Package 'PACVr'

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Title Plastome Assembly Coverage Visualization

Author Michael Gruenstaeudl [aut, cre],
Nils Jenke [ctb]

Maintainer Michael Gruenstaeudl <m.gruenstaeudl@fu-berlin.de>

Depends R (>= 3.3.0)

Imports RCircos (>= 1.2.0), optparse (>= 1.6.0), genbankr (>= 1.2.1),
BiocGenerics (>= 0.20.0)

SystemRequirements mosdepth

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 (2019) <doi:10.1101/697821>.

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OS_type unix

NeedsCompilation no

R topics documented:

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

Software Dependencies

For full functionality, **PACVr** requires the installation of mosdepth (https://github.com/brentp/mosdepth) on the system.

Input Requirements

The input to **PACVr** consists of two input files that contain information on genome sequence and structure as well as 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 that contains a sequence features for each of the inverted repeat regions. Specifically, the inverted repeat regions must be named 'IRa' and 'IRb', or 'Inverted Repeat a' and 'Inverted Repeat b'. Moreover, the total sequence length of the sequence record must be between 100kb and 200kb.

Author(s)

Michael Gruenstaeudl, Nils Jenke

Maintainer: Michael Gruenstaeudl <m.gruenstaeudl@fu-berlin.de>

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,
               mosdepthCmd = 'mosdepth',
               threshold = 25,
               delete = TRUE,
               output = NA)
```

Arguments

`gbk.file`	a character vector that specifies the name of, and path to, the GenBank input file
`bam.file`	a character vector 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
`mosdepthCmd`	a character vector that specifies the command to execute mosdepth on system
`threshold`	a numeric value that specifies the threshold for plotting coverage at different color
`delete`	the decision to delete temporary files upon program execution
`output`	a character vector that specifies the name of, and path to, the output file

Examples

```
gbkFile <- system.file("extdata", "MH161174/MH161174.gb", package="PACVr")
bamFile <- system.file("extdata", "MH161174/MH161174_PlastomeReadsOnly.sorted.bam",
                        package="PACVr")
outFile <- paste(tempdir(), "/MH161174_AssemblyCoverage_viz.pdf", sep="")

PACVr.complete(gbk.file=gbkFile, bam.file=bamFile, windowSize=250,
               mosdepthCmd='mosdepth', threshold=15, delete=TRUE,
               output=outFile)
```

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 pkgRCircos within pkgPACVr 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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