Package ‘MinimumDistance’

March 26, 2015

Type Package
Title A package for de novo CNV detection in case-parent trios
Version 1.11.3
Date Tue Oct 21 22:11:13 EDT 2014
Author Robert B Scharpf and Ingo Ruczinski
Maintainer Robert B Scharpf <rscharpf@jhu.edu>
Description Analysis of de novo copy number variants in trios from high-dimensional genotyping platforms
License Artistic-2.0
Depends R (>= 3.01)
Imports methods, oligoClasses, S4Vectors, VanillaICE (>= 1.29.3), Biobase, DNAcopy, BiocGenerics, ff, foreach, matrixStats, IRanges, lattice, GenomicRanges (>= 1.17.16), GenomeInfoDb, data.table, grid
Suggests human610quadv1bCrlmm (>= 1.0.3), SNPchip, RUnit
Collate 'help.R' 'AllClasses.R' 'AllGenerics.R' 'coercion-methods.R'
'datasets.R' 'defunct.R' 'functions.R' 'generator-funs.R'
'lattice-methods.R' 'mad-methods.R'
'methods-AnnotatedDataFrame.R' 'methods-AssayData.R'
'methods-FileViews.R' 'methods-FilterParamMD.R'
'methods-ILimit.R' 'methods-MDRanges.R'
'methods-MinDistExperiment.R' 'methods-MinDistGRanges.R'
'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
R topics documented:

### Local Variables
### time-stamp-pattern ``8/Date: %3a %3b %2d %02H:%02M:%02S %Z %:y\{}n''
### End

NeedsCompilation no

R topics documented:

acf2 ......................................................... 3
calculateMindist .......................................... 4
coerce ....................................................... 5
denovoHemizygous ......................................... 5
DNAcopyParam ............................................. 6
exampleTripSetList ......................................... 7
filterExperiment ........................................... 7
FilterParamMD ............................................... 8
FilterParamMD-class ......................................... 9
mad2 .......................................................... 10
MAP ........................................................... 10
MAP2 .......................................................... 11
mdLegend ....................................................... 12
MDRanges-class ............................................. 12
md_exp ........................................................ 13
md_gr .......................................................... 14
mindist ......................................................... 15
MinDistExperiment .......................................... 15
MinDistExperiment-class .................................... 16
MinDistGRanges ............................................ 17
MinDistGRanges-class ....................................... 18
MinDistParam ............................................... 19
MinDistParam-class ......................................... 20
MinDistPosterior-class ...................................... 20
MinimumDistance ........................................... 21
nMAD ............................................................ 21
offspringNames .............................................. 22
ParentOffspring-class ....................................... 22
ParentOffspringList-class ................................... 24
Pedigree ......................................................... 25
Pedigree-class ............................................... 25
pedigreeGrid ................................................. 26
pedigreeName ................................................ 27
pedigreeViewports .......................................... 28
PennParam ...................................................... 28
plotDenovo .................................................. 29
range,ILimit-method ....................................... 30
segment2 ....................................................... 30
TrioSet ........................................................ 31
Function for computing autocorrelations

Description

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

Usage

\[ \text{acf2}(x, \text{lag.max} = 10, \text{type} = \text{c("correlation","covariance","partial")}, \]
\[ \text{plot} = \text{FALSE}, \text{na.action} = \text{na.omit}, \text{demean} = \text{TRUE}, ...) \]

Arguments

- \( x \): a numeric vector
- \( \text{lag.max} \): see \text{acf}
- \( \text{type} \): see \text{acf}
- \( \text{plot} \): logical, as in \text{acf}
- \( \text{na.action} \): ignored. Missing values are automatically omitted.
- \( \text{demean} \): logical, as in \text{acf}
- \( ... \): additional arguments passed to \text{acf}

See Also

\text{acf}

Examples

\[ x \leftarrow \text{rnorm}(100) \]
\[ x[5] \leftarrow \text{NA} \]
\[ \text{acf2}(x) \]
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**

```r
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, ...)

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

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

**Arguments**

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

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")))
denoDuction(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

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)
```
exampleTrioSetList

