Debugging step: Verify installations

Antonia Chroni for SJCRH DNB_BINF_Core

Contents

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/libopenblasp-r0.3.20.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] motifmatchr_1.28.0              enrichplot_1.26.6
##   [3] RcppPlanc_2.0.13               rliger_2.2.1
##   [5] flextable_0.9.10               clusterProfiler_4.14.6
##   [7] biovizBase_1.54.0             cicero_1.3.9
##   [9] Gviz_1.46.1                   monocle3_1.4.26
##  [11] BSgenome.Hsapiens.UCSC.hg19_1.4.3  BSgenome.Mmusculus.UCSC.mm10_1.4.3
##  [13] BSgenome_1.74.0               BiocIO_1.16.0
##  [15] Biostrings_2.74.1             XVector_0.46.0
##  [17] TFBSTools_1.44.0              JASPAR2020_0.99.10
##  [19] org.Mm.eg.db_3.20.0          org.Hs.eg.db_3.20.0
##  [21] htmlwidgets_1.6.4            rtracklayer_1.66.0
##  [23] ensembldb_2.30.0             AnnotationFilter_1.30.0
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##   [25] GenomicFeatures_1.58.0           AnnotationDbi_1.68.0
##   [27] AnnotationHub_3.14.0             BiocFileCache_2.14.0
##   [29] dbplyr_2.5.0                     ggdendro_0.2.0
##   [31] DT_0.34.0                        shinyhelper_0.3.2
##   [33] ShinyCell_2.1.0                  glue_1.8.0
##   [35] gridExtra_2.3                    reticulate_1.37.0
##   [37] yaml_2.3.10                      tinytex_0.57
##   [39] lubridate_1.9.4                  dplyr_1.1.4
##   [41] readr_2.1.5                      tidyr_1.3.1
##   [43] tibble_3.3.0                     tidyverse_2.0.0
##   [45] tidytext_0.4.3                   stringr_1.5.2
##   [47] SoupX_1.6.2                      Signac_1.15.9002
##   [49] shiny_1.11.1                     SeuratWrappers_0.2.0
##   [51] SeuratObject_5.2.0              Seurat_4.4.0
##   [53] R.utils_2.13.0                   R.oo_1.26.0
##   [55] R.methodsS3_1.8.2               rlist_0.4.6.2
##   [57] reshape2_1.4.4                   RColorBrewer_1.1-3
##   [59] purrr_1.1.0                      patchwork_1.3.2
##   [61] optparse_1.7.5                   leiden_0.4.3.1
##   [63] knitr_1.50                       irlba_2.3.5.1
##   [65] igraph_2.1.4                     hdf5r_1.3.10
##   [67] harmony_1.2.3                    Rcpp_1.0.12
##   [69] ggthemes_5.1.0                   ggrepel_0.9.6
##   [71] ggpmisc_0.6.2                    ggpp_0.5.9
##   [73] ggh4x_0.3.1                      GGally_2.4.0
##   [75] future_1.67.0                    fs_1.6.6
##   [77] forcats_1.0.1                    flexmix_2.3-20
##   [79] lattice_0.22-6                   data.table_1.17.8
##   [81] cowplot_1.2.0                    clustree_0.5.1
##   [83] ggraph_2.2.1                     numbat_1.4.0
##   [85] Matrix_1.7-0                     scooter_0.0.0.9004
##   [87] infercnv_1.22.0                  SingleR_2.8.0
##   [89] celldex_1.16.0                   scDblFinder_1.20.2
##   [91] scater_1.34.1                    ggplot2_4.0.0
##   [93] scuttle_1.16.0                   SingleCellExperiment_1.28.1
##   [95] SummarizedExperiment_1.36.0     Biobase_2.66.0
##   [97] GenomicRanges_1.58.0            GenomeInfoDb_1.42.3
##   [99] IRanges_2.40.1                   S4Vectors_0.44.0
##  [101] BiocGenerics_0.52.0             MatrixGenerics_1.18.1
##  [103] matrixStats_1.5.0               miQC_1.14.0
##  [105] remotes_2.5.0                    devtools_2.4.5
##  [107] usethis_2.2.3                    BiocManager_1.30.23
##
## loaded via a namespace (and not attached):
##    [1] DBI_1.2.3                       bslib_0.7.0
##    [3] httr_1.4.7                      TFMPvalue_0.0.9
##    [5] BiocParallel_1.40.2            prettyunits_1.2.0
##    [7] yulab.utils_0.2.1              ProtGenerics_1.38.0
##    [9] ggplotify_0.1.2                GenomicAlignments_1.42.0
##   [11] sparseMatrixStats_1.18.0       spatstat.geom_3.2-9
##   [13] pillar_1.11.1                  R6_2.6.1
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##  [15] boot_1.3-30                 mime_0.12
