Package: MinimumDistance (via r-universe)

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`acf2` *Function for computing autocorrelations*

Description

By default, this function returns the lag-10 autocorrelations of a numeric vector and omits missing values.

Usage

```
acf2(
  x,
  lag.max = 10,
  type = c("correlation", "covariance", "partial"),
  plot = FALSE,
  na.action = na.omit,
  demean = TRUE,
  ...
)
```

Arguments

`x`	a numeric vector
`lag.max`	see `acf`
`type`	see `acf`
`plot`	logical, as in `acf`
`na.action`	ignored. Missing values are automattically omitted.
`demean`	logical, as in `acf`
`...`	additional arguments passed to `acf`

See Also

`acf`

Examples

```
x <- rnorm(100)
x[5] <- NA
acf2(x)
```

`calculateMindist` *Deprecated function to calculate the minimum distance*

Description

The 'minimum distance' is the minimum signed absolute difference of the parental log R ratios and the offspring log R ratios. Specifically, let |O-F| denote the absolute difference in the log R ratios comparing offspring to father and |O-M| the absolute difference in the log R ratios comparing offspring to mother. The minimum distance at a marker is the signed minimum of |O-M| and |O-F|. After segmentation of the minimum distance, non-zero segments can indicate a de novo difference in the log R ratio of the offspring and either parent. For example, a positive minimum distance suggests that the log R ratio from the offspring is greater than the log R ratio of either parent.

Usage

```
calculateMindist(object, ...)

## S4 method for signature 'TrioSet'
calculateMindist(object, verbose = TRUE, ...)

## S4 method for signature 'TrioSetList'
calculateMindist(object)

## S4 method for signature 'list'
calculateMindist(object, outdir = ldPath(), ...)

## S4 method for signature 'arrayORff_array'
calculateMindist(object, outdir, center, ...)

## S4 method for signature 'matrix'
calculateMindist(object, ...)
```

Arguments

`object`	see `showMethods("calculateMindist")`
`...`	Ignored
`verbose`	logical. Whether to display messages indicating progress.
`outdir`	character string indicating path to save output
`center`	ignored

coerce *Coercion methods in MinimumDistance package*

Description

Coercion methods in MinimumDistance package

Coerces a TrioSetList to a TrioSet

Usage

```
as(from, to)

## S4 method for signature 'TrioSetList'
stack(x, ...)
```

Arguments

x	a TrioSetList
...	ignored
from	see showMethods("coerce")
to	see showMethods("coerce")

Value

a TrioSet

---

denovoHemizygous *Filter the genomic intervals for denovo copy number states*

Description

This function filters the genomic intervals for denovo events.

Usage

```
denovoHemizygous(object, filters = FilterParamMD(state = "221"))

denovoHomozygous(object, filters = FilterParamMD(state = "220"))

denovo(object, filters = FilterParamMD(state = c("220", "221", "224")))

denovoDuplication(object, filters = FilterParamMD(state = "224"))

## S4 method for signature 'MinDistPosterior'
```

```
denovoHemizygous(object, filters = FilterParamMD(state = "221"))

## S4 method for signature 'MinDistPosterior'
denovoHomozygous(object, filters = FilterParamMD(state = "220"))

## S4 method for signature 'MinDistPosterior'
denovoDuplication(object, filters = FilterParamMD(state = "224"))

## S4 method for signature 'MinDistPosterior'
denovo(object, filters = FilterParamMD(state = c("220", "221", "224")))
```

Arguments

object	see showMethods(denovo) for a list of defined methods
filters	an object of class FilterParamMD

Details

The function denovo filters genomic intervals for states '220', '221', and '224', corresponding to denovo homozygous deletion, denovo hemizygous deletion, and denovo duplication, respectively.

denovoHemizygous filters genomic intervals for state '221'.

denovoHomozygous filters genomic intervals for state '220'

See Also

FilterParamMD-class

DNAcopyParam *Constructor for DNAcopyParam class*

Description

Creates an instance of a parameter class for circular binary segmentation of the minimum distance and the log R ratios. Parameters in this object are passed to the segment function in the package DNAcopy.

Usage

```
DNAcopyParam(
  alpha = 0.01,
  min.width = 2L,
  undo.splits = c("none", "prune", "sdundo"),
  undo.SD = 3
)
```

Arguments

alpha	see segment
min.width	see segment
undo.splits	see segment
undo.SD	see segment

See Also

segment

Examples

```
segment_params <- DNAcopyParam(alpha=0.01)
params <- MinDistParam(dnacopy=segment_params)
```

---

exampleTrioSetList *An example* TrioSetList *object*

Description

A dataset containing log R ratios and B allele frequencies for two chromosomes, organized as a TrioSetList. Each element in the list class is a TrioSet object. Both TrioSetList and TrioSet classes are deprecated; the example data will be removed in a future release.

