Package ‘PACVr’

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Title Plastome Assembly Coverage Visualization

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Depends R (>= 3.3.0)

Imports Biostrings (>= 2.48.0), dplyr, GenomicAlignments (>= 1.18.1), GenomicRanges, IRanges, logger, read.gb (>= 2.2), RCircos (>= 1.2.0), grDevices, stats, utils, tidyr, R6

Description Visualizes the coverage depth of a complete plastid genome as well as the equality of its inverted repeat regions in relation to the circular, quadripartite genome structure and the location of individual genes. For more information, please see Gruenstaeudl and Jenke (2020) <doi:10.1186/s12859-020-3475-0>.

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RoxygenNote 7.3.1

URL `https://github.com/michaelgruenstaeudl/PACVr`

BugReports `https://github.com/michaelgruenstaeudl/PACVr/issues`

Suggests testthat (>= 3.0.0), rentrez

Config/testthat/edition 3

Encoding UTF-8

NeedsCompilation no

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R topics documented:

`PACVr.complete` *Execute the complete pipeline of* **PACVr**

Description

This function executes the complete pipeline of **PACVr** via a single command.

Usage

```
PACVr.complete(
  gbkFile,
  bamFile,
  windowSize = 250,
  logScale = FALSE,
  threshold = 0.5,
  IRCheck = NA,
  relative = TRUE,
  textSize = 0.5,
  tabularCovStats = FALSE,
  output = NA
)
```

Arguments

`gbkFile`	a character string that specifies the name of, and path to, the GenBank input file; alternatively, a character string of GenBank data
`bamFile`	a character string that specifies the name of, and path to, the BAM input file
`windowSize`	a numeric value that specifies window size in which the coverage is calculated
`logScale`	a boolean that specifies if the coverage depth is to be log-transformed before visualizing it
`threshold`	a numeric value that specifies the threshold for plotting coverage depth bars in red as opposed to the default black
`IRCheck`	a numeric value that specifies if tests for IRs of input genome should be performed, and - if IRs are present - which line type to be used for visualizing gene synteny between IRs; 0 = IR presence test but no synteny visualization, 1 = IR presence test and synteny visualization, with ribbon lines between IRs, 2 = IR presence test and synteny visualization, with solid lines between IRs, otherwise = neither IR presence test nor synteny visualization
`relative`	a boolean that specifies whether the threshold is a relative value of the average coverage instead of an absolute value
`textSize`	a numeric value that specifies the relative font size of the text element in the visualization
`tabularCovStats`	a boolean, that when TRUE, generates additional files with detailed genomic region information
`output`	a character string that specifies the name of, and path to, the output file

Value

A file in pdf format containing a circular visualization of the input plastid genome and its sequence reads. As a function, returns 0 in case of visualization success.

Examples

```
## Not run:
gbkFile <- system.file("extdata", "NC_045072/NC_045072.gb", package="PACVr")
bamFile <- system.file("extdata", "NC_045072/NC_045072_subsampled.bam", package="PACVr")
outFile <- paste(tempdir(), "/NC_045072__all_reads.pdf", sep="")
PACVr.complete(gbkFile=gbkFile, bamFile=bamFile, windowSize=250, logScale=FALSE,
               threshold=0.5, IRCheck=1, relative=TRUE, textSize=0.5,
               tabularCovStats=FALSE, output=outFile)

## End(Not run)
## Not run:
gbkFile <- system.file("extdata", "MG936619/MG936619.gb", package="PACVr")
bamFile <- system.file("extdata", "MG936619/MG936619_subsampled.bam", package="PACVr")
outFile <- paste(tempdir(), "/MG936619_CoverageViz.pdf", sep="")
PACVr.complete(gbkFile=gbkFile, bamFile=bamFile, windowSize=50, logScale=FALSE,
               threshold=0.5, IRCheck=NA, relative=TRUE, textSize=0.5,
               tabularCovStats=FALSE, output=outFile)

## End(Not run)
```

`RCircos.Env` *Export the custom environment 'RCircos.Env'*

Description

This function exports the custom environment 'RCircos.Env' used by **RCircos**.

Details

PACVr employs **RCircos** as its visualization engine. In its operation, **RCircos** defines a custom environment (called 'RCircos.Env') and reads/writes variables to this environment from various of its functions. In order to make this environment accessible to **RCircos** within **PACVr** and, simultaneously, fulfil the requirements of CRAN, this export command was created. For more information, please see the Stackoverflow post at `https://stackoverflow.com/questions/56875962/r-package-transferring-environment-from-imported-package`.

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