

# CODECHECK certificate 2025-XYZ

<https://doi.org/10.5281/zenodo.FIXME>




| Item          | Value   |
|---------------|---|
| Title         | AbSolution Report v.0.71  |
| Authors       | García Rodrigo  |
| Reference     | None yet  |
| Codechecker   | Sam Langton                        |
| Date of check | 2025-01-29 12:00:00   |
| Summary       | RMarkdown file with embedded R code created from the AbSolution Shiny app for the purposes of reproducibility.        |
| Repository    | <a href="https://github.com/langtonhugh/absolution_codecheck">https://github.com/langtonhugh/absolution_codecheck</a> |

Table 1: CODECHECK summary

| Output                  | Comment             | Size (b) |
|-------------------------|---------------------|----------|
| screenshots/table1.png  | Screenshot Table 1  | 9749     |
| screenshots/figure1.png | Screenshot Figure 1 | 19642    |
| screenshots/figure2.png | Screenshot Figure 2 | 11448    |
| screenshots/figure3.png | Screenshot Figure 3 | 33635    |
| screenshots/figure4.png | Screenshot Figure 4 | 27092    |

Table 2: Summary of output files generated

## Summary

This code was straightforward to codecheck. As per the documentation, there was a `renv` lockfile located in the `0_SoftwareEnvironment` folder. I created an `.RProj` file in the root directory and copied over the lock file so that upon executing `renv::restore()` it would be easily recognised. I updated my R version to match

the lockfile too. The AbSolution package itself was installed from the pre-existing `0_SoftwareEnvironment` folder using `install.packages("0_SoftwareEnvironment/R/AbSolution_0.0.5.9550.tar", repos = NULL, type="source")`.

I could then knit the RMarkdown file and it executed with no errors first time. The tables and figures are printed directly in the HTML output. The figures are interactive. For the purposes of this codecheck, I made a screenshot of each one. The resulting HTML output file matches the given file as expected. I did not test the docker file as the outputs were reproduced on a Windows machine using `renv` so there was no need to delve into this.

## Recommendations

The project was straightforward to reproduce so there are no specific recommendations for improvement.

## Manifest files

table1.png

Comment: Screenshot Table 1

```
## [1] "Original sizes: "  
## [1] 382  
## [1] 12600  
## [1] "HealthyDonor__PBMC"  
## [1] "Filtering samples"  
## [1] 382  
## [1] 382  
## [1] "Big_summary for"  
## [1] 292  
## [1] 286  
## [1] "Filter passed by: "  
## [1] 191  
## [1] 286
```

