Package `MinimumDistance`

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**Title**  A Package for De Novo CNV Detection in Case-Parent Trios

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**Description**  Analysis of de novo copy number variants in trios from high-dimensional genotyping platforms.

**License**  Artistic-2.0

**Depends**  R (>= 3.3), VanillaICE (>= 1.31.3)

**Imports**  methods, BiocGenerics, Biobase, S4Vectors (>= 0.9.25),
IRanges, GenomeInfoDb, GenomicRanges (>= 1.17.16),
SummarizedExperiment (>= 0.2.0), oligoClasses, DNAcopy, ff,
foreach, matrixStats, lattice, data.table, grid, stats, utils

**Suggests**  human610quadv1bCrlmm (>= 1.0.3), BSgenome.Hsapiens.UCSC.hg18,
BSgenome.Hsapiens.UCSC.hg19, SNPchip, RUnit

**Collate**  'help.R' 'AllClasses.R' 'AllGenerics.R' 'coercion-methods.R'
'datasets.R' 'defunct.R' 'functions.R' 'generator-funs.R'
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'methods-ILimit.R' 'methods-MDRanges.R'
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'methods-MinDistParam.R' 'methods-MinDistPosterior.R'
'methods-ParentOffspring.R' 'methods-ParentOffspringList.R'
'methods-Pedigree.R' 'methods-PennParam.R'
'methods-ShallowSimpleList.R' 'methods-SummarizedExperiment.R'
'methods-TrioSet.R' 'methods-TrioSetList.R'
'methods-ff_array.R' 'methods-grid.R' 'methods-list.R'
'methods-matrix.R' 'segment2-methods.R' 'utils.R' 'zzz.R'

**Enhances**  snow, doSNOW

**LazyLoad**  yes

**biocViews**  Microarray, SNP, CopyNumberVariation

**RoxygenNote**  5.0.1

**NeedsCompilation**  no
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**Function for computing autocorrelations**

**Description**

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

**Usage**

```r
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 automatically omitted.
- `demean`: logical, as in `acf`
- `...`: additional arguments passed to `acf`

**See Also**

`acf`

**Examples**

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

**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 IO-Fl denote the absolute difference in the log R ratios comparing offspring to father and IO-MI the absolute difference in the log R ratios comparing offspring to mother. The minimum distance at a marker is the signed minimum of IO-MI and IO-Fl. 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

```r
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

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"))
```

```R
## 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  
min.width  
undo.splits  
undo.SD  

see segment

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

```r
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 function is deprecated and will be defunct in a future release. The replacement function is `MAP2`.

**Usage**

```r
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

```r
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)
```

**mdLegend**

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

### Description
Text summary of information encapsulated in a MDRanges object for a particular interval

### Usage

```r
mdLegend(g)
```

### Arguments

- `g` a MDRanges object

### Description
Contains maximum a posteriori estimates for each genomic interval

### Usage

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

### Arguments

- `...` additional arguments to GRanges constructor
- `posteriors` a DataFrame

### Examples

```r
MDRanges()
```
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

```r
## 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))
))
```

Prior to inferring de novo trio copy number states, the log R ratios are segmented independently for each individual in a ParentOffspring 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

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-class

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'
MinDistGRanges

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 propagated 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 accommodate 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

```r
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

```r
MinDistGRanges()
```
MinDistParam

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
object
value

A MinDistGRanges object
A MinDistGRanges object
A GRangesList object

Slots

mindist
offspring
father
mother
pedigree

A GRangesList object
A GRangesList object
A GRanges object
A GRanges object
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 probabilities (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

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'
MinDistParam

nMAD(object)

## S4 replacement method for signature 'MinDistParam,numeric'
MinDistParam(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

- \texttt{nMAD} a length-one numeric vector
- \texttt{dnacopy} an object of class \texttt{DNACopyParam}
- \texttt{penncnv} an object of class \texttt{PennParam}
- \texttt{emission} an object of class \texttt{EmissionParam}
- \texttt{thin} a length-one non-negative integer

---

\texttt{MinDistPosterior-class}

\textit{Container for the segmentation results from a \texttt{MinDistExperiment}}

Description

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

Usage

\begin{verbatim}
## S4 method for signature 'MinDistPosterior,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]

## S4 method for signature 'MinDistPosterior'
show(object)
\end{verbatim}

Arguments

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

See Also

- \texttt{denovo}

---

\texttt{MinimumDistance} \textit{De novo copy number alterations in parent-offspring trios}

Description

\textit{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

Constructor for `ParentOffspring` class

**Usage**

```r
offspring(object)
```

```r
father(object)
```

```r
mother(object)
```

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

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

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

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

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

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

```r
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. Constructor for ParentOffspringList class

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

```r
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**

```r
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**

```r
Pedigree()
```
Pedigree-class  

Deprecated class for storing pedigree data

Description

Deprecated class for storing pedigree data

Usage

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

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

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

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

```r
## 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
**pedigreeName**

**Usage**

```r
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**

```r
library(VanillaICE)
require(grid)
## marker-level summaries
data(md_exp)
seqlevels(md_exp, force=TRUE) <- "chr22"
## segmentation results
data(md_gr)
priorCalls <- MAP2(md_exp, md_gr, MinDistParam())
g <- denovoHemizygous(priorCalls)
g
vps <- MinimumDistance:::pedigreeViewports()
param <- HmmTrellisParam()
p <- plotDenovo(md_exp, g[1], param)
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(priorCalls), 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

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**

```r
plotDenovo(object, g, param)
```

### Arguments

- **object**
  - see showMethods("plotDenovo")

- **g**
  - a MDRanges object

- **param**
  - a HmmTrellisParam object
Description

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

Usage

```r
## 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.

Description

Methods for circular binary segmentation.

Usage

```r
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

**Examples**

```r
path <- system.file("extdata", package="MinimumDistance")
load(file.path(path, "logRratio.rda"))
load(file.path(path, "baf.rda"))
load(file.path(path, "pedigreeInfo.rda"))
trioSet <- TrioSet(lrr=logRratio,
                   baf=baf,
                   pedigree=Pedigree(pedigreeInfo),
                   cdfname="human610quadv1bcrlmm",
                   genome="hg18")
```

---

**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**

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

**Usage**

```r
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
TrioSetList-class

Description

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

Usage

```r
## 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'

```r
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 a different state.
- `tauMAX`: the maximum allowed transition probability
- `cnStates`: a length-six numeric vector providing 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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