

Debugging step: Verify installations

Antonia Chroni for SJCRH DNB_BINF_Core

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1 Set up

2 Session Info

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## R version 4.4.0 (2024-04-24)
## Platform: x86_64-pc-linux-gnu
## Running under: Ubuntu 22.04.4 LTS
##
## Matrix products: default
## BLAS:   /usr/lib/x86_64-linux-gnu/openblas-pthread/libblas.so.3
## LAPACK: /usr/lib/x86_64-linux-gnu/openblas-pthread/libopenblas-p0.3.20.so; LAPACK vers
##
## locale:
## [1] C
##
## time zone: Etc/UTC
## tzcode source: system (glibc)
##
## attached base packages:
## [1] grid      stats4    stats      graphics  grDevices  utils      datasets
## [8] methods   base
##
## other attached packages:
##  [1] gg dendro_0.2.0          DT_0.33
##  [3] shinyhelper_0.3.2       ShinyCell_2.1.0
##  [5] glue_1.8.0              gridExtra_2.3
##  [7] reticulate_1.40.0       yaml_2.3.10
##  [9] tinytex_0.54            lubridate_1.9.4
## [11] dplyr_1.1.4             readr_2.1.5
## [13] tidyr_1.3.1             tibble_3.2.1
## [15] tidyverse_2.0.0         tidytext_0.4.2
## [17] stringr_1.5.1           SoupX_1.6.2
## [19] Signac_1.14.9002        shiny_1.10.0
## [21] SeuratWrappers_0.2.0    SeuratObject_5.0.2
## [23] Seurat_4.4.0            R.utils_2.12.3
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## [25] R.oo_1.27.0                R.methodsS3_1.8.2
## [27] rlist_0.4.6.2              rliger_2.1.0
## [29] reshape2_1.4.4             RColorBrewer_1.1-3
## [31] purrr_1.0.2                patchwork_1.3.0
## [33] optparse_1.7.5             leiden_0.4.3.1
## [35] knitr_1.49                 irlba_2.3.5.1
## [37] Matrix_1.7-0               igraph_2.1.4
## [39] hdf5r_1.3.12              harmony_1.2.3
## [41] Rcpp_1.0.14                ggthemes_5.1.0
## [43] ggrepel_0.9.6              ggpmisc_0.6.1
## [45] ggpp_0.5.8-1              ggh4x_0.3.0
## [47] GGally_2.2.1              future_1.34.0
## [49] fs_1.6.5                  forcats_1.0.0
## [51] flextable_0.9.7           flexmix_2.3-19
## [53] lattice_0.22-6            data.table_1.16.4
## [55] cowplot_1.1.3             clustree_0.5.1
## [57] ggraph_2.2.1              RcppPlanc_1.0.0
## [59] scooter_0.0.0.9004         SingleR_2.8.0
## [61] scater_1.34.0             ggplot2_3.5.1
## [63] scuttle_1.16.0            SingleCellExperiment_1.28.1
## [65] SummarizedExperiment_1.36.0 Biobase_2.66.0
## [67] GenomicRanges_1.58.0      GenomeInfoDb_1.42.3
## [69] IRanges_2.40.1            S4Vectors_0.44.0
## [71] BiocGenerics_0.52.0       MatrixGenerics_1.18.1
## [73] matrixStats_1.5.0         miQC_1.14.0
## [75] remotes_2.5.0             devtools_2.4.5
## [77] usethis_3.1.0             BiocManager_1.30.25
##
## loaded via a namespace (and not attached):
## [1] bitops_1.0-9              spatstat.sparse_3.1-0
## [3] httr_1.4.7                ggsci_3.2.0
## [5] profvis_0.4.0             tools_4.4.0
## [7] sctransform_0.4.1         R6_2.5.1
## [9] lazyeval_0.2.2            uwot_0.2.2
## [11] urlchecker_1.0.1         withr_3.0.2
## [13] sp_2.2-0                  progressr_0.15.1
## [15] quantreg_6.00             cli_3.6.3
## [17] textshaping_1.0.0        spatstat.explore_3.3-4
## [19] officer_0.6.7            sass_0.4.9
## [21] spatstat.data_3.1-4       ggribes_0.5.6
## [23] pbapply_1.7-2             askpass_1.2.1
## [25] Rsamtools_2.22.0         systemfonts_1.2.1
## [27] parallelly_1.42.0        sessioninfo_1.2.2
## [29] generics_0.1.3           ica_1.0-3
## [31] spatstat.random_3.3-2     zip_2.3.2
## [33] ggbeeswarm_0.7.2         abind_1.4-8
## [35] lifecycle_1.0.4          SparseArray_1.6.1
## [37] Rtsne_0.17               promises_1.3.2
## [39] crayon_1.5.3             miniUI_0.1.1.1
## [41] beachmat_2.22.0          pillar_1.10.1
## [43] future.apply_1.11.3       codetools_0.2-20

