

# SVbyEye: A visual approach to study genomic structural variation.

*David Porubsky*

2022-12-07

## **Abstract**

To be filled in.

## **Package**

SVbyEye 0.0.0.9000

## Contents

## 1 Introduction

---

SVbyEye relies on assembly to reference alignments produced by tools such as minimap2 (Li 2016) or other tools able to report alignments in a PAF format.

## 2 Functionalities

---

Here are the minimal parameters required to successfully run genome scaffolding using SaaRclust.

**Low-level functions:** List of function...

**High-level functions:** List of function...

For more details on available functions and their parameters, please run.

```
library(SVbyEye)
help(package="SVbyEye")
```

For more details on function specific parameters, please run.

```
library(SVbyEye)
?<function_name> (e.g. ?filterPaf)
```

## 3 Quick Start

---

To demonstrate the functionality of SVbyEye ...

```
## Load the SVbyEye package
library(SVbyEye)
```

Run the code below in order to create simple plot.

```
## Get PAF to plot
paf.file <- system.file("extdata", "test1.paf",
                        package="SVbyEye")

## Read in PAF
paf.table <- readPaf(paf.file = paf.file,
                   include.paf.tags = TRUE, restrict.paf.tags = 'cg')

## Make a plot
## Color by alignment directionality
plotMiro(paf.table = paf.table, color.by = 'direction')
```

## 4 Session Info

```
devtools::session_info()
## - Session info -----
## setting value
## version R version 4.2.1 (2022-06-23)
## os      Ubuntu 20.04.3 LTS
## system x86_64, linux-gnu
## ui      RStudio
## language (EN)
## collate en_US.UTF-8
## ctype   en_US.UTF-8
## tz      America/Los_Angeles
## date    2022-12-07
## rstudio 2022.07.2+576 Spotted Wakerobin (desktop)
## pandoc  2.19.2 @ /usr/lib/rstudio/bin/quarto/bin/tools/ (via rmarkdown)
##
## - Packages -----
## package      * version      date (UTC) lib source
## assertthat    0.2.1        2019-03-21 [1] CRAN (R 4.2.1)
## Biobase       2.58.0       2022-11-01 [1] Bioconductor
## BiocGenerics  0.44.0       2022-11-01 [1] Bioconductor
## BiocIO        1.8.0        2022-11-01 [1] Bioconductor
## BiocManager   1.30.19      2022-10-25 [1] CRAN (R 4.2.1)
## BiocParallel  1.32.1       2022-11-07 [1] Bioconductor
## BiocStyle     * 2.26.0      2022-11-01 [1] Bioconductor
## Biostrings    2.66.0       2022-11-01 [1] Bioconductor
## bitops        1.0-7        2021-04-24 [1] CRAN (R 4.2.1)
## bookdown      0.30         2022-11-09 [1] CRAN (R 4.2.1)
## BSgenome      1.66.1       2022-11-03 [1] Bioconductor
## cachem        1.0.6        2021-08-19 [1] CRAN (R 4.2.1)
## callr         3.7.3        2022-11-02 [1] CRAN (R 4.2.1)
## cli           3.4.1        2022-09-23 [1] CRAN (R 4.2.1)
## codetools     0.2-18       2020-11-04 [4] CRAN (R 4.0.3)
## colorspace    2.0-3        2022-02-21 [1] CRAN (R 4.2.1)
## crayon        1.5.2        2022-09-29 [1] CRAN (R 4.2.1)
## DBI           1.1.3        2022-06-18 [1] CRAN (R 4.2.1)
## DelayedArray  0.24.0       2022-11-01 [1] Bioconductor
## devtools      2.4.5        2022-10-11 [1] CRAN (R 4.2.1)
## digest        0.6.30       2022-10-18 [1] CRAN (R 4.2.1)
## dplyr         1.0.10       2022-09-01 [1] CRAN (R 4.2.1)
## ellipsis      0.3.2        2021-04-29 [1] CRAN (R 4.2.1)
## evaluate      0.18         2022-11-07 [1] CRAN (R 4.2.1)
## fansi         1.0.3        2022-03-24 [1] CRAN (R 4.2.1)
## farver        2.1.1        2022-07-06 [1] CRAN (R 4.2.1)
## fastmap       1.1.0        2021-01-25 [1] CRAN (R 4.2.1)
## fs            1.5.2        2021-12-08 [1] CRAN (R 4.2.1)
## generics      0.1.3        2022-07-05 [1] CRAN (R 4.2.1)
## GenomeInfoDb  1.34.3       2022-11-10 [1] Bioconductor
## GenomeInfoDbData 1.2.9       2022-11-21 [1] Bioconductor
```