Format

a TrioSetList

---

filterExperiment *Methods for filtering MinDistExperiment objects*

Description

Filter a MinDistExperiment object to exclude markers with missing values in the low-level summaries, exclude markers that lie in segments (granges argument) with small minimum distance values (unlikely to be de novo)

Usage

```
filterExperiment(object, granges, param)

## S4 method for signature 'MinDistExperiment,GRanges'
filterExperiment(object, granges, param)

## S4 method for signature 'MinDistExperiment,GRangesList'
filterExperiment(object, granges, param)

## S4 method for signature 'MinDistExperiment,MinDistGRanges'
filterExperiment(object, granges, param)
```

Arguments

object	A MinDistExperiment
granges	A GRanges, GRangesList, or MinDistGRanges object
param	a MinDistParam object

Value

a MinDistExperiment

FilterParamMD *Parameters for filtering results from the segmentation and copy number inference*

Description

A container for criteria used to filter the segmentation results post-hoc. Options including filtering on the posterior call, the posterior probability of the posterior call, the minimum number of markers spanned by the segment, the minimum width of the segment, and chromosome. Convenience functions are available for commonly used filters.

Usage

```
FilterParamMD(state = trioStateNames(), seqnames = paste0("chr", 1:22), ...)
```

Arguments

state	trio copy number states to select
seqnames	chromosome names to select
...	additional arguments passed to FilterParam-class

Examples

```
library(VanillaICE)
data(md_gr)
data(md_exp)
mdparam <- MinDistParam()
fit <- MAP2(md_exp, md_gr, mdparam)
## return all segments
segs(fit)

## Default filters
param <- FilterParamMD()
param
cnvFilter(fit, param)

param2 <- FilterParamMD(seqnames="chr22", probability=0.9, numberFeatures=10)
cnvFilter(fit, param2)
denovoHemizygous(fit)
```

FilterParamMD-class *A class for filtering genomic intervals called by MinimumDistance*

Description

Options for filtering include the number of markers spanned by a segment, the posterior probability of the maximum a posteriori estimate of the trio copy number state, and the trio copy number state.

Usage

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

Arguments

object	a FilterParamMD object

See Also

denovo

mad2 *Deprecated wrapper for computing the median absolute deviation of low-level summaries*

Description

Deprecated wrapper for computing the median absolute deviation of low-level summaries

Usage

```
mad2(object, byrow = FALSE, ...)

## S4 method for signature 'list'
mad2(object, byrow, pedigree, ...)

## S4 method for signature 'TrioSetList'
mad2(object, byrow = FALSE, ...)

## S4 method for signature 'matrix'
mad2(object, byrow, pedigree, ...)

## S4 method for signature 'array'
mad2(object, byrow, pedigree, ...)
```

Arguments

object	see showMethods("mad2")
byrow	logical if TRUE, compute the median absolute deviation of the rows of a matrix
...	additional arguments to mad
pedigree	an object of class Pedigree

MAP *Computes the maximum a posteriori trio copy number state for the segmented minimum distance*

Description

This functions is deprecated and will be defunct in a future release. The replacement function is MAP2.

Usage

```
MAP(
  object,
  ranges,
  id,
  TAUP = 1e+10,
  tauMAX = 1 - 5e-08,
  cnStates = c(-2, -0.4, 0, 0, 0.4, 1),
  pr.nonmendelian = 1.5e-06,
  mdThr = 0.9,
  ...
)
```

Arguments

object	see showMethods(MAP)
ranges	A GRanges object
id	character string for sample identifier
TAUP	scalar for transition probabilities
tauMAX	the maximum probability that the current state is the same as the previous state
cnStates	character vector for hidden Markov model state labels
pr.nonmendelian	numeric: the a priori probability of a non-Mendelian copy number alteration
mdThr	a length-one numeric vector. A minimum distance below this threshold in absolute value will not be evaluated for copy number alterations.
...	Ignored.

MAP2 *Computes maximum a posteriori estimate for the trio copy number state*

Description

Computes maximum a posteriori estimate for the trio copy number state

Usage

```
MAP2(object, mdgr, param = MinDistParam(), ...)

## S4 method for signature 'MinDistExperiment,MinDistGRanges'
MAP2(object, mdgr, param = MinDistParam(), ...)

## S4 method for signature 'MinDistExperiment,GRangesList'
MAP2(object, mdgr, param = MinDistParam(), ...)

## S4 method for signature 'MinDistExperiment,GRanges'
MAP2(object, mdgr, param = MinDistParam(), ...)
```

Arguments

object	An object of class MinDistExperiment
mdgr	An object of class MinDistGRanges, GRangesList, or GRanges.
param	An object of class MinDistParam.
...	ignored

Value

An object of class MinDistPosterior

Examples

```
  library(oligoClasses)
  library(VanillaICE)
  ## A MinDistExperiment object:
  data(md_exp)
  ## Segmented data
  data(md_gr)
  e_param <- EmissionParam(temper=1, p_outlier=1/100)
  param <- MinDistParam(thin=1L, emission=e_param)
## Not run:
  md_g <- MAP2(md_exp, md_gr, param)

## End(Not run)
```

---

md_exp *An example* MinDistExperiment

Description

This dataset contains log R ratios and B allele frequencies from a parent-offspring trio (three individuals). Only markers from chromosomes 7 and 22 are included in this object. The MinDistExperiment class extends RangedSummarizedExperiment, and so many of the methods defined for RangedSummarizedExperiment such as findOverlaps are available through inheritance.

