

# Package ‘uncoverappLib’

September 24, 2021

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

**Version** 1.3.0

**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.

**License** MIT + file LICENSE

**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

**git\_url** <https://git.bioconductor.org/packages/uncoverappLib>

**git\_branch** master

**git\_last\_commit** 6de931b

**git\_last\_commit\_date** 2021-05-19

**Date/Publication** 2021-09-24

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| .get_cache | <i>wrapper function for getting BiocFileCache associated with uncoverapp package wrapper function for getting BiocFileCache associated with uncoverapp package</i> |
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### 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

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|            |                         |
|------------|-------------------------|
| buildInput | <i>Build input file</i> |
|------------|-------------------------|

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### 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)
```

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|--------------------|--|
| getAnnotationFiles | <i>download and rename sorted.bed.gz and sorted.bed.gz.tbi files for annotation of low-coverage positions.</i> |
|--------------------|--|

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**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)
```

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|                |                       |
|----------------|-----------------------|
| run.uncoverapp | <i>run.uncoverapp</i> |
|----------------|-----------------------|

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**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
```

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uncoverappLib

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

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## 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)

**Maintainer:** Emanuela Iovino <emanuela.iovino@unibo.it>

Authors:

- Tommaso Pippucci <tommaso.pippucci@unibo.it>

## See Also

Useful links:

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

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