

Debugging step: Verify installations

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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-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] yaml_2.3.10          tinytex_0.54
##  [3] lubridate_1.9.4      dplyr_1.1.4
##  [5] readr_2.1.5          tidyr_1.3.1
##  [7] tibble_3.2.1         tidyverse_2.0.0
##  [9] tidytext_0.4.2       stringr_1.5.1
## [11] SoupX_1.6.2          Signac_1.14.9001
## [13] shiny_1.10.0         SeuratObject_5.0.2
## [15] Seurat_4.4.0         R.utils_2.12.3
## [17] R.oo_1.27.0          R.methodsS3_1.8.2
## [19] rlist_0.4.6.2        rliger_2.1.0
## [21] reshape2_1.4.4       RColorBrewer_1.1-3
## [23] purrr_1.0.2          patchwork_1.3.0
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## [25] optparse_1.7.5          leiden_0.4.3.1
## [27] knitr_1.49              irlba_2.3.5.1
## [29] igraph_2.1.2            hdf5r_1.3.11
## [31] harmony_1.2.3           Rcpp_1.0.13-1
## [33] ggthemes_5.1.0          ggrepel_0.9.6
## [35] ggpmisc_0.6.1           ggpp_0.5.8-1
## [37] ggh4x_0.3.0             GGally_2.2.1
## [39] future_1.34.0           fs_1.6.5
## [41] forcats_1.0.0           flextable_0.9.7
## [43] flexmix_2.3-19          lattice_0.22-6
## [45] data.table_1.16.4       cowplot_1.1.3
## [47] clustree_0.5.1          ggraph_2.2.1
## [49] numbat_1.4.2            Matrix_1.7-0
## [51] RcppPlanc_1.0.0         scooter_0.0.0.9004
## [53] infercnv_1.22.0         SingleR_2.8.0
## [55] celldex_1.16.0          scDblFinder_1.20.0
## [57] scater_1.34.0           ggplot2_3.5.1
## [59] scuttle_1.16.0          SingleCellExperiment_1.28.1
## [61] SummarizedExperiment_1.36.0 Biobase_2.66.0
## [63] GenomicRanges_1.58.0    GenomeInfoDb_1.42.1
## [65] IRanges_2.40.1          S4Vectors_0.44.0
## [67] BiocGenerics_0.52.0     MatrixGenerics_1.18.0
## [69] matrixStats_1.4.1       miQC_1.14.0
## [71] remotes_2.5.0           devtools_2.4.5
## [73] usethis_3.1.0           BiocManager_1.30.25
##
## loaded via a namespace (and not attached):
## [1] ica_1.0-3                plotly_4.10.4
## [3] zlibbioc_1.52.0          tidysselect_1.2.1
## [5] bit_4.5.0.1              doParallel_1.0.17
## [7] rjson_0.2.23             blob_1.2.4
## [9] urlchecker_1.0.1         S4Arrays_1.6.0
## [11] parallel_4.4.0           png_0.1-8
## [13] cli_3.6.3                ggplotify_0.1.2
## [15] askpass_1.2.1            openssl_2.3.0
## [17] goftest_1.2-3            textshaping_0.4.1
## [19] BiocIO_1.16.0            bluster_1.16.0
## [21] officer_0.6.7            tokenizers_0.3.0
## [23] BiocNeighbors_2.0.1      uwot_0.2.2
## [25] curl_6.0.1              mime_0.12
## [27] evaluate_1.0.1           tidytree_0.4.6
## [29] coin_1.4-3               stringi_1.8.4
## [31] rjags_4-16               parallelDist_0.2.6
## [33] XML_3.99-0.18            httpuv_1.6.15
## [35] AnnotationDbi_1.68.0     magrittr_2.0.3
## [37] rappdirs_0.3.3           splines_4.4.0
## [39] RcppRoll_0.3.1           getopt_1.20.4
## [41] logger_0.4.0            sctransform_0.4.1
## [43] ggbeeswarm_0.7.2         sessioninfo_1.2.2
## [45] DBI_1.2.3                HDF5Array_1.34.0
## [47] jquerylib_0.1.4          withr_3.0.2

