Package 'uncoverappLib'

October 14, 2021

Title Interactive graphical application for clinical assessment of sequence coverage at the base-pair level

Version 1.2.0

Imports markdown, shiny, shinyjs, shinyBS, shinyWidgets,shinycssloaders, DT, Gviz, Homo.sapiens, openxlsx, condformat, stringr, org.Hs.eg.db, TxDb.Hsapiens.UCSC.hg38.knownGene, BiocFileCache,rappdirs, TxDb.Hsapiens.UCSC.hg19.knownGene, rlist, utils, EnsDb.Hsapiens.v75, EnsDb.Hsapiens.v86, OrganismDbi, BSgenome.Hsapiens.UCSC.hg19, processx, Rsamtools, GenomicRanges

Description a Shiny application containing a suite of graphical and statistical tools to support clinical assessment of low coverage regions.It displays three web pages each providing a different analysis module: Coverage analysis, calculate AF by allele frequency app and binomial distribution.

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.0

URL https://github.com/Manuelaio/uncoverappLib

BugReports https://github.com/Manuelaio/uncoverappLib/issues

VignetteBuilder knitr

Suggests BiocStyle, knitr, testthat, rmarkdown, dplyr

biocViews Software, Visualization, Annotation, Coverage

NeedsCompilation no

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R topics documented:

`.get_cache` *wrapper function for getting BiocFileCache associated with uncoverapp package wrapper function for getting BiocFileCache associated with uncoverapp package*

Description

wrapper function for getting BiocFileCache associated with uncoverapp package wrapper function for getting BiocFileCache associated with uncoverapp package

Usage

```
.get_cache()
```

Value

BiocFileCache object associated with uncoverappLib

`buildInput` *Build input file*

Description

Function to build input file for unCOVERAPP when the number of genes to analyze is > 50.

Usage

```
buildInput(
  geneList,
  genome,
  type_bam,
  bamList,
  outDir,
  MAPQ.min = 1,
  base.quality = 1
)
```

Arguments

geneList	a text file, named with .txt extension, containing HGNC official gene name(s) one per row.
genome	(char) reference genome, hg19 or hg38
type_bam	(char) chromosome notation of their BAM file(s). Use "number" or "chr". In the BAM file, the number option refers to 1, 2, ..., X,.M chromosome notation, while the chr option refers to chr1, chr2, ... chrX, chrM chromosome notation.
bamList	a text file, named with .list extension, containing the absolute paths to BAM file(s) one per row.
outDir	(char) directory where pileup output will be stored
MAPQ.min	(integer) minimum MAPQ value for an alignment to be included in output file.
base.quality	(integer) minimum QUAL value for each nucleotide in an alignment.

Value

A file.bed containing tab-separated specifications of genomic coordinates (chromosome, start position, end position), the coverage value, and the reference:alternate allele counts for each position.

Examples

```
gene.list<- system.file("extdata", "mygene.txt", package = "uncoverappLib")

bam_example <- system.file("extdata", "example_POLG.bam",
package = "uncoverappLib")
cat(bam_example, file = "bam.list", sep = "\n")
temp_dir=tempdir()
buildInput(geneList= gene.list, genome= "hg19", type_bam= "chr",
bamList= "bam.list", outDir= temp_dir)
```

`getAnnotationFiles` *download and rename sorted.bed.gz and sorted.bed.gz.tbi files for annotation of low-coverage positions.*

Description

download and rename sorted.bed.gz and sorted.bed.gz.tbi files for annotation of low-coverage positions.

Usage

```
getAnnotationFiles(verbose = FALSE, vignette = FALSE)
```

Arguments

`verbose`	(logical) print messages
`vignette`	(logical) download example annotation-file in vignette mode

Value

(char) Path to local cached file or initial download is required

Examples

```
getAnnotationFiles(verbose = TRUE, vignette= TRUE)
```

`run.uncoverapp` *run.uncoverapp*

Description

This function launches `unCOVERApp`, a `Shiny` application for clinical assessment of sequence coverage.

Usage

```
run.uncoverapp()
```

Value

This return a Shiny App. The is no value

Author(s)

Emanuela Iovino

Examples

```
file.name='../path/sorted.bed.gz'
tbi='.../path/sorted.bed.gz.tbi'
run.uncoverapp()


## Only run this example in interactive R sessions

if (interactive()) {
run.uncoverapp()
}

#After running `run.uncoverapp()` the shiny app appears in your browser
```

`uncoverappLib` *uncoverappLib: Interactive graphical application for clinical assessment of sequence coverage at the base-pair level*

Description

a Shiny application containing a suite of graphical and statistical tools to support clinical assessment of low coverage regions.It displays three web pages each providing a different analysis module: Coverage analysis, calculate AF by allele frequency app and binomial distribution.

Author(s)

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Authors:

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See Also

Useful links:

- https://github.com/Manuelaio/uncoverappLib
- Report bugs at https://github.com/Manuelaio/uncoverappLib/issues

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