Package: MDTS (via r-universe)

November 25, 2026

Title Detection of de novo deletion in targeted sequencing trios

Version 1.34.0

Description A package for the detection of de novo copy number deletions in targeted sequencing of trios with high sensitivity and positive predictive value.

Depends R (>= 3.5.0)

Imports GenomicAlignments, GenomicRanges, IRanges, Biostrings, DNAcopy, Rsamtools, parallel, stringr

Suggests testthat, knitr

VignetteBuilder knitr

License Artistic-2.0

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

biocViews StatisticalMethod, Technology, Sequencing, TargetedResequencing, Coverage, DataImport

Config/pak/sysreqs libbz2-dev libicu-dev liblzma-dev xz-utils zlib1g-dev

Repository Bioconductor 3.24

Date/Publication 2026-11-23 22:40:26 UTC

RemoteUrl https://github.com/bioc/MDTS

RemoteRef RELEASE_3_24

RemoteSha ca1fecee3a340ebb8d00f7629a60df0b25aba575

Contents

MDTS-package 2
calcBins 2
calcCounts 3
calcMD 4
denovoDeletions 4

getMetaData 5
normalizeCounts 6
segmentMD 6
visualizeDeletion 7

Index **9**

`MDTS-package` *The MDTS package for Detection of Denovo Deletions from Targeted Sequencing Data Using Minimum-Distance*

Description

The MDTS package for Detection of Denovo Deletions from Targeted Sequencing Data Using Minimum-Distance

---

`calcBins` *Sample driven calculation of bins for counting*

Description

This function will randomly select a sample of bam files to calculate dynamic MDTS bins for subsequent read-depth analysis.

Usage

```
calcBins(metaData, n, readLength, medianCoverage, minimumCoverage, genome,
  mappabilityFile, seed = 1337)
```

Arguments

`metaData`	A table in the format of the output of getMetaData().
`n`	The number of subsamples to use.
`readLength`	The read length of the experiment.
`medianCoverage`	The median number of reads across sub-samples to reach before creating a new bin.
`minimumCoverage`	The miminum number of coverage across all sub-samples required to create the proto-region.
`genome`	The BSGenome object that assists in calculations of the GC content of the bins.
`mappabilityFile`	A path to the bigwig file of 100mer mappability of the corresponding genome.
`seed`	Sets the seed so results are reproducible. Defaults to 1337.

Value

Returns a GRanges object depicting the dynamic bins that MDTS calculates.

Examples

```
load(system.file("extdata", 'bins.RData', package = "MDTS"))
bins
```

---

calcCounts *Creating the raw count matrix*

Description

This function will return a matrix of read counts where ecah column is a sample, and each row is a bin.

Usage

```
calcCounts(metaData, bins, rl, mc.cores = 1)
```

Arguments

metaData	A table in the format of the output of getMetaData().
bins	The set of bins determined by calcBins().
rl	The read length of the experiment.
mc.cores	The number of cores to use for multi-threaded analysis. Defaults to 1.

Value

A data.frame that contains the counts for each sample in the metaData input that fall into each segment of bins.

Examples

```
## Not run:
pD <- getMetaData(
'https://raw.githubusercontent.com/JMF47/MDTSData/master/data/pD.ped')
genome = BSgenome.Hsapiens.UCSC.hg19
map_file <-
"https://raw.githubusercontent.com/JMF47/MDTSData/master/data/chr1.map.bw"
bins = calcBins(pD, n=5, rl=100, med=150, min=5, genome, map_file)

## End(Not run)
load(system.file("extdata", 'bins.RData', package = "MDTS"))
load(system.file("extdata", 'counts.RData', package = "MDTS"))
counts
```

calcMD *Calculating the Minimum Distance matrix*

Description

This function will return a matrix of minimum distances where ecah column is a family, and each row is a bin.

Usage

```
calcMD(mCounts, metaData)
```

Arguments

mCounts	A matrix of normalized coverage output by normalizedCounts().
metaData	A table in the format of the output of metaData().

Value

A `data.frame` of minimum distances. Each column is a trio, while each row is an entry in `bins`

Examples

```
load(system.file("extdata", 'bins.RData', package = "MDTS"))
load(system.file("extdata", 'counts.RData', package = "MDTS"))
load(system.file("extdata", 'pD.RData', package = "MDTS"))
mCounts <- normalizeCounts(counts, bins)
md <- calcMD(mCounts, pD)
```

denovoDeletions *Denovo Deletion Calling*

Description

This function will return a single GRanges object containing all denovo deletions that passed filtering from a Circular Binary Segmentation object with supplementary information.

Usage

```
denovoDeletions(cbs, mCounts, bins)
```

Arguments

cbs	The output from segmentMD().
mCounts	The normalized counts matrix output by normalizeCounts().
bins	The set of bins determined by calcBins().

Value

A GRanges object that reports all detected denovo deletions passing requite filters.

Examples

```
load(system.file("extdata", 'bins.RData', package = "MDTS"))
load(system.file("extdata", 'counts.RData', package = "MDTS"))
load(system.file("extdata", 'pD.RData', package = "MDTS"))
mCounts = normalizeCounts(counts, bins)
md = calcMD(mCounts, pD)
cbs = segmentMD(md, bins)
denovo = denovoDeletions(cbs, mCounts, bins)
```

---

getMetaData *Constructor for metadata*

Description

This function allows constructor of phenotype information necessary for downstream analysis. See format of required fields. Function will also rearrange the rows such that trios are grouped together - with proband first, mother second, and father third.