figure1.png

Comment: Screenshot Figure 1

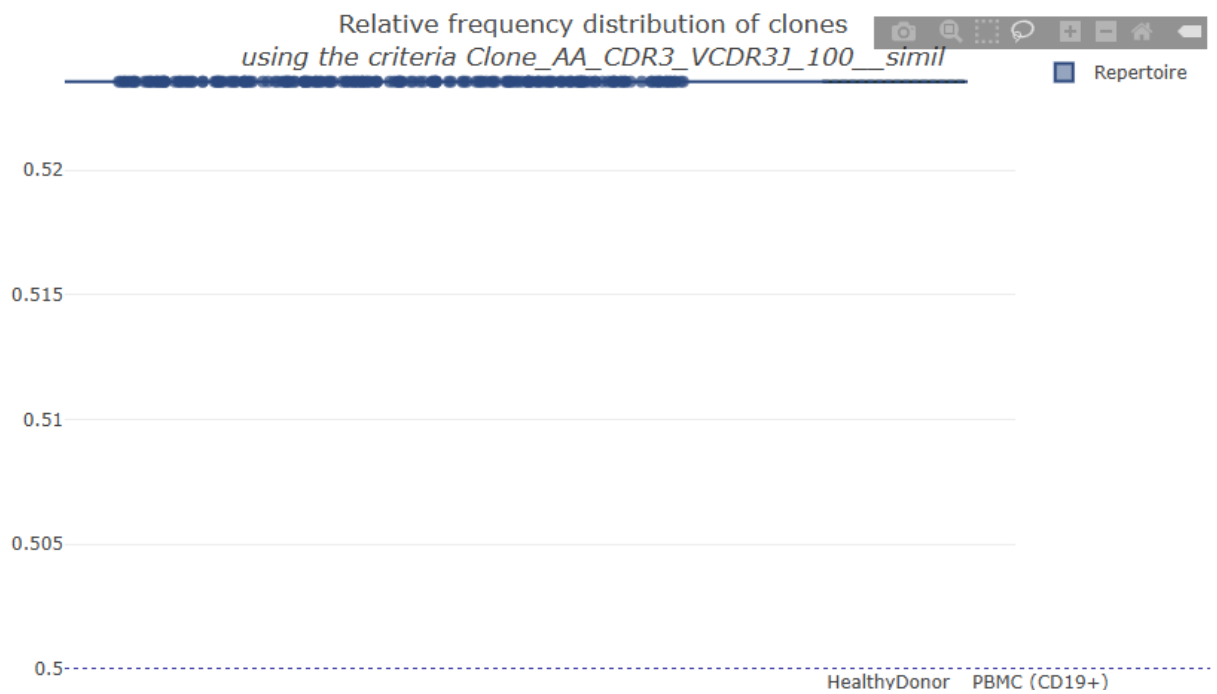


figure2.png

Comment: Screenshot Figure 2

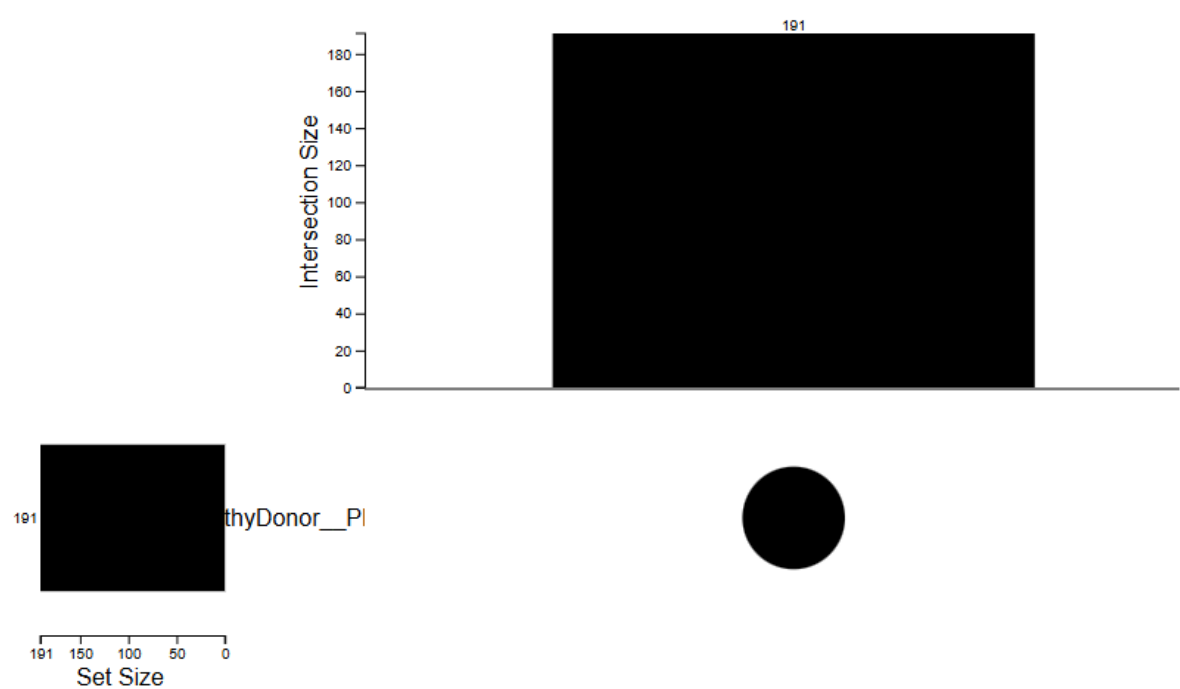


figure3.png

Comment: Screenshot Figure 3

