

CODECHECK certificate 2025-020

<https://doi.org/10.5281/zenodo.16758977>



Item	Value
Title	AbSolution Report v.0.71
Authors	Rodrigo García Valiente
Reference	See 'report template' in Results folder
Codechecker	Sam Langton
Date of check	2025-01-29 14:00:00
Summary	RMarkdown file with embedded R code created from the AbSolution Shiny app for the purposes of reproducibility.
Repository	https://github.com/langtonhugh/absolution_codecheck

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 ENCORE¹ structure, 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`

¹<https://github.com/EDS-Bioinformatics-Laboratory/ENCORE>

```
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 for a codecheck.

Recommendations

The project was straightforward to reproduce so there are no specific recommendations for improvement. I'd be interested to know how the authors predict users will make use of the `renv` lock file in the absence of any instructions. The lock file in the pre-existing software environment folder is a `.prod` file extension (i.e., not `.lock`, which is the default for `renv`). For me, `renv` did not recognise the lock file until I changed the file extension to `.lock` and placed it in the root folder.

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

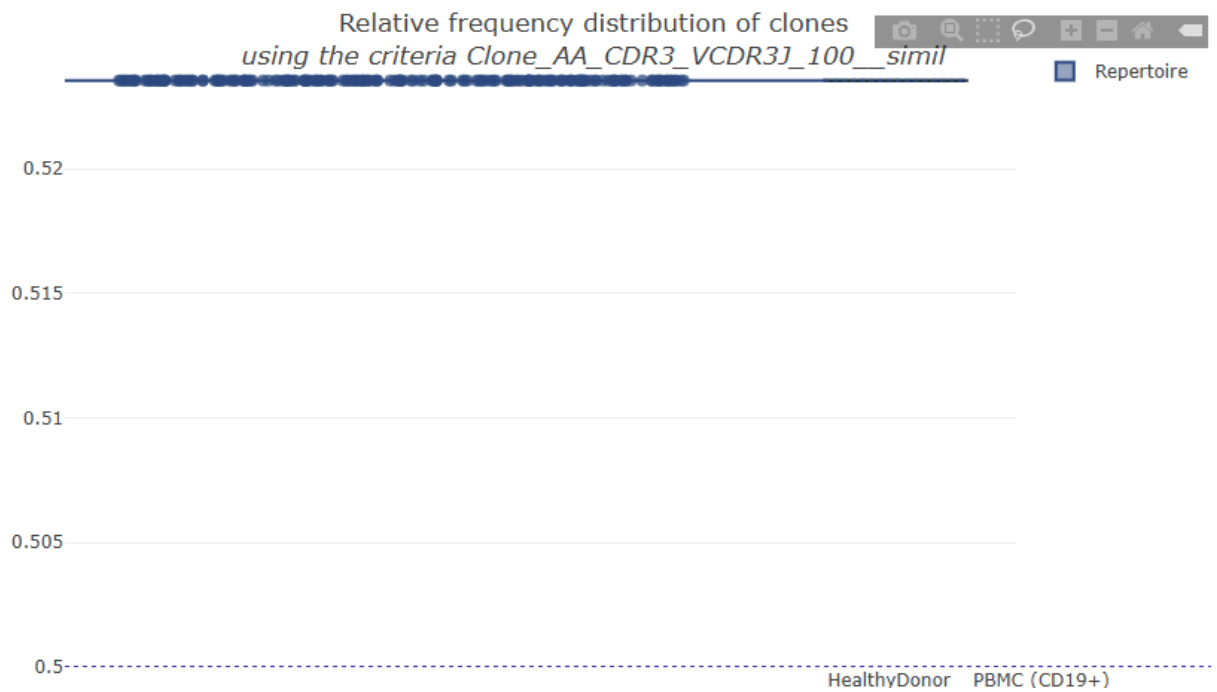


figure2.png