Usage

```
getMetaData(path, id = "subj_id", familyId = "family_id",
  fatherId = "father_id", motherId = "mother_id", bamPath = "bam_path")
```

Arguments

path	The path pointing to the file that contains information on each subject in the dataset.
id	The column name that identifies each sample. Defaults to 'subj_id'.
familyId	The column name that identifies which family the sample belongs to. Defaults to 'family_id'.
fatherId	The column name that identifies the id of the father. Defaults to 'father_id'.
motherId	The column name that identifies the id of the mother. Defaults to 'mother_id'.
bamPath	The column name that identifies where to find the bam file for each subject. Defaults to 'bam_path'.

Value

Returns a data.frame of required sample information for running MDTS.

Examples

```
meta <- getMetaData(
'https://raw.githubusercontent.com/JMF47/MDTSData/master/data/pD.ped')
```

normalizeCounts *Calculating the normalized M scores*

Description

This function will return a matrix of normalized M scores where ecah column is a sample, and each row is a bin.

Usage

```
normalizeCounts(counts, bins, GC = TRUE, map = TRUE, mc.cores = 1)
```

Arguments

counts	A matrix of raw coverage output by calcCounts().
bins	The set of bins determined by calcBins().
GC	Whether to loess adjust for GC. Defaults to TRUE.
map	Whether to loess adjust for mappability. Defaults to TRUE. Defaults to 1.
mc.cores	The number of cores to use for multi-threaded analysis.

Value

A data.frame of normalized counts. Each column is a sample, and each row is a entry of bins.

Examples

```
load(system.file("extdata", 'bins.RData', package = "MDTS"))
load(system.file("extdata", 'counts.RData', package = "MDTS"))
load(system.file("extdata", 'pD.RData', package = "MDTS"))
mCounts <- normalizeCounts(counts, bins)
```

segmentMD *Circular Binary Segmentation on Minimum Distances*

Description

This function will return a GRanges object containing the copy number segments of all families in the input minimum distance matrix. It calls segment() from DNAcopy (alpha=0.001, undo.splits="sdundo", undo.SD=4).

Usage

```
segmentMD(md, bins, alpha = 0.001, undo.splits = "sdundo", undo.SD = 4,
  mc.cores = 1)
```

Arguments

md	The minimum distance matrix produced by calcMD.
bins	The set of bins determined by calcBins.
alpha	Controls the alpha option in calling DNAcopy::segment()
undo.splits	Controls the undo.splits option in DNAcopy::segment()
undo.SD	Controls the undo.SD option in calling DNAcopy::segment()
mc.cores	The number of cores to use for multi-threaded analysis. Defaults to 1.

Value

A data.frame containing the segmented regions based to be parsed by denovoDeletions() minimum distance.

Examples

```
load(system.file("extdata", 'bins.RData', package = "MDTS"))
load(system.file("extdata", 'counts.RData', package = "MDTS"))
load(system.file("extdata", 'pD.RData', package = "MDTS"))
mCounts <- normalizeCounts(counts, bins)
md <- calcMD(mCounts, pD)
cbs <- segmentMD(md, bins)
```

---

visualizeDeletion *Visualization for deletions*

Description

This function plots the raw read information from the location of interest for a trio.

Usage

```
visualizeDeletion(deletion, bins, metaData, mCounts, md, save = FALSE)
```

Arguments

deletion	A GRanges object in the format of the output of denovoDeletions().
bins	The set of bins determined by calcBins().
metaData	A table in the format of the output of getMetaData().
mCounts	A matrix of normalized coverage output by normalizedCounts().
md	The minimum distance matrix output by calcMD()
save	If TRUE will save plot to current working directory instead of rendering.

Value

The file name if the plot was saved.

Examples

```
## Not run:
load(system.file("extdata", 'bins.RData', package = "MDTS"))
load(system.file("extdata", 'counts.RData', package = "MDTS"))
load(system.file("extdata", 'pD.RData', package = "MDTS"))
mCounts <- normalizeCounts(counts, bins)
md <- calcMD(mCounts, pD)
cbs <- segmentMD(md, bins)
denovo <- denovoDeletions(cbs, mCounts, bins)
visualizeDeletion(denovo[1], bins, pD, mCounts, md)

## End(Not run)
```

Index

∗ **calcBins**
    calcBins, 2
∗ **calcCounts**
    calcCounts, 3
∗ **calcMD**
    calcMD, 4
∗ **denovoDeletions**
    denovoDeletions, 4
∗ **normalizeCounts**
    normalizeCounts, 6
∗ **segmentMD**
    segmentMD, 6
∗ **visualizeDeletion**
    visualizeDeletion, 7

calcBins, 2
calcCounts, 3
calcMD, 4

denovoDeletions, 4

getMetaData, 5

MDTS *(*MDTS-package*)*, 2
MDTS-package, 2

normalizeCounts, 6

segmentMD, 6

visualizeDeletion, 7