##  [17] edgeR_4.4.2                 uwot_0.2.2
##  [19] viridis_0.6.5               Rhdf5lib_1.28.0
##  [21] libcoin_1.0-10              ROCR_1.0-11
##  [23] Hmisc_5.1-3                 limma_3.62.2
##  [25] S7_0.2.0                    parallelly_1.45.1
##  [27] caTools_1.18.3              polyclip_1.10-6
##  [29] beachmat_2.22.0             htmltools_0.5.8.1
##  [31] lambda.r_1.2.4              fgsea_1.32.4
##  [33] spatstat.utils_3.0-4        rpart_4.1.23
##  [35] fitdistrplus_1.1-11         goftest_1.2-3
##  [37] tidyselect_1.2.1            RSQLite_2.3.7
##  [39] GenomeInfoDbData_1.2.13     ScaledMatrix_1.14.0
##  [41] scattermore_1.2             sessioninfo_1.2.2
##  [43] spatstat.data_3.0-4         xgboost_1.7.7.1
##  [45] sctransform_0.4.1           future.apply_1.11.2
##  [47] CNEr_1.42.0                 uuid_1.2-1
##  [49] vipor_0.4.7                 Rtsne_0.17
##  [51] tokenizers_0.3.0            DelayedMatrixStats_1.28.1
##  [53] lazyeval_0.2.2              sass_0.4.9
##  [55] scales_1.4.0                treeio_1.30.0
##  [57] profvis_0.3.8               pracma_2.4.4
##  [59] bitops_1.0-7                KEGGREST_1.46.0
##  [61] ggstats_0.11.0              promises_1.3.3
##  [63] rhdf5filters_1.18.1         poweRlaw_0.80.0
##  [65] zoo_1.8-12                  locfit_1.5-9.9
##  [67] DelayedArray_0.32.0         scistreer_1.2.0
##  [69] multcomp_1.4-25             tools_4.4.0
##  [71] ape_5.8                     rlang_1.1.6
##  [73] generics_0.1.4              BiocSingular_1.22.0
##  [75] ggridges_0.5.6              evaluate_0.24.0
##  [77] httr2_1.2.1                 fastcluster_1.2.6
##  [79] colorspace_2.1-0            ellipsis_0.3.2
##  [81] withr_3.0.2                 RCurl_1.98-1.14
##  [83] futile.logger_1.4.3         restfulr_0.0.15
##  [85] xtable_1.8-4                alabaster.se_1.6.0
##  [87] plyr_1.8.9                  lme4_1.1-35.3
##  [89] aplot_0.2.2                 systemfonts_1.1.0
##  [91] MatrixModels_0.5-4          httpuv_1.6.15
##  [93] rmarkdown_2.27              metapod_1.14.0
##  [95] latticeExtra_0.6-30         officer_0.7.0
##  [97] MASS_7.3-60.2               dqrng_0.4.1
##  [99] deldir_2.0-4                GO.db_3.20.0
## [101] sandwich_3.1-0              rhdf5_2.50.2
## [103] tensor_1.5                  ragg_1.5.0
## [105] vctrs_0.6.5                 lifecycle_1.0.4
## [107] logger_0.3.0                codetools_0.2-20
## [109] nlme_3.1-164                progress_1.2.3
## [111] pkgload_1.3.4               jquerylib_0.1.4
## [113] rstudioapi_0.16.0           stringi_1.8.4
## [115] VGAM_1.1-11                 hms_1.1.3
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## [117] pbapply_1.7-2                minqa_1.2.7