Format

a MinDistExperiment

Examples

```
## Not run:
    library(oligoClasses)
    library(VanillaICE)
    library(data.table)
    library(BSgenome.Hsapiens.UCSC.hg18)
    extdir <- system.file("extdata", package="VanillaICE")
    features <- suppressWarnings(fread(file.path(extdir, "SNP_info.csv")))
```

```
fgr <- GRanges(paste0("chr", features$Chr), IRanges(features$Position, width=1),
               isSnp=features[["Intensity Only"]]==0)
fgr <- SnpGRanges(fgr)
names(fgr) <- features[["Name"]]
sl <- seqlevels(BSgenome.Hsapiens.UCSC.hg18)
seqlevels(fgr) <- sl[sl %in% seqlevels(fgr)]
seqinfo(fgr) <- seqinfo(BSgenome.Hsapiens.UCSC.hg18)[seqlevels(fgr),]
fgr <- sort(fgr)
files <- list.files(extdir, full.names=TRUE, recursive=TRUE, pattern="FinalReport")
## parse files
parsedDir <- "ParsedFiles"
if(!file.exists(parsedDir)) dir.create(parsedDir)
views <- ArrayViews(rowRanges=fgr, sourcePaths=files, parsedPath=parsedDir)
dat <- fread(files[1])
select_columns <- match(c("SNP Name", "Allele1 - AB", "Allele2 - AB",
                          "Log R Ratio", "B Allele Freq"), names(dat))
index_genome <- match(names(fgr), dat[["SNP Name"]])
scan_params <- CopyNumScanParams(index_genome=index_genome, select=select_columns,
                                 cnvar="Log R Ratio",
                                 bafvar="B Allele Freq",
                                 gtvar=c("Allele1 - AB", "Allele2 - AB"))
invisible(sapply(views, parseSourceFile, param=scan_params))
ped_hapmap <- ParentOffspring(id = "hapmap", father="12287_03",
                              mother="12287_02",
                              offspring="12287_01",
                              parsedPath=parsedPath(views))
ped_list <- ParentOffspringList(pedigrees=list(
                                  ParentOffspring(id = "hapmap", father="12287_03",
                                                  mother="12287_02",
                                                  offspring="12287_01",
                                                  parsedPath=parsedPath(views)),
                                  ParentOffspring(id = "cleft",
                                                  father="22169_03",
                                                  mother="22169_02",
                                                  offspring="22169_01",
                                                  parsedPath=parsedPath(views))))
sample_info <- read.csv(file.path(extdir, "sample_data.csv"), stringsAsFactors=FALSE)
ind_id <- setNames(gsub(" ", "", sample_info$IndividualID), sample_info$File)
colnames(views) <- ind_id[gsub(".csv", "", colnames(views))]
md_exp <- MinDistExperiment(views, pedigree=ped_list[[2]])
seqlevels(md_exp, pruning.mode="coarse") <- "chr22"
params <- MinDistParam()
md_gr <- segment2(md_exp, params)
save(md_exp, file="~/Software/bridge/MinimumDistance/data/md_exp.rda")
save(md_gr, file="~/Software/bridge/MinimumDistance/data/md_gr.rda")

## End(Not run)
```

---

md_gr *An example* MinDistGRanges *object*

Description

Prior to inferring de novo trio copy number states, the log R ratios are segmented independently for each individual in a ParentOffsping class. The segmentation results are recorded in separate GRanges objects for the parents. For segmentation of the offspring log R ratios and the minimum distance, the segments are stored in separate GRangesList objects. For convenience, these GRanges, GRangesList, and pedigree information are bound in a single container referred to as a MinDistGRanges object. The example MinDistGRanges object provided in this package was obtained from the segmentation of the data stored in the example MinDistExperiment object.