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## [49] systemfonts_1.1.0	xgboost_1.7.8.1
## [51] lmtest_0.9-40	tidygraph_1.3.1
## [53] formatR_1.14	rtracklayer_1.66.0
## [55] htmlwidgets_1.6.4	SparseArray_1.6.0
## [57] reticulate_1.40.0	zoo_1.8-12
## [59] XVector_0.46.0	hahmmr_1.0.0
## [61] UCSC.utils_1.2.0	RhpcBLASctl_0.23-42
## [63] timechange_0.3.0	foreach_1.5.2
## [65] caTools_1.18.3	ggtree_3.10.1
## [67] rhdf5_2.50.1	quantreg_5.99.1
## [69] janeaustenr_1.0.0	alabaster.schemas_1.6.0
## [71] gridGraphics_0.5-1	ellipsis_0.3.2
## [73] lazyeval_0.2.2	phyclust_0.1-34
## [75] survival_3.5-8	scattermore_1.2
## [77] BiocVersion_3.20.0	crayon_1.5.3
## [79] RcppAnnoy_0.0.22	progressr_0.15.1
## [81] tweenr_2.0.3	scistreer_1.2.0
## [83] later_1.4.1	ggridges_0.5.6
## [85] codetools_0.2-20	profvis_0.4.0
## [87] KEGGREST_1.46.0	Rtsne_0.17
## [89] limma_3.62.1	gdtools_0.4.1
## [91] Rsamtools_2.22.0	filelock_1.0.3
## [93] pkgconfig_2.0.3	xml2_1.3.6
## [95] spatstat.univar_3.1-1	GenomicAlignments_1.42.0
## [97] aplot_0.2.4	spatstat.sparse_3.1-0
## [99] alabaster.base_1.6.1	ape_5.8-1
## [101] viridisLite_0.4.2	xtable_1.8-4
## [103] fastcluster_1.2.6	plyr_1.8.9
## [105] httr_1.4.7	tools_4.4.0
## [107] globals_0.16.3	pkgbuild_1.4.5
## [109] beeswarm_0.4.0	nlme_3.1-164
## [111] futile.logger_1.4.3	lambda.r_1.2.4
## [113] dbplyr_2.5.0	ExperimentHub_2.14.0
## [115] MatrixModels_0.5-3	digest_0.6.37
## [117] farver_2.1.2	tzdb_0.4.0
## [119] SnowballC_0.7.1	yulab.utils_0.1.8
## [121] viridis_0.6.5	glue_1.8.0
## [123] cachem_1.1.0	BiocFileCache_2.14.0
## [125] polyclip_1.10-7	generics_0.1.3
## [127] Biostrings_2.74.1	mvtnorm_1.3-2
## [129] parallelly_1.41.0	pkgload_1.4.0
## [131] statmod_1.5.0	ragg_1.3.3
## [133] ScaledMatrix_1.14.0	fontBitstreamVera_0.1.1
## [135] pbapply_1.7-2	httr2_1.0.7
## [137] spam_2.11-0	dqrng_0.4.1
## [139] graphlayouts_1.2.1	gtools_3.9.5
## [141] alabaster.se_1.6.0	gridExtra_2.3
## [143] GenomeInfoDbData_1.2.13	rhdf5filters_1.18.0
## [145] RCurl_1.98-1.16	memoise_2.0.1
## [147] rmarkdown_2.29	scales_1.3.0
## [149] gypsum_1.2.0	RANN_2.6.2

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## [151] fontLiberation_0.1.0      spatstat.data_3.1-4
## [153] cluster_2.1.6            spatstat.utils_3.1-1
## [155] hms_1.1.3                fitdistrplus_1.2-1
## [157] munsell_0.5.1            colorspace_2.1-1
## [159] rlang_1.1.4              quadprog_1.5-8
## [161] DelayedMatrixStats_1.28.0 sparseMatrixStats_1.18.0
## [163] dotCall64_1.2            ggforce_0.4.2
## [165] xfun_0.49                alabaster.matrix_1.6.1
## [167] coda_0.19-4.1            TH.data_1.1-2
## [169] iterators_1.0.14         modeltools_0.2-23
## [171] abind_1.4-8              libcoin_1.0-10
## [173] treeio_1.26.0            ggsci_3.2.0
## [175] Rhdf5lib_1.28.0          futile.options_1.0.1
## [177] bitops_1.0-9             promises_1.3.2
## [179] RSQLite_2.3.9            sandwich_3.1-1
## [181] DelayedArray_0.32.0      compiler_4.4.0
## [183] alabaster.ranges_1.6.0   beachmat_2.22.0
## [185] SparseM_1.84-2           polynom_1.4-1
## [187] listenv_0.9.1            fontquiver_0.2.1
## [189] edgeR_4.4.1              AnnotationHub_3.14.0
## [191] BiocSingular_1.22.0      tensor_1.5
## [193] MASS_7.3-60.2            uuid_1.2-1
## [195] BiocParallel_1.40.0      spatstat.random_3.3-2
## [197] R6_2.5.1                 fastmap_1.2.0
## [199] multcomp_1.4-26          fastmatch_1.1-6
## [201] vipor_0.4.7              ROCR_1.0-11
## [203] ggstats_0.7.0            rsvd_1.0.5
## [205] nnet_7.3-19              gtable_0.3.6
## [207] phangorn_2.12.1          KernSmooth_2.23-22
## [209] miniUI_0.1.1.1           deldir_2.0-4
## [211] htmltools_0.5.8.1        RcppParallel_5.1.9
## [213] bit64_4.5.2              spatstat.explore_3.3-3
## [215] lifecycle_1.0.4          zip_2.3.1
## [217] restfulr_0.0.15          sass_0.4.9
## [219] vctrs_0.6.5              spatstat.geom_3.3-4
## [221] scan_1.34.0              ggfun_0.1.8
## [223] sp_2.1-4                 future.apply_1.11.3
## [225] bslib_0.8.0              pillar_1.10.0
## [227] gplots_3.2.0             metapod_1.14.0
## [229] locfit_1.5-9.10          jsonlite_1.8.9
## [231] argparse_2.2.5

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