

Debugging step: Verify installations

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1 Set up

2 Session Info

```
## 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_2.1.0.9004
## [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] igraph_2.1.4         hdf5r_1.3.12
## [39] harmony_1.2.3        Rcpp_1.0.14
## [41] ggthemes_5.1.0       ggrepel_0.9.6
## [43] ggpmisc_0.6.1        ggpp_0.5.8-1
## [45] ggh4x_0.3.0          GGally_2.2.1
## [47] future_1.34.0        fs_1.6.5
## [49] forcats_1.0.0        flextable_0.9.7
## [51] flexmix_2.3-19       lattice_0.22-6
## [53] data.table_1.16.4    cowplot_1.1.3
## [55] clustree_0.5.1       ggraph_2.2.1
## [57] numbat_1.4.2         Matrix_1.7-2
## [59] RcppPlanc_1.0.0      scooter_0.0.0.9004
## [61] infercnv_1.22.0      SingleR_2.8.0
## [63] celldex_1.16.0       scDblFinder_1.20.0
## [65] scater_1.34.0        ggplot2_3.5.1
## [67] scuttle_1.16.0       SingleCellExperiment_1.28.1
## [69] SummarizedExperiment_1.36.0 Biobase_2.66.0
## [71] GenomicRanges_1.58.0 GenomeInfoDb_1.42.3
## [73] IRanges_2.40.1       S4Vectors_0.44.0
## [75] BiocGenerics_0.52.0  MatrixGenerics_1.18.1
## [77] matrixStats_1.5.0    miQC_1.14.0
## [79] remotes_2.5.0        devtools_2.4.5
## [81] 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      tidyselect_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_2.3.2
## [17] goftest_1.2-3        textshaping_1.0.0
## [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_6.2.0           mime_0.12
## [27] evaluate_1.0.3       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

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|----------|--------------------------|-------------------------|
| ## [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 |
| ## [49] | systemfonts_1.2.1 | 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_1.6.1 |
| ## [57] | zoo_1.8-12 | XVector_0.46.0 |
| ## [59] | hahmmr_1.0.0 | UCSC.utils_1.2.0 |
| ## [61] | RhpcBLASctl_0.23-42 | timechange_0.3.0 |
| ## [63] | foreach_1.5.2 | caTools_1.18.3 |
| ## [65] | ggtree_3.15.0 | rhdf5_2.50.2 |
| ## [67] | quantreg_6.00 | janeaustrer_1.0.0 |
| ## [69] | alabaster.schemas_1.6.0 | gridGraphics_0.5-1 |
| ## [71] | ellipsis_0.3.2 | lazyeval_0.2.2 |
| ## [73] | phyclust_0.1-34 | survival_3.8-3 |
| ## [75] | scattermore_1.2 | BiocVersion_3.20.0 |
| ## [77] | crayon_1.5.3 | RcppAnnoy_0.0.22 |
| ## [79] | progressr_0.15.1 | tweenr_2.0.3 |
| ## [81] | scistree_1.2.0 | later_1.4.1 |
| ## [83] | ggridges_0.5.6 | codetools_0.2-20 |
| ## [85] | profvis_0.4.0 | KEGGREST_1.46.0 |
| ## [87] | Rtsne_0.17 | limma_3.62.2 |
| ## [89] | gdtools_0.4.1 | Rsamtools_2.22.0 |
| ## [91] | filelock_1.0.3 | pkgconfig_2.0.3 |
| ## [93] | xml2_1.3.6 | spatstat.univar_3.1-1 |
| ## [95] | GenomicAlignments_1.42.0 | aplot_0.2.4 |
| ## [97] | spatstat.sparse_3.1-0 | alabaster.base_1.6.1 |
| ## [99] | ape_5.8-1 | viridisLite_0.4.2 |
| ## [101] | xtable_1.8-4 | fastcluster_1.2.6 |