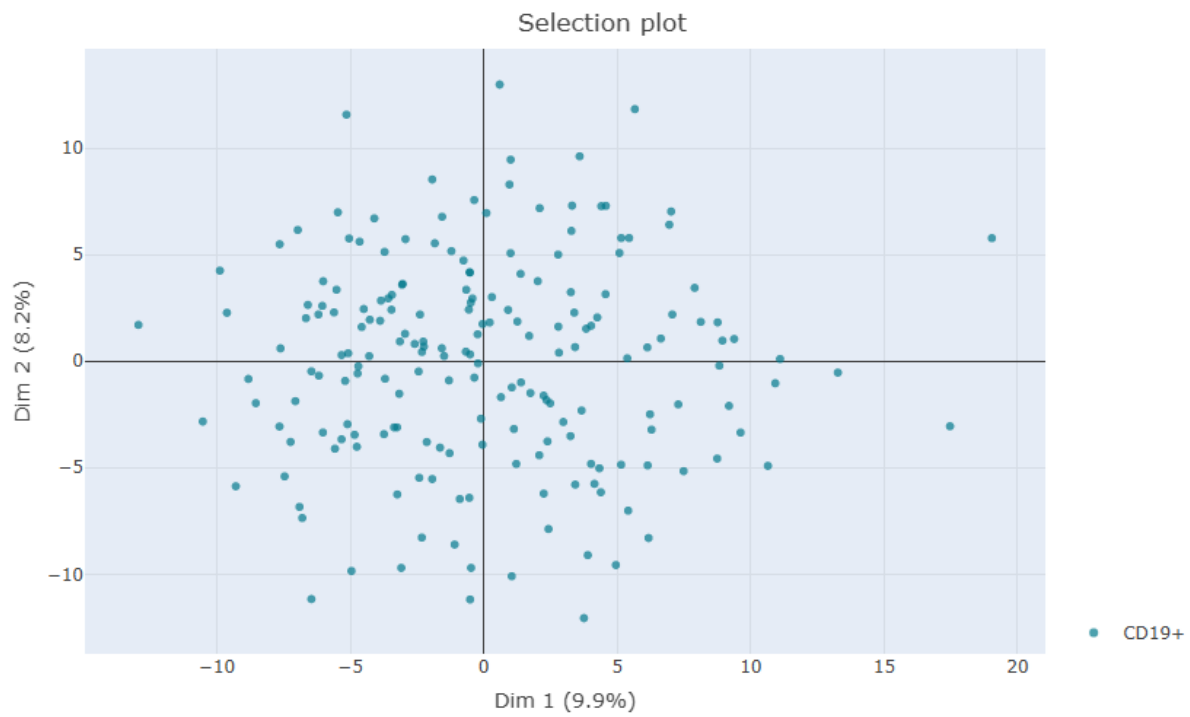
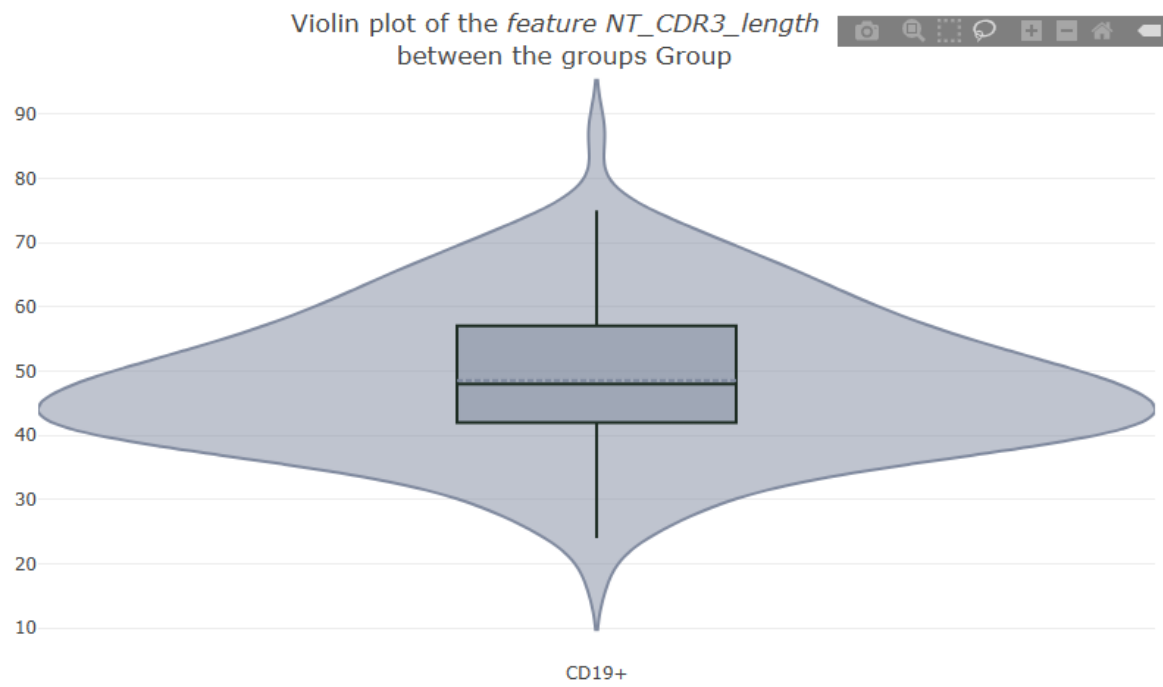


figure4.png

Comment: Screenshot Figure 4





## Citing this document

Sam Langton (2025). CODECHECK Certificate 2025-XYZ. Zenodo. <https://doi.org/10.5281/zenodo.FIXME>

