

Package ‘MDTS’

July 24, 2025

Title Detection of de novo deletion in targeted sequencing trios

Version 1.28.0

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

git_url <https://git.bioconductor.org/packages/MDTS>

git_branch RELEASE_3_21

git_last_commit 2078f3e

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-07-23

Author Jack M.. Fu [aut, cre]

Maintainer Jack M.. Fu <jmfu@jhsp.h.edu>

Contents

MDTS-package	2
calcBins	2
calcCounts	3

calcMD	4
denovoDeletions	4
getMetaData	5
normalizeCounts	6
segmentMD	6
visualizeDeletion	7
Index	9

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

Description

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

calcBins	<i>Sample driven calculation of bins for counting</i>
----------	---

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 each 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/MDTSDData/master/data/pD.ped')
genome = BSgenome.Hsapiens.UCSC.hg19
map_file <-
  "https://raw.githubusercontent.com/JMF47/MDTSDData/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	<i>Calculating the Minimum Distance matrix</i>
--------	--

Description

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

Usage

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

Arguments

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

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	<i>Denovo Deletion Calling</i>
-----------------	--------------------------------

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 <code>segmentMD()</code> .
mCounts	The normalized counts matrix output by <code>normalizeCounts()</code> .
bins	The set of bins determined by <code>calcBins()</code> .

Value

A GRanges object that reports all detected denovo deletions passing require 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	<i>Calculating the normalized M scores</i>
-----------------	--

Description

This function will return a matrix of normalized M scores where each 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	<i>Circular Binary Segmentation on Minimum Distances</i>
-----------	--

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

<code>md</code>	The minimum distance matrix produced by <code>calcMD</code> .
<code>bins</code>	The set of bins determined by <code>calcBins</code> .
<code>alpha</code>	Controls the <code>alpha</code> option in calling <code>DNAcopy::segment()</code>
<code>undo.splits</code>	Controls the <code>undo.splits</code> option in <code>DNAcopy::segment()</code>
<code>undo.SD</code>	Controls the <code>undo.SD</code> option in calling <code>DNAcopy::segment()</code>
<code>mc.cores</code>	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	<i>Visualization for deletions</i>
-------------------	------------------------------------

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

<code>deletion</code>	A GRanges object in the format of the output of <code>denovoDeletions()</code> .
<code>bins</code>	The set of bins determined by <code>calcBins()</code> .
<code>metaData</code>	A table in the format of the output of <code>getMetaData()</code> .
<code>mCounts</code>	A matrix of normalized coverage output by <code>normalizedCounts()</code> .
<code>md</code>	The minimum distance matrix output by <code>calcMD()</code>
<code>save</code>	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](#)