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(dncopy=segment_params)

trioSetList <- exampleTrioSetList

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 Trio 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

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
Examples

```r
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

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

Arguments

- `object`: a FilterParamMD object

See Also

denovo
### 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

### 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.
...

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)
library(MinimumDistance)
## 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

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)

## S4 method for signature 'MDRanges'
reduce(x, ...)

MDRanges-class
Arguments

... additional arguments to GRanges constructor

posterior \( a \) DataFrame

\( x \) a MDRanges object

Examples

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 SummarizedExperiment, and so many of the methods defined for SummarizedExperiment such as findOverlaps are available through inheritance.

Format

a MinDistExperiment

Examples

```r
## Not run:
library(oligoClasses)
library(GenomicRanges)
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(rowData=fgr, sourcePaths=files, parsedPath=parsedDir)
dat <- fread(files[1])
select_columns <- match(c("SNP Name", "Allele1 - AB", "Allele2 - AB"),
```
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
mindist

*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 'SummarizedExperiment'
father(object)

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

## S4 method for signature 'SummarizedExperiment'
MinDistGRanges

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 SummarizedExperiment
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

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
```r
## 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
MinDistParam

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 probabilities (see citation below), and initial values/parameters for computing emission probabilities.

Usage

MinDistParam(nMAD = 0.75, dnacopy = DNACopyParam(), pennnv = 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.
pennnv 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
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

```r
## 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

Description

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

```r
nMAD(object)
nMAD(object) <- value
```

Arguments

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

- `offspring(object)`
- `mother(object)`
- `father(object)`

`ParentOffspring(id = character(), father = character(),
mother = character(), offspring = character(), parsedPath = character())`
## 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 parsed files of the marker-level summaries
- **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

```r
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.
Pedigree

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

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

```r
## 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`
pedigreeName

Examples

library( GenomicRanges )
library( VanillaICE )
require( grid )
## marker-level summaries
data( md_exp )
seqlevels( md_exp, force=TRUE ) <- "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 idio-
gram, 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

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

## S4 method for signature 'MinDistExperiment,MDRanges'
```r
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

```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.

segment2  

A wrapper for DNAcopy's segment function

Description

Methods for circular binary segmentation.

Usage

```r
segment2(object, ...)
```

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

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

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

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

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

Depreciated constructor for TrioSet class

Description

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

Usage

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

Arguments

pedigreeData an object of class Pedigree

sampleSheet a data.frame containing metadata on the trios

row.names a character vector providing row identifiers for the sampleSheet 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

geno 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="human61@quadv1bCr1mm",
                  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 'ff_array,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]

## 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, ...)

### Arguments

- **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.
- **object**: a TrioSet object
- **value**: a matrix
- **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

---

### 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, fname = "", genome)
TrioSetList-class

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
- fname: 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

```r
## S4 method for signature 'TrioSetList,SummarizedExperiment'
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'
MMAP(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 SummarizedExperiment
- `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 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.
TrioSetListLD

md

segmentParents

verbose

pos

chrom

featureNames

genome

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
TrioSetListLD

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
Index

[,MinDistExperiment, ANY, ANY, ANY-method (MinDistExperiment-class), 16
[,MinDistPosterior, ANY, ANY, ANY-method (MinDistPosterior-class), 20
[,ParentOffspringList, ANY, ANY, ANY-method (ParentOffspringList-class), 24
[,ParentOffspringList, ANY-method (ParentOffspringList-class), 24
[,Pedigree, ANY, ANY, ANY-method (Pedigree-class), 25
[,Pedigree, ANY-method (Pedigree-class), 25
[,TrioSet, ANY, ANY, ANY-method (TrioSet-class), 32
[,TrioSet, ANY-method (TrioSet-class), 32
[,TrioSetList, ANY, ANY, ANY-method (TrioSetList-class), 34
[,TrioSetList, ANY-method (TrioSetList-class), 34
[,ff_array, ANY, ANY, ANY-method (TrioSet-class), 32
[,ff_array, ANY-method (TrioSet-class), 32
[[,ParentOffspringList, ANY, ANY-method (ParentOffspringList-class), 24
[[,TrioSetList, ANY, ANY-method (TrioSetList-class), 34
$,TrioSetList-method (TrioSetList-class), 34