Format

a MinDistGRanges object

---

mdLegend *Text summary of information encapculated in a MDRanges object for a particular interval*

Description

Text summary of information encapculated in a MDRanges object for a particular interval

Usage

```
mdLegend(g)
```

Arguments

g	a MDRanges object

MDRanges-class *A GRanges-derived class*

Description

Contains maximum a posteriori estimates for each genomic interval

Usage

```
MDRanges(..., posteriors)
```

Arguments

...	additional arguments to GRanges constructor
posteriors	a DataFrame

Examples

```
MDRanges()
```

mindist *Getter and setter for the minimum distance statistic*

Description

Getter and setter for the minimum distance statistic

Usage

```
mindist(object)

mindist(object) <- value
```

Arguments

object	see showMethods("mindist")
value	a matrix of the minimum distance

MinDistExperiment *Constructor for* MinDistExperiment *class*

Description

Constructor for MinDistExperiment class

Usage

```
MinDistExperiment(object = ArrayViews(), pedigree = ParentOffspring(), ...)

## S4 method for signature 'ArrayViews,ParentOffspring'
MinDistExperiment(object = ArrayViews(), pedigree = ParentOffspring(), ...)
```

Arguments

object	see showMethods(MinDistExperiment)
pedigree	a ParentOffspring object
...	ignored

Value

an object of class MinDistExperiment

MinDistExperiment-class *Class and methods for MinDistExperiment*

Description

Class and methods for MinDistExperiment

Usage

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

## S4 method for signature 'MinDistExperiment'
pedigree(object)

## S4 replacement method for signature 'MinDistExperiment'
pedigree(object) <- value

## S4 method for signature 'MinDistExperiment'
mindist(object)

## S4 replacement method for signature 'MinDistExperiment,ANY'
mindist(object) <- value

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

## S4 method for signature 'MinDistExperiment'
offspring(object)

## S4 method for signature 'MinDistExperiment'
father(object)

## S4 method for signature 'MinDistExperiment'
mother(object)

## S4 method for signature 'MinDistExperiment'
segment2(object, param = MinDistParam())

## S4 method for signature 'RangedSummarizedExperiment'
father(object)

## S4 method for signature 'RangedSummarizedExperiment'
mother(object)

## S4 method for signature 'RangedSummarizedExperiment'
```

```
offspring(object)
```

Arguments

object	a MinDistExperiment object
value	a ParentOffspring object
x	a MinDistExperiment object
i	a numeric-vector for indexing the rows (optional)
j	a numeric-vector for indexing the columns (optional)
...	additional arguments propogated to subsetting methods for RangedSummarizedExperiment
drop	logical. Whether to simplify a one-row or one-column matrix to a vector. In most cases, this should always be FALSE.
param	a MinDistParam object

Slots

mindist a matrix

pedigree a ParentOffspring object

MinDistGRanges *Constructor for* MinDistGRanges *class*

Description

The MinDistGRanges class contains the segmentation of the father, mother, offspring, and the minimum distance for each possible parent-offspring trio. For the parents, the segmentation results are expected to be in GRanges format. To accomodate multiple-offspring families, both the offspring segments and minimum distance segments should be of class GRangesList where the length of the list corresponds to the number of offspring.

Usage

```
MinDistGRanges(
  mindist = GRangesList(),
  offspring = GRangesList(),
  father = GRanges(),
  mother = GRanges(),
  pedigree = ParentOffspring()
)
```

Arguments

mindist	a GRangesList object
offspring	a GRangesList object
father	a GRanges object
mother	a GRanges object
pedigree	a ParentOffspring object

Examples

```
MinDistGRanges()
```

`MinDistGRanges-class` *A container for storing segmentation data for members in a* `ParentOffspring` *family*

Description

A container for storing segmentation data for members in a `ParentOffspring` family

Usage

```
## S4 method for signature 'MinDistGRanges'
names(x)

## S4 method for signature 'MinDistGRanges'
mindist(object)

## S4 replacement method for signature 'MinDistGRanges,GRangesList'
mindist(object) <- value

## S4 method for signature 'MinDistGRanges'
offspring(object)

## S4 method for signature 'MinDistGRanges'
mother(object)

## S4 method for signature 'MinDistGRanges'
father(object)

## S4 method for signature 'MinDistGRanges'
pedigree(object)

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

## S4 method for signature 'GRangesList'
offspring(object)
```

Arguments

`x`	a `MinDistGRanges` object
`object`	a `MinDistGRanges` object
`value`	a `GRangesList` object

Slots

`mindist` a `GRangesList` object

`offspring` a `GRangesList` object

`father` a `GRanges` object

`mother` a `GRanges` object

`pedigree` a `ParentOffspring` object

Examples

```
data(md_gr)
offspring(md_gr)
father(md_gr)
mother(md_gr)
mindist(md_gr)
```

`MinDistParam` *Constructor for* `MinDistParam` *class*

Description

The `MinDistParam` class contains parameters used for the segmentation implemented in the `DNAcopy` package, parameters extracted from the `PennCNV` HMM such as parent-offspring transmission parobabilities (see citation below), and initial values / parameters for computing emission probabilities.

Usage

