Package 'uncoverappLib'

November 26, 2024

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

Version 1.17.0

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,S4Vectors, EnsDb.Hsapiens.v75, EnsDb.Hsapiens.v86, OrganismDbi, 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. uncoverAPP provides a statisticl summary of coverage given target file or genes name.

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Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

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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`.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,
  type_input,
  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
type_input	(char) type of input target. Use "target" or "genes". If you use a list of gene names use "genes", if you use a target bed use "target".
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

Two file: 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 and a file.txt with statistical summary of coverage

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",type_input="genes", 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` *Location for uncoverapp in RStudio enviroment*

Description

This function controls the ‘shiny.launch.browser‘ option to launch uncoverapp in an external ‘browser‘, the RStudio viewer ‘"viewer"‘, or a new ‘"window"‘ in RStudio.

Usage

```
run.uncoverapp(where = c("browser", "viewer", "window"))
```

Arguments

`where`	accept ‘"browser‘" , ‘"viewer‘" or ‘"window‘". The option sets where uncoverapp will be launched. Using NULL, uncoverapp will use default After running ‘run.uncoverapp(where="window")‘ the shiny app appears in your chosen location.

Value

This return a Shiny App. The is no value

Examples

```
## Only run this example in interactive R sessions

if (interactive()) {
run.uncoverapp(where="window")
}
```

---

uncoverAPP *run.uncoverapp*

Description

This function launches unCOVERApp, a Shiny application for clinical assessment of sequence coverage. Setting where uncoverapp will be launched with following where option: ‘"browser‘" in user default browser, ‘"viewer‘" RStudio viewer and ‘"window‘" in a new Rstudio window.

Usage

```
uncoverAPP()
```

Value

This return a Shiny App. The is no value

Author(s)

Emanuela Iovino

Examples

```
## Not run:
file.name='../path/sorted.bed.gz'
tbi='.../path/sorted.bed.gz.tbi'
app()

## End(Not run)

## Only run this example in interactive R sessions

if (interactive()) {
app()
}
```

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. uncoverAPP provides a statisticl summary of coverage given target file or genes name.

Author(s)

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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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