## About CODECHECK

This certificate confirms that the codechecker could independently reproduce the results of a computational analysis given the data and code from a third party. A CODECHECK does not check whether the original computation analysis is correct. However, as all materials required for the reproduction are freely available by following the links in this document, the reader can then study for themselves the code and data.

## About this document

This document was created using R Markdown using the `codecheck` R package. `make codecheck.pdf` will regenerate the report file.

```
read.delim("sessionInfo.txt")
```

```
##                                R.version.4.3.1..2023.06.16.ucrt.
## 1                             Platform: x86_64-w64-mingw32/x64 (64-bit)
## 2                             Running under: Windows 11 x64 (build 22621)
## 3                             Matrix products: default
## 4                             locale:
## 5                             [1] LC_COLLATE=English_United States.utf8
## 6                             [2] LC_CTYPE=English_United States.utf8
## 7                             [3] LC_MONETARY=English_United States.utf8
## 8                             [4] LC_NUMERIC=C
## 9                             [5] LC_TIME=English_United States.utf8
## 10                            time zone: Europe/Amsterdam
## 11                            tzcode source: internal
## 12                            attached base packages:
## 13 [1] stats      graphics  grDevices utils      datasets  methods  base
## 14                            other attached packages:
## 15      [1] plotly_4.10.1      ggplot2_3.5.1      dplyr_1.1.2
## 16                        [4] shiny_1.7.4        AbSolution_0.0.5.9550
## 17                        loaded via a namespace (and not attached):
## 18          [1] shinythemes_1.2.0      later_1.3.1
## 19          [3] bitops_1.0-7           tibble_3.2.1
## 20          [5] Peptides_2.4.5         R.oo_1.25.0
## 21          [7] shinymanager_1.0.410   lifecycle_1.0.3
## 22          [9] shinyjs_0.4.1          doParallel_1.0.17
## 23         [11] rprojroot_2.0.3        lattice_0.20-45
## 24         [13] MASS_7.3-58.2          crosstalk_1.2.0
## 25         [15] magrittr_2.0.3         sass_0.4.6
## 26         [17] rmarkdown_2.21         jquerylib_0.1.4
## 27         [19] yaml_2.3.7             bigparallelr_0.3.2
## 28         [21] httpuv_1.6.11          askpass_1.1
## 29         [23] reticulate_1.34.0      cowplot_1.1.1
## 30         [25] DBI_1.2.3              RColorBrewer_1.1-3
```