```
MinDistParam(
  nMAD = 0.75,
  dnacopy = DNAcopyParam(),
  penncnv = PennParam(),
  emission = EmissionParam(),
  thin = 10L
)
```

Arguments

`nMAD`	a length-one numeric vector indicating the minimal number of median absolute deviations of the mean segmented minimum distance from zero. For non-zero segments (# median absolute deviations > nMAD), maximum a posteriori estimates of the parent-offspring copy number states are computed. Segments with minimum distance values near zero are not called as they are less likely to correspond to regions with de novo copy number alterations.
`dnacopy`	an object of class `DNAcopyParam`.
`penncnv`	probabilities/parameters of the PennCNV hidden Markov model
`emission`	an object of class `EmissionParam`
`thin`	a length-one vector indicating whether to thin the data. This is primarily for internal use in conjunction with the `filterExperiment` function.

See Also

segment

MinDistParam-class *Class and methods for parameters of minimum distance algorithm*

Description

Contains parameters used for circular binary segmentation (package DNAcopy), parameters in the PennCNV hidden Markov model, and parameters used for computing emission probabilities.

Usage

```
## S4 method for signature 'MinDistParam'
nMAD(object)

## S4 replacement method for signature 'MinDistParam,numeric'
nMAD(object) <- value

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

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

Arguments

object	a MinDistParam object
value	a length-one numeric vector.

Slots

nMAD a length-one numeric vector

dnacopy an object of class DNAcopyParam

penncnv an object of class PennParam

emission an object of class EmissionParam

thin a length-one non-negative integer

MinDistPosterior-class *Container for the segmentation results from a MinDistExperiment*

Description

MinDistPosterior is a GRangesList-derived container for the segmentation and maximum a posteriori trio copy number states.

Usage

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

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

Arguments

x	a MinDistPosterior object
i	an index for subsetting rows
j	an index for subsetting columns
...	additional arguments passed to subsetting matrices
drop	logical – whether to coerce single-row matrices to vectors
object	a MinDistPosterior object

See Also

denovo

MinimumDistance *De novo copy number alterations in parent-offspring trios*

nMAD *Setter and getter for number of median absolute deviations the mean minimum distance of a genomic interval is from zero*

Description

Setter and getter for number of median absolute deviations the mean minimum distance of a genomic interval is from zero

Usage

```
nMAD(object)

nMAD(object) <- value
```

Arguments

object	see showMethods("nMAD")
value	a length-one numeric vector

offspringNames *Deprecated functions and methods*

Description

These functions will be defunct in a future release.

Usage

```
offspringNames(object)

offspringNames(object) <- value

trios(object)

pedigree(object)

pedigree(object) <- value
```

Arguments

object	see showMethods("offspringNames")
value	a character vector of offspring identifiers

ParentOffspring-class *Object containing the sample identifiers for members in a pedigree*

Description

Container for registering sample identifiers with membership in a pedigree. For representing multiple pedigrees, see ParentOffspringList.

Accessor for the sample identifiers for the members in a pedigree

Usage

```
offspring(object)

mother(object)

father(object)

ParentOffspring(
  id = character(),
  father = character(),
  mother = character(),
  offspring = character(),
  parsedPath = character()
)

## S4 method for signature 'ParentOffspring'
pedigreeName(object)

## S4 method for signature 'ParentOffspring'
father(object)

## S4 method for signature 'ParentOffspring'
mother(object)

## S4 method for signature 'ParentOffspring'
offspring(object)

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

## S4 method for signature 'ParentOffspring'
names(x)
```

Arguments

object	a ParentOffspring object

id	length-one character vector providing a family-level id
father	length-one character vector providing sample ids for father
mother	length-one character vector providing sample ids for mother
offspring	character vector providing sample ids for offspring (can have length greater than one if there is more than one offspring)
parsedPath	character vector providing path to low-level data
x	a ParentOffspring object

Slots

id length-one character vector providing a family-level id

father length-one character vector providing sample ids for father

mother length-one character vector providing sample ids for mother

offspring character vector providing sample ids for offspring (can have length greater than one if there is more than one offspring)

parsedPath character vector providing path to parsed files of the marker-level summaries

See Also

ParentOffspringList-class

Examples

```
ParentOffspring()
```

ParentOffspringList-class

A list of ParentOffspring *objects*

Description

Each element of the list is an element of class ParentOffspring.

Usage

```
ParentOffspringList(pedigrees = list(), id)

## S4 method for signature 'ParentOffspringList'
pedigreeName(object)

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

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

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

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

Arguments

pedigrees	a list of ParentOffspring objects
id	identifier for a pedigree
object	a ParentOffspringList object
x	a ParentOffspringList object
i	a numeric vector for subsetting the list (optional)
j	ignored
...	ignored
drop	ignored

Slots

`id` a character vector of identifiers for the pedigrees. `id` must have the same length as `pedigrees`

`pedigrees` A list of ParentOffspring objects.

Examples

```
ParentOffspringList()
```

Pedigree *Deprecated function for constructing an instance of class Pedigree*

Description

This function is deprecated and will be removed in a future release.

Usage