| ## [103] | plyr_1.8.9 | httr_1.4.7 |
| ## [105] | tools_4.4.0 | globals_0.16.3 |
| ## [107] | pkgbuild_1.4.6 | beeswarm_0.4.0 |
| ## [109] | nlme_3.1-167 | futile.logger_1.4.3 |
| ## [111] | lambda.r_1.2.4 | dbplyr_2.5.0 |
| ## [113] | ExperimentHub_2.14.0 | MatrixModels_0.5-3 |
| ## [115] | digest_0.6.37 | farver_2.1.2 |
| ## [117] | tzdb_0.4.0 | SnowballC_0.7.1 |
| ## [119] | yulab.utils_0.2.0 | viridis_0.6.5 |
| ## [121] | cachem_1.1.0 | BiocFileCache_2.14.0 |
| ## [123] | polyclip_1.10-7 | generics_0.1.3 |
| ## [125] | Biostrings_2.74.1 | mvtnorm_1.3-3 |
| ## [127] | parallelly_1.42.0 | pkgload_1.4.0 |
| ## [129] | statmod_1.5.0 | ragg_1.3.3 |
| ## [131] | ScaledMatrix_1.14.0 | fontBitstreamVera_0.1.1 |
| ## [133] | pbapply_1.7-2 | httr2_1.1.0 |
| ## [135] | spam_2.11-1 | dqrng_0.4.1 |
| ## [137] | graphlayouts_1.2.2 | gtools_3.9.5 |
| ## [139] | alabaster.se_1.6.0 | GenomeInfoDbData_1.2.13 |
| ## [141] | rhdf5filters_1.18.0 | RCurl_1.98-1.16 |

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| ## [143] memoise_2.0.1 | rmarkdown_2.29 |
| ## [145] scales_1.3.0 | gypsum_1.2.0 |
| ## [147] RANN_2.6.2 | fontLiberation_0.1.0 |
| ## [149] spatstat.data_3.1-4 | cluster_2.1.8 |
| ## [151] spatstat.utils_3.1-2 | hms_1.1.3 |
| ## [153] fitdistrplus_1.2-2 | munsell_0.5.1 |
| ## [155] colorspace_2.1-1 | rlang_1.1.5 |
| ## [157] quadprog_1.5-8 | DelayedMatrixStats_1.28.1 |
| ## [159] sparseMatrixStats_1.18.0 | dotCall64_1.2 |
| ## [161] ggforce_0.4.2 | xfun_0.50 |
| ## [163] alabaster.matrix_1.6.1 | coda_0.19-4.1 |
| ## [165] TH.data_1.1-3 | iterators_1.0.14 |
| ## [167] modeltools_0.2-23 | abind_1.4-8 |
| ## [169] libcoin_1.0-10 | treeio_1.30.0 |
| ## [171] ggsci_3.2.0 | Rhdf5lib_1.28.0 |
| ## [173] futile.options_1.0.1 | bitops_1.0-9 |
| ## [175] promises_1.3.2 | RSQLite_2.3.9 |
| ## [177] sandwich_3.1-1 | DelayedArray_0.32.0 |
| ## [179] compiler_4.4.0 | alabaster.ranges_1.6.0 |
| ## [181] beachmat_2.22.0 | SparseM_1.84-2 |
| ## [183] polynom_1.4-1 | listenv_0.9.1 |
| ## [185] fontquiver_0.2.1 | edgeR_4.4.2 |
| ## [187] AnnotationHub_3.14.0 | BiocSingular_1.22.0 |
| ## [189] tensor_1.5 | MASS_7.3-64 |
| ## [191] uuid_1.2-1 | BiocParallel_1.40.0 |
| ## [193] spatstat.random_3.3-2 | R6_2.5.1 |
| ## [195] fastmap_1.2.0 | multcomp_1.4-28 |
| ## [197] fastmatch_1.1-6 | vipor_0.4.7 |
| ## [199] ROCR_1.0-11 | ggstats_0.8.0 |
| ## [201] rsvd_1.0.5 | nnet_7.3-20 |
| ## [203] gtable_0.3.6 | phangorn_2.12.1 |
| ## [205] KernSmooth_2.23-26 | miniUI_0.1.1.1 |
| ## [207] deldir_2.0-4 | htmltools_0.5.8.1 |
| ## [209] RcppParallel_5.1.10 | bit64_4.6.0-1 |
| ## [211] spatstat.explore_3.3-4 | lifecycle_1.0.4 |
| ## [213] zip_2.3.2 | restfulr_0.0.15 |
| ## [215] sass_0.4.9 | vctrs_0.6.5 |
| ## [217] spatstat.geom_3.3-5 | scraper_1.34.0 |
| ## [219] ggfun_0.1.8 | sp_2.2-0 |
| ## [221] future.apply_1.11.3 | bslib_0.9.0 |
| ## [223] pillar_1.10.1 | gplots_3.2.0 |
| ## [225] metapod_1.14.0 | locfit_1.5-9.11 |
| ## [227] jsonlite_1.8.9 | argparse_2.2.5 |