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## [45] fastmatch_1.1-6	spatstat.univar_3.1-1
## [47] fontLiberation_0.1.0	vctrs_0.6.5
## [49] png_0.1-8	spam_2.11-1
## [51] gtable_0.3.6	cachem_1.1.0
## [53] xfun_0.50	S4Arrays_1.6.0
## [55] mime_0.12	tidygraph_1.3.1
## [57] survival_3.5-8	RcppRoll_0.3.1
## [59] ellipsis_0.3.2	fitdistrplus_1.2-2
## [61] ROCR_1.0-11	nlme_3.1-164
## [63] bit64_4.6.0-1	fontquiver_0.2.1
## [65] RcppAnnoy_0.0.22	SnowballC_0.7.1
## [67] bslib_0.9.0	vipor_0.4.7
## [69] KernSmooth_2.23-22	colorspace_2.1-1
## [71] nnet_7.3-19	tidyselect_1.2.1
## [73] bit_4.5.0.1	compiler_4.4.0
## [75] BiocNeighbors_2.0.1	SparseM_1.84-2
## [77] xml2_1.3.6	fontBitstreamVera_0.1.1
## [79] DelayedArray_0.32.0	plotly_4.10.4
## [81] scales_1.3.0	lmtest_0.9-40
## [83] rappdirs_0.3.3	digest_0.6.37
## [85] goftest_1.2-3	spatstat.utils_3.1-2
## [87] rmarkdown_2.29	XVector_0.46.0
## [89] htmltools_0.5.8.1	pkgconfig_2.0.3
## [91] sparseMatrixStats_1.18.0	fastmap_1.2.0
## [93] rlang_1.1.5	htmlwidgets_1.6.4
## [95] UCSC.utils_1.2.0	DelayedMatrixStats_1.28.1
## [97] farver_2.1.2	jquerylib_0.1.4
## [99] zoo_1.8-12	jsonlite_1.8.9
## [101] BiocParallel_1.40.0	tokenizers_0.3.0
## [103] BiocSingular_1.22.0	magrittr_2.0.3
## [105] polynom_1.4-1	modeltools_0.2-23
## [107] GenomeInfoDbData_1.2.13	dotCall64_1.2
## [109] munsell_0.5.1	viridis_0.6.5
## [111] gdtools_0.4.1	stringi_1.8.4
## [113] zlibbioc_1.52.0	MASS_7.3-60.2
## [115] plyr_1.8.9	pkgbuild_1.4.6
## [117] ggstats_0.8.0	parallel_4.4.0
## [119] listenv_0.9.1	deldir_2.0-4
## [121] Biostrings_2.74.1	graphlayouts_1.2.2
## [123] splines_4.4.0	tensor_1.5
## [125] hms_1.1.3	uuid_1.2-1
## [127] spatstat.geom_3.3-5	ScaledMatrix_1.14.0
## [129] pkgload_1.4.0	evaluate_1.0.3
## [131] tzdb_0.4.0	tweenr_2.0.3
## [133] httpuv_1.6.15	MatrixModels_0.5-3
## [135] getopt_1.20.4	RANN_2.6.2
## [137] openssl_2.3.2	polyclip_1.10-7
## [139] scattermore_1.2	ggforce_0.4.2
## [141] rsvd_1.0.5	xtable_1.8-4
## [143] janeaustenr_1.0.0	later_1.4.1
## [145] viridisLite_0.4.2	ragg_1.3.3

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## [147] memoise_2.0.1      beeswarm_0.4.0
## [149] cluster_2.1.6       timechange_0.3.0
## [151] globals_0.16.3
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