acf, 3
acf2, 3
as (coerce), 5

calculateMindist, 4
calculateMindist, arrayORff_array-method (calculateMindist), 4
calculateMindist, list-method (calculateMindist), 4
calculateMindist, matrix-method (calculateMindist), 4
calculateMindist, TrioSet-method (calculateMindist), 4
calculateMindist, TrioSetList-method (calculateMindist), 4
calculateMindist, MinDistExperiment-method (coerce), 5
calculateMindist, MinDistPosterior-method (denovoHemizygous), 5
calculateMindist, MinDistPosterior-method (denovoHemizygous), 5
calculateMindist, MinDistPosterior-method (DNAcopyParam), 6
calculateMindist, MinDistPosterior-method (TrioSet-class), 32
calculateMindist, MinDistPosterior-method (TrioSet-class), 32
coerce, 5
denovo, 21
denovo (denovoHemizygous), 5
denovo, MinDistPosterior-method (denovoHemizygous), 5
denovoDuplication (denovoHemizygous), 5
denovoDuplication, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
denovoHemizygous, MinDistPosterior-method (denovoHemizygous), 5
father, MinDistExperiment-method
   (MinDistExperiment-class), 16
father, MinDistGRanges-method
   (MinDistGRanges-class), 18
father, ParentOffspring-method
   (ParentOffspring-class), 22
father, SummarizedExperiment-method
   (MinDistExperiment-class), 16
filterExperiment, 7
filterExperiment, MinDistExperiment, GRanges-method
   (filterExperiment), 7
filterExperiment, MinDistExperiment, GRangesList-method
   (filterExperiment), 7
filterExperiment, MinDistExperiment, MinDistGRanges-method
   (filterExperiment), 7
FilterParam, 8
FilterParamMD, 8
FilterParamMD-class, 9
length, ParentOffspringList-method
   (ParentOffspringList-class), 24
length, TrioSetList-method
   (TrioSetList-class), 34
mad, 10
mad2, 10
mad2, array-method (mad2), 10
mad2, list-method (mad2), 10
mad2, matrix-method (mad2), 10
mad2, TrioSetList-method (mad2), 10
MAP, 10
MAP, TrioSet, GRanges-method
   (TrioSet-class), 32
MAP, TrioSetList, GRanges-method
   (TrioSetList-class), 34
MAP2, 11
MAP2, MinDistExperiment, GRanges-method
   (MAP2), 11
MAP2, MinDistExperiment, GRangesList-method
   (MAP2), 11
MAP2, MinDistExperiment, MinDistGRanges-method
   (MAP2), 11
mad_exp, 13
mad_gr, 14
madLegend, 12
MDRanges (MDRanges-class), 12
MDRanges-class, 12
mindist, 15
mindist, MinDistExperiment-method
   (MinDistExperiment-class), 16
mindist, MinDistGRanges-method
   (MinDistGRanges-class), 18
mindist, TrioSet-method (TrioSet-class), 32
mindist<- (mindist), 15
mindist<-, MinDistExperiment, ANY-method
   (MinDistExperiment-class), 16
mindist<-, MinDistGRanges, GRangesList-method
   (MinDistGRanges-class), 18
mindist<-, MinDistGRanges, GRangesList-method
   (TrioSet-class), 32
MindDistExperiment, 15
MindDistExperiment, ArrayViews, ParentOffspring-method
   (MindDistExperiment), 15
MindDistExperiment-class, 16
MindDistGRanges, 17
MindDistGRanges-class, 18
MindDistParam, 19
MindDistParam-class, 20
MindDistPosterior-class, 20
MinimumDistance, 21
MinimumDistance-package
   (MinimumDistance), 21
mother (ParentOffspring-class), 22
mother, MinDistExperiment-method
   (MinDistExperiment-class), 16
mother, MinDistGRanges-method
   (MinDistGRanges-class), 18
mother, ParentOffspring-method
   (ParentOffspring-class), 22
mother, SummarizedExperiment-method
   (MinDistExperiment-class), 16
names, MinDistGRanges-method
   (MinDistGRanges-class), 18
names, ParentOffspring-method
   (ParentOffspring-class), 22
nMAD, 21
nMAD, MinDistParam-method
   (MinDistParam-class), 20
nMAD<- (nMAD), 21
nMAD<-, MinDistParam, numeric-method
   (MinDistParam-class), 20
offspring (ParentOffspring-class), 22
offspring, GRangesList-method
   (MinDistGRanges-class), 18
offspring, MinDistExperiment-method
   (MinDistExperiment-class), 16
offspring, MinDistGRanges-method
   (MinDistGRanges-class), 18
offspring, ParentOffspring-method
   (ParentOffspring-class), 22
offspring, SummarizedExperiment-method
   (MinDistExperiment-class), 16
offspringNames, 22
offspringNames, Pedigree-method
   (Pedigree-class), 25
offspringNames, TrioSetList-method
   (TrioSetList-class), 34
offspringNames <- (offspringNames), 22

