

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] ggseqlogo_0.1                  chromVAR_1.28.0
## [3] BSgenome.Mmusculus.UCSC.mm39_1.4.3 motifmatchr_1.28.0
## [5] enrichplot_1.26.6               RcppPlanc_2.0.13
## [7] rlier_2.2.1.9001                flextable_0.9.10
## [9] clusterProfiler_4.14.6          biovizBase_1.54.0
## [11] cicero_1.3.9                  Gviz_1.46.1
## [13] monocle3_1.4.26                BSgenome.Hsapiens.UCSC.hg19_1.4.3
## [15] BSgenome.Mmusculus.UCSC.mm10_1.4.3 BSgenome_1.74.0
## [17] BiocIO_1.16.0                 Biostrings_2.74.1
## [19] XVector_0.46.0                TFBSTools_1.44.0
## [21] JASPAR2024_0.99.6              JASPAR2022_0.99.8
## [23] JASPAR2020_0.99.10            JASPAR2018_1.1.1
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## [25] org.Mm.eg.db_3.20.0          org.Hs.eg.db_3.20.0
## [27] htmlwidgets_1.6.4             rtracklayer_1.66.0
## [29] ensemblDb_2.30.0              AnnotationFilter_1.30.0
## [31] GenomicFeatures_1.58.0         AnnotationDbi_1.68.0
## [33] AnnotationHub_3.14.0          BiocFileCache_2.14.0
## [35] dbplyr_2.5.0                 ggdendro_0.2.0
## [37] DT_0.34.0                   shinyhelper_0.3.2
## [39] ShinyCell_2.1.0              glue_1.8.0
## [41] gridExtra_2.3                reticulate_1.37.0
## [43] yaml_2.3.12                  tinytex_0.58
## [45] lubridate_1.9.4              dplyr_1.1.4
## [47] readr_2.1.5                  tidyverse_2.0.0
## [49] tibble_3.3.1                 stringr_1.6.0
## [51] tidytext_0.4.3               Signac_1.16.0
## [53] SoupX_1.6.2                 SeuratWrappers_0.2.0
## [55] shiny_1.12.1                 Seurat_4.4.0
## [57] SeuratObject_5.2.0           R.oo_1.26.0
## [59] R.utils_2.13.0               rlist_0.4.6.2
## [61] R.methodsS3_1.8.2             RColorBrewer_1.1-3
## [63] reshape2_1.4.5               patchwork_1.3.2
## [65] purrr_1.2.1                  leiden_0.4.3.1
## [67] optparse_1.7.5               irlba_2.3.7
## [69] knitr_1.51                   hdf5r_1.3.10
## [71] igraph_2.2.1                 Rcpp_1.0.12
## [73] harmony_1.2.4                ggrepel_0.9.6
## [75] ggthemes_5.2.0               ggpp_0.6.0
## [77] ggpmisc_0.6.3               GGally_2.4.0
## [79] ggh4x_0.3.1                  fs_1.6.6
## [81] future_1.69.0                flexmix_2.3-20
## [83]forcats_1.0.1                 data.table_1.18.2.1
## [85] lattice_0.22-6               clustree_0.5.1
## [87] cowplot_1.2.0                numbat_1.4.0
## [89] ggraph_2.2.1                 scooter_0.0.0.9004
## [91] Matrix_1.7-0                 SingleR_2.8.0
## [93] infercnv_1.22.0              scDblFinder_1.20.2
## [95] celldex_1.16.0              ggplot2_4.0.1
## [97] scater_1.34.1               SingleCellExperiment_1.28.1
## [99] scuttle_1.16.0               Biobase_2.66.0
## [101] SummarizedExperiment_1.36.0 GenomeInfoDb_1.42.3
## [103] GenomicRanges_1.58.0          S4Vectors_0.44.0
## [105] IRanges_2.40.1              MatrixGenerics_1.18.1
## [107] BiocGenerics_0.52.0          miQC_1.14.0
## [109] matrixStats_1.5.0            devtools_2.4.5
## [111] remotes_2.5.0               BiocManager_1.30.23
## [113] usethis_2.2.3

##
## 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_0.2.3               ProtGenerics_1.38.0

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## [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
## [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_0.2.1                parallelly_1.46.1
## [27] caTools_1.18.2           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              uid_1.2-2
## [49] viper_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_0.12.0            promises_1.5.0
## [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_1.1.7
## [73] generics_0.1.4             BiocSingular_1.22.0
## [75] ggridges_0.5.6            evaluate_0.24.0
## [77] httr2_1.2.2               fastcluster_1.2.6
## [79] otel_0.2.0                colorspace_2.1-0
## [81] ellipsis_0.3.2            withr_3.0.2
## [83] RCurl_1.98-1.14           futile.logger_1.4.3
## [85] restfulr_0.0.15           xtable_1.8-4
## [87] alabaster.se_1.6.0         plyr_1.8.9
## [89] lme4_1.1-35.3             subplot_0.2.2
## [91] systemfonts_1.3.1          MatrixModels_0.5-4
## [93] httpuv_1.6.15             rmarkdown_2.27
## [95] metapod_1.14.0            latticeExtra_0.6-30
## [97] officer_0.7.3             MASS_7.3-60.2
## [99] dqrng_0.4.1                deldir_2.0-4
## [101] GO.db_3.20.0              sandwich_3.1-0
## [103] rhdf5_2.50.2              tensor_1.5
## [105] ragg_1.5.0                vctrs_0.7.1
## [107] lifecycle_1.0.5            logger_0.3.0
## [109] codetools_0.2-20           nlme_3.1-164