## SVbyEye: A visual approach to study genomic structural variation.

```
## GenomicAlignments      1.34.0      2022-11-01 [1] Bioconductor
## GenomicRanges          1.50.1      2022-11-06 [1] Bioconductor
## ggfittext              0.9.1       2021-01-30 [1] CRAN (R 4.2.1)
## ggforce                0.4.1       2022-10-04 [1] CRAN (R 4.2.1)
## gggenes               0.4.1       2020-12-10 [1] CRAN (R 4.2.1)
## ggnewscale            0.4.8       2022-10-06 [1] CRAN (R 4.2.1)
## ggplot2               3.4.0       2022-11-04 [1] CRAN (R 4.2.1)
## glue                  1.6.2       2022-02-24 [1] CRAN (R 4.2.1)
## gtable                0.3.1       2022-09-01 [1] CRAN (R 4.2.1)
## htmltools             0.5.3       2022-07-18 [1] CRAN (R 4.2.1)
## htmlwidgets           1.5.4       2021-09-08 [1] CRAN (R 4.2.1)
## httpuv                1.6.6       2022-09-08 [1] CRAN (R 4.2.1)
## IRanges               2.32.0      2022-11-01 [1] Bioconductor
## knitr                 1.41        2022-11-18 [1] CRAN (R 4.2.1)
## later                 1.3.0       2021-08-18 [1] CRAN (R 4.2.1)
## lattice               0.20-45     2021-09-22 [4] CRAN (R 4.1.1)
## lifecycle             1.0.3       2022-10-07 [1] CRAN (R 4.2.1)
## magrittr              2.0.3       2022-03-30 [1] CRAN (R 4.2.1)
## MASS                  7.3-58.1    2022-08-03 [1] CRAN (R 4.2.1)
## Matrix               1.5-3       2022-11-11 [1] CRAN (R 4.2.1)
## MatrixGenerics        1.10.0      2022-11-01 [1] Bioconductor
## matrixStats           0.63.0      2022-11-18 [1] CRAN (R 4.2.1)
## memoise               2.0.1       2021-11-26 [1] CRAN (R 4.2.1)
## mime                  0.12        2021-09-28 [1] CRAN (R 4.2.1)
## miniUI                0.1.1.1     2018-05-18 [1] CRAN (R 4.2.1)
## munsell               0.5.0       2018-06-12 [1] CRAN (R 4.2.1)
## pillar                1.8.1       2022-08-19 [1] CRAN (R 4.2.1)
## pkgbuild              1.3.1       2021-12-20 [1] CRAN (R 4.2.1)
## pkgconfig             2.0.3       2019-09-22 [1] CRAN (R 4.2.1)
## pkgload               1.3.2       2022-11-16 [1] CRAN (R 4.2.1)
## polyclip             1.10-4      2022-10-20 [1] CRAN (R 4.2.1)
## prettyunits           1.1.1       2020-01-24 [1] CRAN (R 4.2.1)
## processx              3.8.0       2022-10-26 [1] CRAN (R 4.2.1)
## profvis              0.3.7       2020-11-02 [1] CRAN (R 4.2.1)
## promises              1.2.0.1     2021-02-11 [1] CRAN (R 4.2.1)
## ps                    1.7.2       2022-10-26 [1] CRAN (R 4.2.1)
## purrr                 0.3.5       2022-10-06 [1] CRAN (R 4.2.1)
## R6                    2.5.1       2021-08-19 [1] CRAN (R 4.2.1)
## Rcpp                  1.0.9       2022-07-08 [1] CRAN (R 4.2.1)
## RCurl                 1.98-1.9    2022-10-03 [1] CRAN (R 4.2.1)
## remotes               2.4.2       2021-11-30 [1] CRAN (R 4.2.1)
## restfulr              0.0.15      2022-06-16 [1] CRAN (R 4.2.1)
## rjson                 0.2.21      2022-01-09 [1] CRAN (R 4.2.1)
## rlang                 1.0.6       2022-09-24 [1] CRAN (R 4.2.1)
## rmarkdown             2.18        2022-11-09 [1] CRAN (R 4.2.1)
## Rsamtools             2.14.0      2022-11-01 [1] Bioconductor
## rstudioapi            0.14        2022-08-22 [1] CRAN (R 4.2.1)
## rtracklayer           1.58.0      2022-11-01 [1] Bioconductor
## S4Vectors             0.36.0      2022-11-01 [1] Bioconductor
## scales                1.2.1       2022-08-20 [1] CRAN (R 4.2.1)
## sessioninfo           1.2.2       2021-12-06 [1] CRAN (R 4.2.1)
```

