReadsAtPos = 20,
  maximumMajorAlleleFrequency = 0.9,
  minimumBiAllelicFrequency = 0.9,
  maxReads = 15000,
  verbose = TRUE
)
```

## Arguments

| | |
|---|---|
| BamList | A GAlignmentsList object |
| minimumReadsAtPos | minimum number of reads required to call a SNP at a given position |
| maximumMajorAlleleFrequency | maximum frequency allowed for the most common allele. Setting this parameter lower will minimise the SNP calls resulting from technical read errors, at the cost of missing loci with potential strong ASE |
| minimumBiAllelicFrequency | minimum frequency allowed for the first and second most common allele. Setting a Lower value for this parameter will minimise the identification of loci with three or more alleles in one sample. This is useful if sequencing errors are suspected to be common. |
| maxReads | max number of reads of one list-element allowed |
| verbose | logical indicating if process information should be displayed |

## Details

This function scans all reads stored in a GAlignmentsList for possible heterozygote positions. The user can balance the sensitivity of the search by modifying the minimumReadsAtPos, maximumMajorAlleleFrequency and minimumBiAllelicFrequency arguments.

## Value

scanForHeterozygotes.old returns a GRanges object with the SNPs for the BamList object that was used as input.

## Author(s)

Jesper R. Gadin, Lasse Folkersen

## See Also

- The getAlleleCounts which is a function that count the number of reads overlapping a site.

## Examples

```
data(reads)
s <- scanForHeterozygotes.old(reads,verbose=FALSE)
```

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