ParentOffspring, 24, 28
ParentOffspring
   (ParentOffspring-class), 22
ParentOffspringList, 22, 28
ParentOffspringList
   (ParentOffspringList-class), 24
ParentOffspringList-class, 24
Pedigree, 25
pedigree (offspringNames), 22
pedigree, MinDistExperiment-method
   (MinDistExperiment-class), 16
pedigree, MinDistGRanges-method
   (MinDistGRanges-class), 18
pedigree, TrioSet-method
   (TrioSet-class), 32
pedigree, TrioSetList-method
   (TrioSetList-class), 34
Pedigree-class, 25
pedigree <- (offspringNames), 22
pedigree <-, MinDistExperiment-method
   (MinDistExperiment-class), 16
pedigreeGrid, 26, 28
pedigreeName, 27
pedigreeName, ParentOffspring-method
   (ParentOffspring-class), 22
pedigreeName, ParentOffspringList-method
   (ParentOffspringList-class), 24
pedigreeViewports, 26, 28
PennParam, 28
plotDenovo, 26, 28, 29
plotDenovo, MinDistExperiment, MDRanges-method
   (plotDenovo), 29
range, ILimit-method, 30
reduce, MDRanges-method
   (MDRanges-method), 12
segment, 7, 19, 31
segment2, 30
segment2, arrayORff_array-method
   (segment2), 30
segment2, ff_matrix-method (segment2), 30
segment2, list-method
   (TrioSetList-class), 34
segment2, matrix-method (segment2), 30
segment2, MinDistExperiment-method
   (MinDistExperiment-class), 16
segment2, TrioSet-method (segment2), 30
segment2, TrioSetList-method
   (TrioSetList-class), 34
show, DNAcopyParam-method
   (MinDistParam-class), 20
show, FilterParamMID-method
   (FilterParamMID-class), 9
show, MinDistExperiment-method
   (MinDistExperiment-class), 16
show, MinDistGRanges-method
   (MinDistGRanges-class), 18
show, MinDistParam-method
   (MinDistParam-class), 20
show, MinDistPosterior-method
   (MinDistPosterior-class), 20
show, ParentOffspring-method
   (ParentOffspring-class), 22
show, ParentOffspringList-method
   (ParentOffspringList-class), 24
show, Pedigree-method (Pedigree-class), 25
show, PennParam-method (PennParam), 28
show, TrioSet-method (TrioSet-class), 32
show, TrioSetList-method
   (TrioSetList-class), 34
stack, TrioSetList-method (coerce), 5
stack, TrioSetList-method (coerce), 5
trios (offspringNames), 22
trios, Pedigree-method (Pedigree-class), 25
trios, TrioSet-method (TrioSet-class), 32
trios, TrioSetList-method
   (TrioSetList-class), 34
TrioSet, 31
TrioSet-class, 32
TrioSetList, 33, 37
trioSetList (exampleTrioSetList), 7
TrioSetList-class, 34
TrioSetListLD, 36