Comment: Screenshot Figure 2

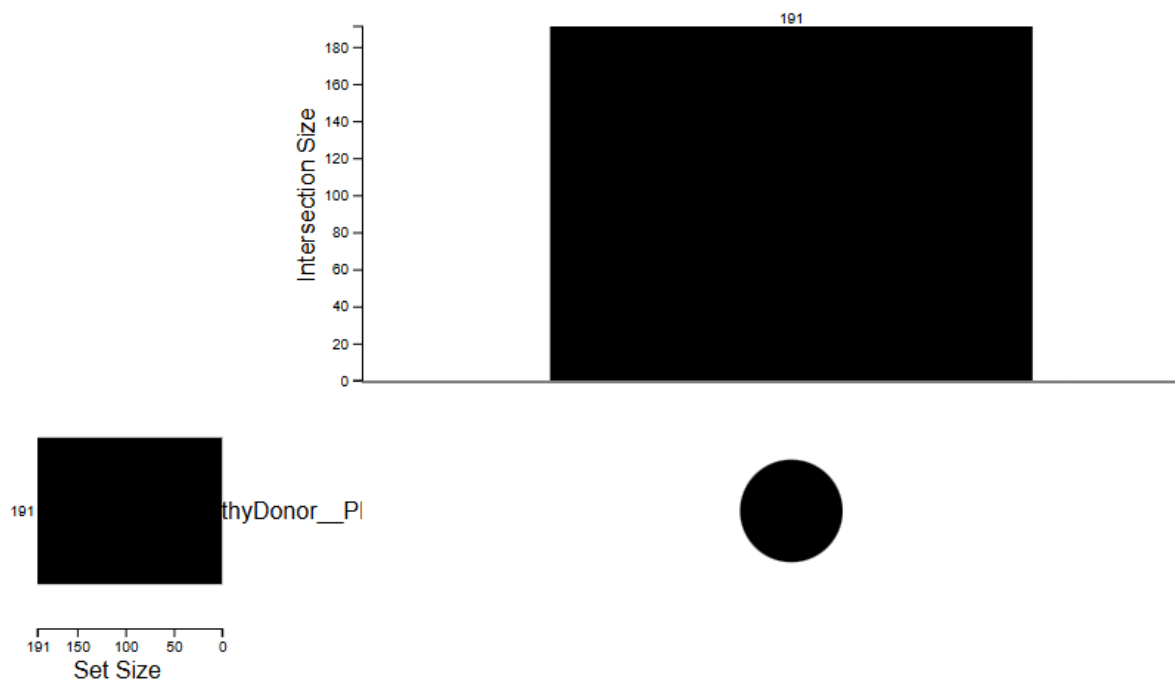


figure3.png

Comment: Screenshot Figure 3

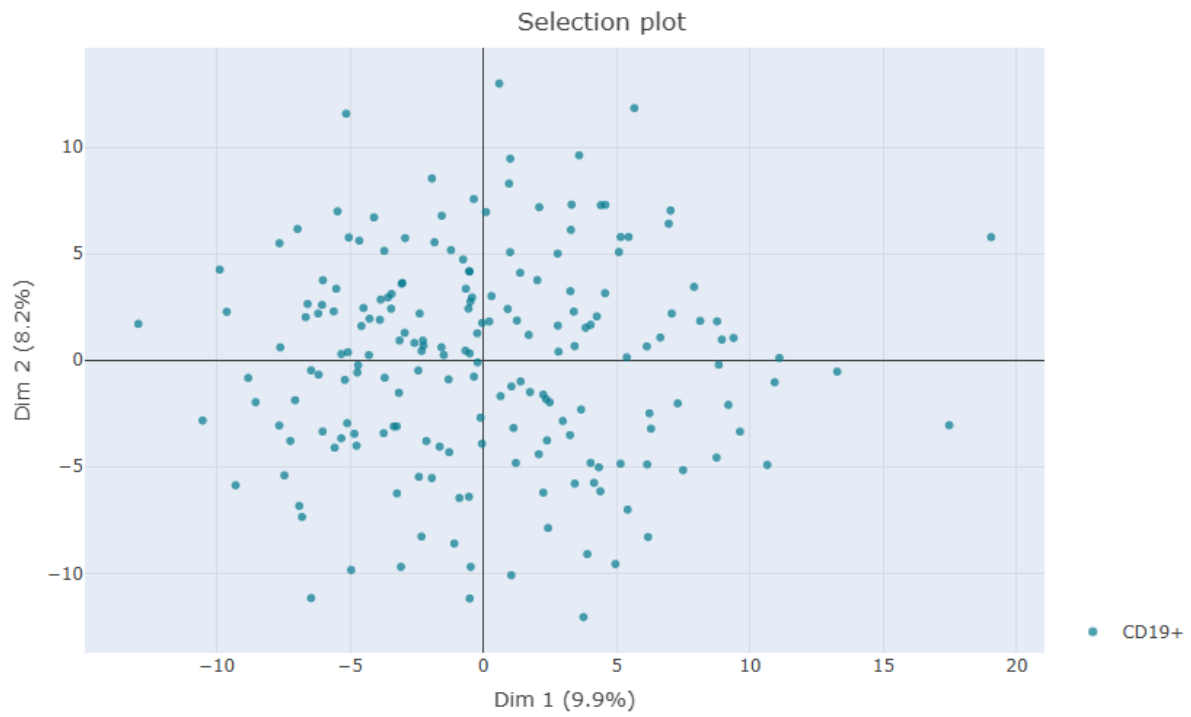
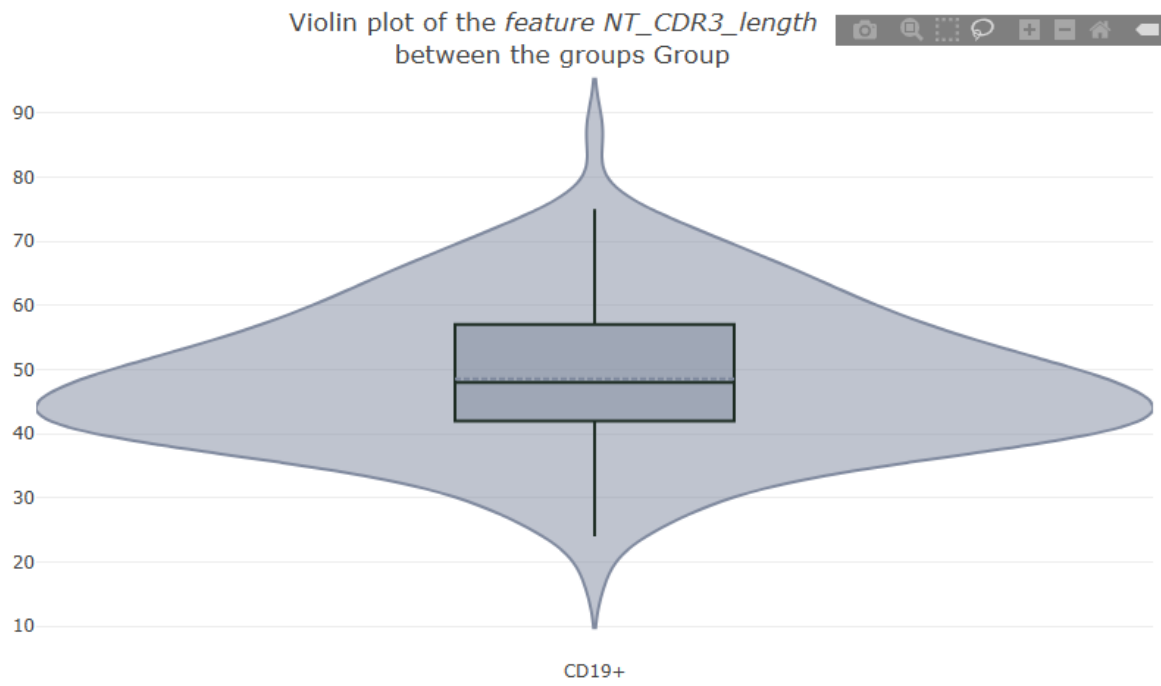


figure4.png

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.

Session info

The following session info was saved after successful completion of the codecheck.

```
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] shinyjqui_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] RSpecra_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] tidyselect_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	sorttable_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