SVbyEye: A visual approach to study genomic structural variantion.

David Porubsky

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Abstract

To be filled in.

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.

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)
```

Quick Start

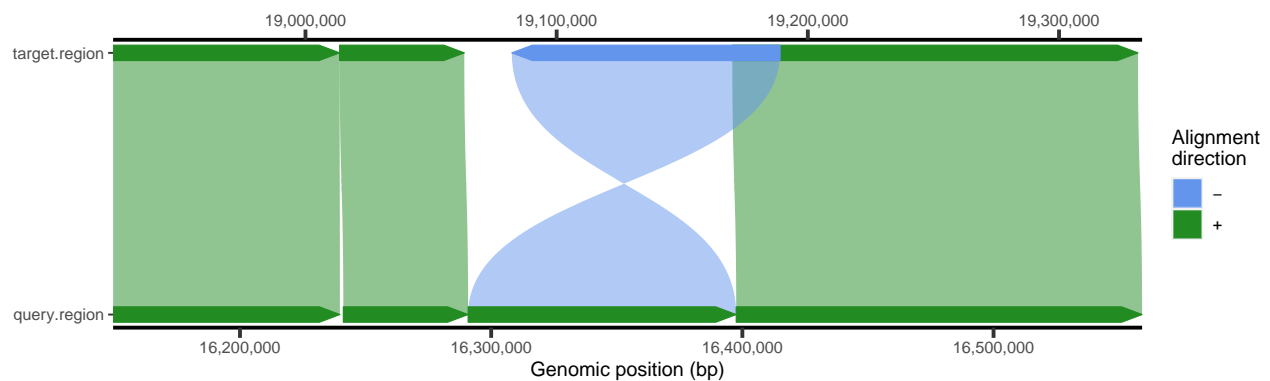To demonstrate the functionality of SVbyEye ...

```
## 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')
```

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       X11
##  language (EN)
##  collate  en_US.UTF-8
##  ctype    en_US.UTF-8
##  tz       America/Los_Angeles
##  date     2022-11-22
##  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
##  BiocParallel       1.32.1   2022-11-07 [1] Bioconductor
##  Biostrings         2.66.0   2022-11-01 [1] Bioconductor
##  bitops             1.0-7    2021-04-24 [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
##  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)
##   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   2022-11-22 [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)
##   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

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