```
Pedigree(
  pedigreeInfo,
  fatherIds = character(),
  motherIds = character(),
  offspringIds = character()
)
```

Arguments

pedigreeInfo	a data.frame with column names 'F' (father), 'M' (mother), and 'O' (offspring). Elements of the data.frame are the sample names.
fatherIds	character vector of identifiers for the father
motherIds	character vector of identifiers for the mother
offspringIds	character vector of identifiers for the offspring

Examples

```
Pedigree()
```

Pedigree-class *Deprecated class for storing pedigree data*

Description

Deprecated class for storing pedigree data

Usage

```
## S4 method for signature 'Pedigree'
trios(object)

## S4 method for signature 'Pedigree'
offspringNames(object)

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

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

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

Arguments

object	a Pedigree object
x	a Pedigree object
i	a numeric vector for subsetting (optional)
j	ignored
...	ignored
drop	ignored

Slots

`trios` a `data.frame` with colnames 'F', 'M', and 'O' containing sample identifiers for the father (F), mother (M), and offspring (O).

`trioIndex` a `data.frame`

`pedigreeGrid` *Plot the log R ratios and BAFs on a grid given by precomputed viewports*

Description

Plot the log R ratios and BAFs on a grid given by precomputed viewports

Usage

```
pedigreeGrid(g, vps, figs)
```

Arguments

`g`	a `MDRanges` object
`vps`	a list of viewports. See `pedigreeViewports`.
`figs`	a list of trellis objects created by the function `plotDenovo`.

See Also

`plotDenovo` `pedigreeViewports`

Examples

```
library(VanillaICE)
require(grid)
##marker-level summaries
data(md_exp)
seqlevels(md_exp, pruning.mode="coarse") <- "chr22"
## segmentation results
data(md_gr)
posteriorCalls <- MAP2(md_exp, md_gr, MinDistParam())
g <- denovoHemizygous(posteriorCalls)
g
vps <- MinimumDistance:::pedigreeViewports()
param <- HmmTrellisParam()
p <- plotDenovo(md_exp, g[1], param)
p <- pedigreeGrid(g=g[1], vps=vps, figs=p)
leg <- mdLegend(g[1])
upViewport(0)
pushViewport(vps[["legend"]])
grid.text(leg, x=unit(0.02, "npc"), y=unit(0.95, "npc"), just=c("left", "top"),
          gp=gpar(cex=0.6, fontfamily="mono"))
```

```
##
## combine adjacent denovo hemizygous
##
g2 <- reduce(denovoHemizygous(posteriorCalls), min.gapwidth=500e3)
post <- MAP2(md_exp, g2)
g2 <- denovoHemizygous(post)
p <- plotDenovo(md_exp, g2, param)
p <- pedigreeGrid(g=g2, vps=vps, figs=p)
leg <- mdLegend(g2)
upViewport(0)
pushViewport(vps[["legend"]])
grid.text(leg, x=unit(0.02, "npc"), y=unit(0.95, "npc"), just=c("left", "top"),
          gp=gpar(cex=0.6, fontfamily="mono"))
```

---

pedigreeName *Accessor for pedigree name*

Description

Accessor for pedigree name

Usage

```
pedigreeName(object)
```

Arguments

object	a ParentOffspring or ParentOffspringList object

See Also

ParentOffspring ParentOffspringList

---

pedigreeViewports *Default viewports for plotting log R ratios, BAFs, chromosome idiogram, and a legend for a case-parent trio*

Description

Default viewports for plotting log R ratios, BAFs, chromosome idiogram, and a legend for a case-parent trio

Usage

```
pedigreeViewports()
```

See Also

plotDenovo pedigreeGrid

Examples

```
vps <- pedigreeViewports()
```

PennParam *Constructor for class* PennParam

Description

Parameters for the PennCNV Hidden Markov model

Usage

```
PennParam(
  states,
  referenceState = "222",
  prLessLikelyCN = 9e-04,
  prNonMendelian = 1.5e-06,
  prInitialStateNotDiploid = 4/5,
  prTransitionToNewState = 0.5,
  tauNM = 0.01
)

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

Arguments

states	character vector of possible trio states
referenceState	the reference (normal) trio copy number state (typically '222')
prLessLikelyCN	as defined in Wang et al. 2007, this is the probability of the less likely allele-specific copy numbers for the trio
prNonMendelian	the prior probability of a non-Mendelian copy number alteration
prInitialStateNotDiploid	initial probability for non-diploid states
prTransitionToNewState	probability of transitioning to a new state
tauNM	probability of transitioning from a Mendelian given previous event was non-Mendelian (and vice versa).
object	a PennParam object

References

Wang et al., Genome Res. 2007 Nov;17(11):1665-74. PMID: 17921354

plotDenovo *Plot marker-level summaries for a genomic interval of interest*

Description

Plot marker-level summaries for a genomic interval of interest

Usage

```
plotDenovo(object, g, param)

## S4 method for signature 'MinDistExperiment,MDRanges'
plotDenovo(object, g, param)
```

Arguments

object	see showMethods("plotDenovo")
g	a MDRanges object
param	a HmmTrellisParam object

range,ILimit-method *compute the range of an ILimit instance*

Description

The range method for class ILimit is used internally in MinimumDistance.

Usage

```
## S4 method for signature 'ILimit'
range(x, ..., na.rm = FALSE)
```

Arguments

x	a ILimit object
...	ignored
na.rm	logical. If TRUE, missing values are removed.

segment2 *A wrapper for DNAcopy's segment function*

Description

Methods for circular binary segmentation.

Usage

```
segment2(object, ...)

