Using PACVr

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1 Introduction

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. This vignette provides examples of executing PACVr on an empirical dataset co-supplied with the R package: invokation from within the R interpreter via function `PACVr.complete()`, and invokation from the Unix command-line shell via script `PACVr_Rscript.R`.

2 Requirements

Prior to running PACVr, several dependencies have to be installed.

```
# Mosdepth (a general dependency)
system("conda install -y mosdepth")
# CRAN packages
if (!require("pacman"))
    install.packages("pacman")
pacman::p_load("RCircos", "optparse", install=TRUE)
# Bioconductor packages
if (!requireNamespace("BiocManager", quietly=TRUE))
    install.packages("BiocManager")
if (!requireNamespace("genbankr", quietly=TRUE))
    BiocManager::install("genbankr")
```

3 Executing PACVr via R interpreter

PACVr can be executed from within the R interpreter via function `PACVr.complete()`.

```
library(PACVr)
## Specify input files
gbkFile <- system.file("extdata", "MH161174/MH161174.gb", package="PACVr")
bamFile <- system.file("extdata", "MH161174/MH161174_PlastomeReadsOnly.sorted.bam",
                       package="PACVr")
## Specify output file
outFile <- paste(tempdir(), "/MH161174_AssemblyCoverage_viz.pdf", sep="")
## Run PACVr
PACVr.complete(gbk.file=gbkFile, bam.file=bamFile, windowSize=250,
               mosdepthCmd='mosdepth', threshold=15, delete=TRUE,
               output=outFile)
```

4 Executing PACVr via Unix shell

PACVr can also be executed from the Unix command-line shell via script `PACVr_Rscript.R`.

```
Rscript ./inst/extdata/PACVr_Rscript.R  \
    -k ./inst/extdata/MH161174.gb \
    -b ./inst/extdata/MH161174_PlastomeReadsOnly.sorted.bam \
    -o ./inst/extdata/MH899017_AssemblyCoverage_viz.pdf
```
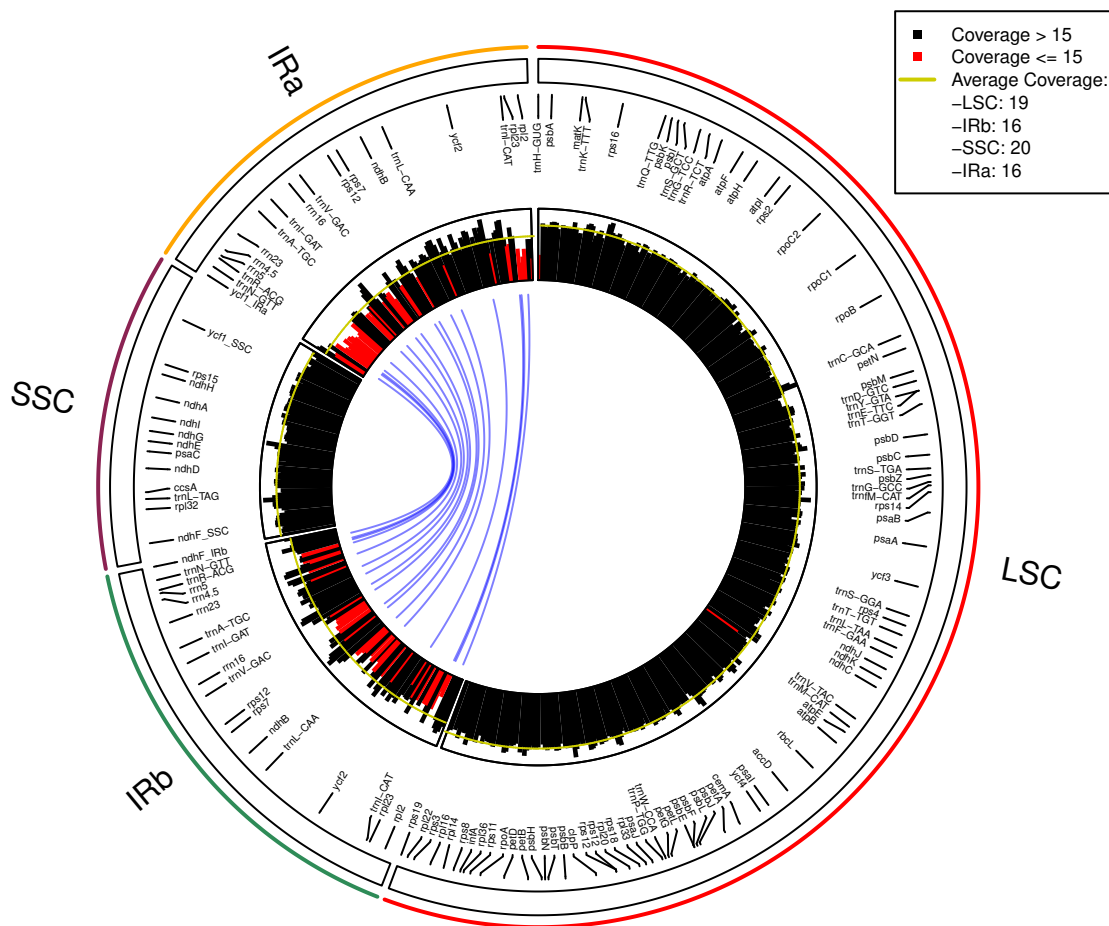
Figure 1: File `MH161174_AssemblyCoverage_viz.svg` as generated via `PACVr.complete()`

5 sessionInfo

```
> sessionInfo()
R version 3.3.3 (2017-03-06)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Debian GNU/Linux 9 (stretch)

locale:
 [1] LC_CTYPE=de_DE.UTF-8       LC_NUMERIC=C
 [3] LC_TIME=de_DE.UTF-8        LC_COLLATE=de_DE.UTF-8
 [5] LC_MONETARY=de_DE.UTF-8    LC_MESSAGES=de_DE.UTF-8
 [7] LC_PAPER=de_DE.UTF-8       LC_NAME=C
 [9] LC_ADDRESS=C               LC_TELEPHONE=C
[11] LC_MEASUREMENT=de_DE.UTF-8 LC_IDENTIFICATION=C

attached base packages:
[1] stats     graphics  grDevices utils     datasets
[6] methods   base

loaded via a namespace (and not attached):
[1] tools_3.3.3
```