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## [111] progress_1.2.3          pkgload_1.3.4
## [113] jquerylib_0.1.4        rstudioapi_0.16.0
## [115] stringi_1.8.4          VGAM_1.1-11
## [117] hms_1.1.3              pbapply_1.7-2
## [119] minqa_1.2.7            cachem_1.1.0
## [121] alabaster.ranges_1.6.0 janeaustenr_1.0.0
## [123] tidytree_0.4.6          listenv_0.9.1
## [125] urlchecker_1.0.1       plotly_4.10.4
## [127] ggtree_3.14.0            jpeg_0.1-10
## [129] alabaster.base_1.6.1    ExperimentHub_2.14.0
## [131] pkgbuild_1.4.4           ggfun_0.2.0
## [133] HDF5Array_1.34.0         ggsci_3.1.0
## [135] ggtangle_0.1.1          SparseArray_1.6.2
## [137] Formula_1.2-5           memoise_2.0.1
## [139] crayon_1.5.2            gridGraphics_0.5-1
## [141] rappdirs_0.3.3          S4Arrays_1.6.0
## [143] xml2_1.5.2              filelock_1.0.3
## [145] interp_1.1-6             GOSemSim_2.32.0
## [147] UCSC.utils_1.2.0         png_0.1-8
## [149] progressr_0.14.0          tzdb_0.4.0
## [151] alabaster.matrix_1.6.1   fastmap_1.2.0
## [153] coda_0.19-4.1            tidygraph_1.3.1
## [155] pkgconfig_2.0.3           cli_3.6.5
## [157] beeswarm_0.4.0           alabaster.schemas_1.6.0
## [159] DOSE_4.0.1               ggforce_0.4.2
## [161] pwalign_1.2.0             nnet_7.3-19
## [163] DirichletMultinomial_1.48.0 lmtest_0.9-40
## [165] textshaping_0.4.0         BiocVersion_3.20.0
## [167] RcppAnnoy_0.0.22          gdtools_0.4.4
## [169] argparse_2.2.3             timechange_0.4.0
## [171] viridisLite_0.4.2          rjags_4-15
## [173] askpass_1.2.0              scran_1.34.0
## [175] foreign_0.8-86            splines_4.4.0
## [177] blob_1.2.4                annotate_1.84.0
## [179] XML_3.99-0.16.1           VariantAnnotation_1.52.0
## [181] globals_0.19.0             ggbeeswarm_0.7.2
## [183] RcppRoll_0.3.0             ica_1.0-3
## [185] spam_2.10-0               dichromat_2.0-0.1
## [187] compiler_4.4.0             rjson_0.2.21
## [189] RcppParallel_5.1.7          biomaRt_2.62.1
## [191] bit_4.0.5                 BiocNeighbors_2.0.1
## [193] sp_2.1-4                  formatR_1.14
## [195] digest_0.6.35              quadprog_1.5-8
## [197] graphlayouts_1.1.1          fontLiberation_0.1.0
## [199] foreach_1.5.2              seqLogo_1.72.0
## [201] fontBitstreamVera_0.1.1    spatstat.random_3.2-3
## [203] SparseM_1.84-2             zlibbioc_1.52.0
## [205] dotCall64_1.1-1            tweenr_2.0.3
## [207] openssl_2.2.0              phangorn_2.11.1
## [209] statmod_1.5.0              gson_0.1.0
## [211] rsrvd_1.0.5               nloptr_2.0.3

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## [213] mvtnorm_1.2-5          qvalue_2.38.0
## [215] later_1.3.2            modeltools_0.2-23
## [217] backports_1.5.0        Rsamtools_2.22.0
## [219] parallel_4.4.0         parallelDist_0.2.6
## [221] fontquiver_0.2.1       quantreg_6.1
## [223] miniUI_0.1.1.1        gtable_0.3.6
## [225] abind_1.4-5           xfun_0.56
## [227] getopt_1.20.4          curl_7.0.0
## [229] doParallel_1.0.17      KernSmooth_2.23-22
## [231] futile.options_1.0.1    gypsum_1.2.0
## [233] survival_3.5-8         jsonlite_1.8.8
## [235] magrittr_2.0.4          coin_1.4-3
## [237] base64enc_0.1-3         iterators_1.0.14
## [239] TH.data_1.1-2           RhpcBLASctl_0.23-42
## [241] fastmatch_1.1-4         checkmate_2.3.1
## [243] gtools_3.9.5            SnowballC_0.7.1
## [245] htmlTable_2.4.2         spatstat.sparse_3.0-3
## [247] RANN_2.6.1              bluster_1.16.0
## [249] phyclus_0.1-34          spatstat.explore_3.2-7
## [251] polynom_1.4-1           bit64_4.0.5
## [253] cluster_2.1.6           farver_2.1.2
## [255] zip_2.3.1                hahmmr_1.0.0
## [257] gplots_3.1.3.1
```