## S4 method for signature 'TrioSet'
segment2(object, md = NULL, segmentParents = TRUE, verbose = TRUE, ...)

## S4 method for signature 'matrix'
segment2(object, pos, chrom, id, featureNames, ...)

## S4 method for signature 'ff_matrix'
segment2(object, pos, chrom, id, featureNames, ...)

## S4 method for signature 'arrayORff_array'
segment2(
  object,
  pos,
  chrom,
  id,
  featureNames,
  segmentParents = TRUE,
  verbose = TRUE,
  ...
)
```

Arguments

object	see showMethods{segment2}
...	Additional arguments passed to DNAcopy's segment.
md	a matrix of the minimum distance
segmentParents	logical. Whether to segment the log R ratios of the parents using circular binary segmentation.
verbose	logical. Whether to display messages that indicate progress.
pos	integer vector of physical position of markers in the genome
chrom	character or integer vector of chromosome names
id	character vector of trio identifiers for subsetting object
featureNames	character vector specifying marker names for subsetting object

See Also

segment

segment

TrioSet *Deprecated constructor for* TrioSet *class*

Description

The TrioSet class has been deprecated and may be removed in a future release.

Usage

```
TrioSet(
  pedigreeData = Pedigree(),
  sample.sheet,
  row.names = NULL,
  lrr,
  baf,
  featureData,
  cdfname,
  drop = TRUE,
  mindist = NULL,
  genome = c("hg19", "hg18")
)
```

Arguments

pedigreeData	an object of class Pedigree
sample.sheet	a data.frame containing metadata on the trios
row.names	a character vector providing row identifiers for the sample.sheet argument that match the names of the trios in the pedigreeData argument.
lrr	a matrix of log R ratios
baf	a matrix of B allele frequencies
featureData	a GenomeAnnotatedDataFrame object for the SNPs/nonpolymorphic markers
cdfname	character string indicating the annotation package used to extract physical position and chromosome of markers
drop	logical. When FALSE, the dimnames on the log R ratio and BAF arrays is set to NULL
mindist	can be either NULL or a matrix of the minimum distance
genome	character string providing the UCSC genome build

Value

TrioSet

TrioSet-class *Deprecated class for storing low-level genomic data for trios*

Description

This class is deprecated and will be defunct in a future release.

Usage

```
## S4 method for signature 'TrioSet'
pedigree(object)

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

## S4 method for signature 'TrioSet'
mindist(object)

## S4 replacement method for signature 'TrioSet,matrix'
mindist(object) <- value

## S4 method for signature 'TrioSet'
dim(x)

## S4 method for signature 'TrioSet'
trios(object)

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

## S4 method for signature 'TrioSet,GRanges'
MAP(
  object,
  ranges,
  transition_param = TransitionParam(),
  emission_param = EmissionParam(),
  mdThr = 0.9,
  ...
)

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

Arguments

object	a TrioSet object
value	a matrix

x	a TrioSet object
i	a numeric vector for subsetting rows (optional)
j	a numeric vector for subsetting trios (optional)
...	additional arguments passed to subsetting methods for matrices and data frames
drop	logical. Whether to simplify matrices to numeric vectors. This should be left as FALSE.
ranges	a GRanges object
transition_param	an object of class TransitionParam
emission_param	an object of class EmissionParam
mdThr	the minimum absolute value of the minimum distance segment mean. Segments with means below mdThr in absolute value will not be called as they are unlikely to be de novo.

Slots

fatherPhenoData AnnotatedDataFrame containing covariates for the father

motherPhenoData AnnotatedDataFrame containing covariates for the mother

pedigree an object of class Pedigree

mindist a numeric matrix of the minimum distance for each trio, or NULL

TrioSetList *Constructor for* TrioSetList *class*

Description

The TrioSetList class has been deprecated and may be removed in a future release. Use MinDistExperiment instead.