## SVbyEye: A visual approach to study genomic structural variation.

```
## shiny                1.7.3      2022-10-25 [1] CRAN (R 4.2.1)
## stringi              1.7.8      2022-07-11 [1] CRAN (R 4.2.1)
## stringr              1.4.1      2022-08-20 [1] CRAN (R 4.2.1)
## SummarizedExperiment 1.28.0    2022-11-01 [1] Bioconductor
## SVbyEye              * 0.0.0.9000 2022-12-07 [1] local
## tibble               3.1.8      2022-07-22 [1] CRAN (R 4.2.1)
## tidyselect           1.2.0      2022-10-10 [1] CRAN (R 4.2.1)
## tinytex              0.42       2022-09-27 [1] CRAN (R 4.2.1)
## tweenr              2.0.2      2022-09-06 [1] CRAN (R 4.2.1)
## urlchecker           1.0.1      2021-11-30 [1] CRAN (R 4.2.1)
## usethis              2.1.6      2022-05-25 [1] CRAN (R 4.2.1)
## utf8                 1.2.2      2021-07-24 [1] CRAN (R 4.2.1)
## vctrs                0.5.1      2022-11-16 [1] CRAN (R 4.2.1)
## wesanderson          0.3.6      2018-04-20 [1] CRAN (R 4.2.1)
## withr                2.5.0      2022-03-03 [1] CRAN (R 4.2.1)
## xfun                 0.35       2022-11-16 [1] CRAN (R 4.2.1)
## XML                  3.99-0.12  2022-10-28 [1] CRAN (R 4.2.1)
## xtable               1.8-4      2019-04-21 [1] CRAN (R 4.2.1)
## XVector              0.38.0     2022-11-01 [1] Bioconductor
## yaml                 2.3.6      2022-10-18 [1] CRAN (R 4.2.1)
## zlibbioc             1.44.0     2022-11-01 [1] Bioconductor
##
## [1] /home/porubsky/R/x86_64-pc-linux-gnu-library/4.2
## [2] /usr/local/lib/R/site-library
## [3] /usr/lib/R/site-library
## [4] /usr/lib/R/library
##
## -----
```

Report any issues [here](#):

## References

- 10 Li, Heng. 2016. "Minimap and Miniasm: Fast Mapping and de Novo Assembly for Noisy Long Sequences." *Bioinformatics* 32 (14): 2103–10.