## [119] cachem_1.1.0                 alabaster.ranges_1.6.0
## [121] janeaustenr_1.0.0            tidytree_0.4.6
## [123] listenv_0.9.1                urlchecker_1.0.1
## [125] plotly_4.10.4                ggtree_3.14.0
## [127] jpeg_0.1-10                  alabaster.base_1.6.1
## [129] ExperimentHub_2.14.0         pkgbuild_1.4.4
## [131] ggfun_0.2.0                  HDF5Array_1.34.0
## [133] ggsci_3.1.0                  ggtangle_0.0.7
## [135] SparseArray_1.6.2            Formula_1.2-5
## [137] memoise_2.0.1                crayon_1.5.2
## [139] gridGraphics_0.5-1           rappdirs_0.3.3
## [141] S4Arrays_1.6.0               xml2_1.4.0
## [143] filelock_1.0.3               interp_1.1-6
## [145] GOSemSim_2.32.0              UCSC.utils_1.2.0
## [147] png_0.1-8                    progressr_0.14.0
## [149] tzdb_0.4.0                   alabaster.matrix_1.6.1
## [151] fastmap_1.2.0                coda_0.19-4.1
## [153] tidygraph_1.3.1              pkgconfig_2.0.3
## [155] cli_3.6.5                    beeswarm_0.4.0
## [157] alabaster.schemas_1.6.0      DOSE_4.0.1
## [159] ggforce_0.4.2                pwalign_1.2.0
## [161] nnet_7.3-19                  DirichletMultinomial_1.48.0
## [163] lmtest_0.9-40                textshaping_0.4.0
## [165] BiocVersion_3.20.0           RcppAnnoy_0.0.22
## [167] gdtools_0.4.3                argparse_2.2.3
## [169] timechange_0.3.0             viridisLite_0.4.2
## [171] rjags_4-15                   askpass_1.2.0
## [173] scran_1.34.0                 foreign_0.8-86
## [175] splines_4.4.0                blob_1.2.4
## [177] annotate_1.84.0              XML_3.99-0.16.1
## [179] VariantAnnotation_1.52.0     globals_0.18.0
## [181] ggbeeswarm_0.7.2             RcppRoll_0.3.0
## [183] ica_1.0-3                    spam_2.10-0
## [185] dichromat_2.0-0.1            compiler_4.4.0
## [187] rjson_0.2.21                 RcppParallel_5.1.7
## [189] biomaRt_2.62.1               bit_4.0.5
## [191] BiocNeighbors_2.0.1          sp_2.1-4
## [193] formatR_1.14                 digest_0.6.35
## [195] quadprog_1.5-8               graphlayouts_1.1.1
## [197] fontLiberation_0.1.0         foreach_1.5.2
## [199] seqLogo_1.72.0               fontBitstreamVera_0.1.1
## [201] spatstat.random_3.2-3        SparseM_1.84-2
## [203] zlibbioc_1.52.0              dotCall64_1.1-1
## [205] tweenr_2.0.3                 openssl_2.2.0
## [207] phangorn_2.11.1              statmod_1.5.0
## [209] rsvd_1.0.5                   gson_0.1.0
## [211] nloptr_2.0.3                 mvtnorm_1.2-5
## [213] qvalue_2.38.0                later_1.3.2
## [215] modeltools_0.2-23            backports_1.5.0
## [217] Rsamtools_2.22.0             parallel_4.4.0
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## [219] parallelDist_0.2.6          fontquiver_0.2.1
## [221] quantreg_6.1                miniUI_0.1.1.1
## [223] gtable_0.3.6                abind_1.4-5
## [225] xfun_0.53                   getopt_1.20.4
## [227] curl_7.0.0                  doParallel_1.0.17
## [229] KernSmooth_2.23-22          futile.options_1.0.1
## [231] gypsum_1.2.0                survival_3.5-8
## [233] jsonlite_1.8.8              magrittr_2.0.4
## [235] coin_1.4-3                  base64enc_0.1-3
## [237] iterators_1.0.14            TH.data_1.1-2
## [239] RhpcBLASctl_0.23-42         fastmatch_1.1-4
## [241] checkmate_2.3.1             gtools_3.9.5
## [243] SnowballC_0.7.1             htmlTable_2.4.2
## [245] spatstat.sparse_3.0-3       RANN_2.6.1
## [247] bluster_1.16.0              phyclust_0.1-34
## [249] spatstat.explore_3.2-7      polynom_1.4-1
## [251] bit64_4.0.5                 cluster_2.1.6
## [253] farver_2.1.2                zip_2.3.1
## [255] hahmmr_1.0.0                gplots_3.1.3.1
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