|       |                              |                          |
|-------|------------------------------|--------------------------|
| ## 31 | [27] ade4_1.7-22             | golem_0.4.1              |
| ## 32 | [29] zlibbioc_1.46.0         | R.cache_0.16.0           |
| ## 33 | [31] GenomicRanges_1.52.0    | purrr_1.0.1              |
| ## 34 | [33] R.utils_2.12.2          | BiocGenerics_0.46.0      |
| ## 35 | [35] RCurl_1.98-1.12         | styler_1.10.0            |
| ## 36 | [37] bigassertr_0.1.6        | reactable_0.4.4          |
| ## 37 | [39] GenomeInfoDbData_1.2.10 | IRanges_2.34.0           |
| ## 38 | [41] S4Vectors_0.38.1        | umap_0.2.10.0            |
| ## 39 | [43] RSpectra_0.16-1         | parallelly_1.35.0        |
| ## 40 | [45] codetools_0.2-19        | DelayedArray_0.26.7      |
| ## 41 | [47] DT_0.28                 | bs4Dash_2.3.4            |
| ## 42 | [49] tidysselect_1.2.0       | bigstatsr_1.5.12         |
| ## 43 | [51] viridis_0.6.3           | shinyWidgets_0.7.6       |
| ## 44 | [53] matrixStats_1.2.0       | stats4_4.3.1             |
| ## 45 | [55] flock_0.7               | GenomicAlignments_1.36.0 |
| ## 46 | [57] jsonlite_1.8.4          | ellipsis_0.3.2           |
| ## 47 | [59] dashboardthemes_1.1.6   | iterators_1.0.14         |
| ## 48 | [61] foreach_1.5.2           | tools_4.3.1              |
| ## 49 | [63] progress_1.2.2          | stringdist_0.9.10        |
| ## 50 | [65] Rcpp_1.0.10             | glue_1.6.2               |
| ## 51 | [67] gridExtra_2.3           | xfun_0.46                |
| ## 52 | [69] MatrixGenerics_1.12.3   | GenomeInfoDb_1.36.0      |
| ## 53 | [71] withr_2.5.0             | formatR_1.14             |
| ## 54 | [73] fastmap_1.1.1           | sourcetools_0.1.7-1      |
| ## 55 | [75] fansi_1.0.4             | shinyjs_2.1.0            |
| ## 56 | [77] openssl_2.0.6           | digest_0.6.31            |
| ## 57 | [79] R6_2.5.1                | mime_0.12                |
| ## 58 | [81] colorspace_2.1-0        | RSQLite_2.3.1            |
| ## 59 | [83] diptest_0.76-0          | R.methodsS3_1.8.2        |
| ## 60 | [85] config_0.3.2            | utf8_1.2.3               |
| ## 61 | [87] tidyr_1.3.0             | generics_0.1.3           |
| ## 62 | [89] data.table_1.16.2       | iterors_1.0              |
| ## 63 | [91] prettyunits_1.1.1       | httr_1.4.6               |
| ## 64 | [93] htmlwidgets_1.6.2       | S4Arrays_1.0.4           |
| ## 65 | [95] pkgconfig_2.0.3         | gtable_0.3.3             |
| ## 66 | [97] blob_1.2.4              | shinymeta_0.2.0.3        |
| ## 67 | [99] XVector_0.40.0          | htmltools_0.5.5          |
| ## 68 | [101] scales_1.3.0           | fresh_0.2.0              |
| ## 69 | [103] Biobase_2.60.0         | sunburstR_2.1.8          |
| ## 70 | [105] png_0.1-8              | attempt_0.3.1            |
| ## 71 | [107] knitr_1.42             | rstudioapi_0.14          |
| ## 72 | [109] tzdb_0.4.0             | nlme_3.1-162             |
| ## 73 | [111] cachem_1.0.8           | stringr_1.5.0            |
| ## 74 | [113] KernSmooth_2.23-20     | parallel_4.3.1           |
| ## 75 | [115] shinycssloaders_1.0.0  | pillar_1.9.0             |
| ## 76 | [117] grid_4.3.1             | vctrs_0.6.5              |
| ## 77 | [119] shazam_1.2.0           | promises_1.2.0.1         |
| ## 78 | [121] shinyFiles_0.9.3       | airr_1.4.1               |
| ## 79 | [123] xtable_1.8-4           | billboarder_0.4.0        |
| ## 80 | [125] evaluate_0.21          | readr_2.1.4              |
| ## 81 | [127] cli_3.6.1              | compiler_4.3.1           |
| ## 82 | [129] Rsamtools_2.16.0       | rlang_1.1.1              |
| ## 83 | [131] crayon_1.5.2           | sortable_0.5.0           |
| ## 84 | [133] fs_1.6.2               | stringi_1.7.12           |

|       |                         |                             |
|-------|-------------------------|-----------------------------|
| ## 85 | [135] viridisLite_0.4.2 | BiocParallel_1.34.1         |
| ## 86 | [137] assertthat_0.2.1  | munsell_0.5.0               |
| ## 87 | [139] Biostrings_2.68.1 | lazyeval_0.2.2              |
| ## 88 | [141] upsetjs_1.11.1    | Matrix_1.6-5                |
| ## 89 | [143] benchmarkme_1.0.8 | scrypt_0.1.6                |
| ## 90 | [145] hms_1.1.3         | alakazam_1.3.0              |
| ## 91 | [147] bit64_4.0.5       | learnr_0.11.5               |
| ## 92 | [149] seqinr_4.2-30     | SummarizedExperiment_1.30.1 |
| ## 93 | [151] igraph_1.6.0      | memoise_2.0.1               |
| ## 94 | [153] bslib_0.4.2       | benchmarkmeData_1.0.4       |
| ## 95 | [155] bit_4.0.5         | ape_5.7-1                   |