

Package ‘PACVr’

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Title Plastome Assembly Coverage Visualization

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Depends R (>= 3.3.0)

Imports RCircos (>= 1.2.0), optparse (>= 1.6.0), genbankr (>= 1.2.1),
BiocGenerics (>= 0.20.0), Biostrings (>= 2.48.0),
GenomicAlignments (>= 1.18.1), GenomicRanges, IRanges

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](https://doi.org/10.1186/s12859-020-3475-0)>.

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PACVr-package

Plastome Assembly Coverage Visualization in R

Description

PACVr 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.

Note**Input Requirements**

The input to **PACVr** consists of two input files that contain information on (a) genome sequence and structure, and (b) on coverage depth. Specifically, users must provide (a) a file in GenBank flat file format that complies with the GenBank record specifications (<https://www.ncbi.nlm.nih.gov/Sitemap/samplerecord.html>), and (b) a file in BAM format that complies with the specifications described in the Sequence Alignment/Map Format documentation (<https://samtools.github.io/hts-specs/SAMv1.pdf>) and is accompanied by an ancillary index file.

Data Requirements

The user-supplied GenBank flat file must contain a sequence record of a complete plastid genome. For effective visualizations, the sequence record should contain a sequence feature for each of the inverted repeat regions, whereby the regions should be named 'IRa' and 'IRb' or 'Inverted Repeat a' and 'Inverted Repeat b', respectively. For effective visualizations, the total sequence length of the complete genome should be between 50 kb and 250 kb.

Author(s)

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References

Gruenstaeudl, M. and Jenke, N. (2019). PACVr: Plastome Assembly Coverage Visualization in R. bioRxiv 697821; doi: <https://doi.org/10.1101/697821>

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

Description

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

Usage

```
PACVr.complete(
  gbk.file,
  bam.file,
  windowSize = 250,
  logScale = FALSE,
  threshold = 0.5,
  syntenyLineType = 1,
  relative = TRUE,
  textSize = 0.5,
  delete = TRUE,
  output = NA
)
```

Arguments

<code>gbk.file</code>	a character vector that specifies the name of, and path to, the GenBank input file
<code>bam.file</code>	a character vector that specifies the name of, and path to, the BAM input file
<code>windowSize</code>	a numeric value that specifies window size in which the coverage is calculated
<code>logScale</code>	a boolean that specifies if the coverage depth is to be log-transformed before visualizing it
<code>threshold</code>	a numeric value that specifies the threshold for plotting coverage depth bars in red as opposed to the default black
<code>syntenyLineType</code>	a numeric value of 1, 2 or 3 that specifies the line type for visualizing IR gene synteny; 1 = ribbon lines, 2 = solid lines, 3 = no line
<code>relative</code>	a boolean that specifies whether the threshold is a relative value of the average coverage instead of an absolute value
<code>textSize</code>	a numeric value that specifies the relative font size of the text element in the visualization
<code>delete</code>	the decision to delete temporary files upon program execution
<code>output</code>	a character vector that specifies the name of, and path to, the output file

Examples

```
## Not run:
gbkFile <- system.file("extdata",
  "NC_045072/NC_045072.gb",
  package="PACVr")
bamFile <- system.file("extdata",
  "NC_045072/NC_045072_PlastomeReadsOnly.sorted.bam",
  package="PACVr")
outFile <- paste(tempdir(), "/NC_045072__all_reads.pdf", sep="")
PACVr.complete(gbk.file=gbkFile, bam.file=bamFile, windowSize=250,
  threshold=0.5, syntenyLineType=1, relative=TRUE, textSize=0.5,
  delete=TRUE, 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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