Usage

```
TrioSetList(
  chromosome = integer(),
  pedigreeData = Pedigree(),
  sample.sheet,
  row.names = NULL,
  lrr,
  baf,
  featureData,
  cdfname,
  ffname = "",
  genome
)
```

Arguments

chromosome	integer vector of chromosome names
pedigreeData	a Pedigree object
sample.sheet	a data.frame containing sample covariates
row.names	a character vector
lrr	a matrix of log R ratios
baf	a matrix of B allele frequencies
featureData	a GenomeAnnotatedDataFrame
cdfname	a character string indicating the annotation package
ffname	prefix for ff-filenames
genome	character string indicating genome build

TrioSetList-class *Deprecated class for storing low-level genomic data for trios*

Description

This class is deprecated and will be defunct in a future release.

Usage

```
## S4 method for signature 'TrioSetList,RangedSummarizedExperiment'
coerce(from, to)

## S4 method for signature 'TrioSetList'
pedigree(object)

## S4 method for signature 'TrioSetList'
trios(object)

## S4 method for signature 'TrioSetList'
offspringNames(object)

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

## S4 method for signature 'TrioSetList,ANY,ANY'
x[[i, j, ..., exact = TRUE]]

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

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

```
## S4 method for signature 'TrioSetList'
x$name

## S4 method for signature 'TrioSetList,GRanges'
MAP(
  object,
  ranges,
  id,
  TAUP = 1e+10,
  tauMAX = 1 - 5e-08,
  cnStates = c(-2, -0.4, 0, 0, 0.4, 1),
  pr.nonmendelian = 1.5e-06,
  mdThr = 0.9,
  ...
)

## S4 method for signature 'TrioSetList'
segment2(object, md = NULL, segmentParents = TRUE, verbose = TRUE, ...)

## S4 method for signature 'list'
segment2(
  object,
  pos,
  chrom,
  id = NULL,
  featureNames,
  segmentParents = TRUE,
  verbose = TRUE,
  genome,
  ...
)
```

Arguments

from	a TrioSetList
to	a RangedSummarizedExperiment
object	a TrioSetList object
x	a TrioSetList
i	a numeric vector for subsetting the chromosomes (optional)
j	a numeric vector for subsetting trios (optional)
...	additional arguments passed to subsetting methods for matrices and data frames
drop	logical. Whether to simplify matrices to numeric vectors. This should be left as FALSE.
exact	ignored
name	character string of a variable name in the phenoData

ranges	a GRanges object
id	a character vector of trio identifiers
TAUP	length-one numeric vector. Larger values decrease the probability of transitioning to an different state.
tauMAX	the maximum allowed transition probability
cnStates	a length-six numeric vector profiving initial values for the mean copy number for each of the 6 states
pr.nonmendelian	a length-one numeric vector indicating the probability of a non-Mendelian copy number alteration in the offspring
mdThr	a length-one numeric vector indicating the minimum value of the mean minimum distance. Segments with absolute mean value less than mdThr are not called.
md	a list of minimum distance matrices. Length of list should be the same as the length of the TrioSetList object.
segmentParents	logical. Whether to segment the parental log R ratios.
verbose	logical. Whether to display messages indicating progress.
pos	a list of the genomic positions (integers)
chrom	list of chromosome names
featureNames	a list of the marker names
genome	a character vector indicating the UCSC genome build used for the annotation (i.e., 'hg18' or 'hg19').

Slots

fatherPhenoData AnnotatedDataFrame containing covariates for the father

motherPhenoData AnnotatedDataFrame containing covariates for the mother

pedigree an object of class Pedigree

TrioSetListLD *Deprecated TrioSetList constructor for large data*

Description

The TrioSetListLD constructor uses ff objects to handle large datasets. This function is defunct. Use MinDistExperiment instead.

Usage

```
TrioSetListLD(
  path,
  fnames,
  ext = "",
  samplesheet,
  row.names,
  pedigreeData,
  featureData,
  annotationPkg,
  outdir = ldPath(),
  ffprefix = "",
  genome = c("hg19", "hg18")
)
```

Arguments

path	Path to plain-text files containing log R ratios and B allele frequencies. Files should contain data for a single sample.
fnames	Character string providing filenames.
ext	Character string indicating whether the fnames has a file extension (e.g., ".txt")
samplesheet	(Optional) data.frame containing phenotypic / experimental covariates on the samples. Note that if samplesheet is provided, row.names must be specified.
row.names	Character vector indicating the sample id for each row in samplesheet. row.names should be unique and, ideally, correspond to fnames
pedigreeData	An object of class Pedigree.
featureData	A GenomeAnnotatedDataFrame
annotationPkg	Character string indicating the annotation package used to extract information on the features (chromosome, physical position, and whether the feature is polymorphic ('isSnp')).
outdir	Character string indicating the path for storing ff objects. Ignored if the **ff** package is not loaded.
ffprefix	Character string indicating the prefix used to name ff objects. Ignored if the **ff** package is not loaded.
genome	character string indicating UCSC genome build. Only "hg19" is allowed for annotation packages that support a single build. Supported builds for most platforms are "hg18" and "hg19".

Value

A TrioSetList object

See Also

TrioSetList

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