

Debugging step: Verify installations

Antonia Chroni for SJCRH DNB_BINF_Core

Contents

| | |
|-----------------------|----------|
| 1 Set up | 1 |
| 2 Session Info | 1 |

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 versi
##
## 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] JASPAR2020_0.99.10            org.Mm.eg.db_3.20.0
## [23] org.Hs.eg.db_3.20.0           htmlwidgets_1.6.4
```

```

## [25] rtracklayer_1.66.0
## [27] AnnotationFilter_1.30.0
## [29] AnnotationDbi_1.68.0
## [31] BiocFileCache_2.14.0
## [33] ggdendro_0.2.0
## [35] shinyhelper_0.3.2
## [37] glue_1.8.0
## [39] reticulate_1.37.0
## [41] tinytex_0.58
## [43] dplyr_1.1.4
## [45] tidyr_1.3.1
## [47] tidyverse_2.0.0
## [49] stringr_1.6.0
## [51] Signac_1.16.9004
## [53] SeuratWrappers_0.2.0
## [55] Seurat_4.4.0
## [57] R.oo_1.26.0
## [59] rlist_0.4.6.2
## [61] RColorBrewer_1.1-3
## [63] patchwork_1.3.2
## [65] leiden_0.4.3.1
## [67] irlba_2.3.5.1
## [69] hdf5r_1.3.10
## [71] Rcpp_1.0.12
## [73] ggrepel_0.9.6
## [75] ggpp_0.5.9
## [77] GGally_2.4.0
## [79] fs_1.6.6
## [81] flexmix_2.3-20
## [83] data.table_1.17.8
## [85] clustree_0.5.1
## [87] numbat_1.4.0
## [89] scooter_0.0.0.9004
## [91] SingleR_2.8.0
## [93] scDblFinder_1.20.2
## [95] ggplot2_4.0.1
## [97] SingleCellExperiment_1.28.1
## [99] Biobase_2.66.0
## [101] GenomeInfoDb_1.42.3
## [103] S4Vectors_0.44.0
## [105] MatrixGenerics_1.18.1
## [107] miQC_1.14.0
## [109] devtools_2.4.5
## [111] BiocManager_1.30.23
##
## loaded via a namespace (and not attached):
## [1] DBI_1.2.3
## [3] httr_1.4.7
## [5] BiocParallel_1.40.2
## [7] yulab.utils_0.2.3
## [9] ggplotify_0.1.2
ensemblDb_2.30.0
GenomicFeatures_1.58.0
AnnotationHub_3.14.0
dplyr_2.5.0
DT_0.34.0
ShinyCell_2.1.0
gridExtra_2.3
yaml_2.3.12
lubridate_1.9.4
readr_2.1.5
tibble_3.3.0
tidytext_0.4.3
SoupX_1.6.2
shiny_1.12.1
SeuratObject_5.3.0
R.utils_2.13.0
R.methodsS3_1.8.2
reshape2_1.4.5
purrr_1.2.0
optparse_1.7.5
knitr_1.50
igraph_2.2.1
harmony_1.2.4
ggthemes_5.2.0
ggpmisc_0.6.3
ggh4x_0.3.1
future_1.68.0
forcats_1.0.1
lattice_0.22-6
cowplot_1.2.0
ggraph_2.2.1
Matrix_1.7-0
infercnv_1.22.0
celldex_1.16.0
scater_1.34.1
scuttle_1.16.0
SummarizedExperiment_1.36.0
GenomicRanges_1.58.0
IRanges_2.40.1
BiocGenerics_0.52.0
matrixStats_1.5.0
remotes_2.5.0
usethis_2.2.3
bslib_0.7.0
TFMPvalue_0.0.9
prettyunits_1.2.0
ProtGenerics_1.38.0
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_1.46.0
## [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_1.5.0
## [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] RSpectra_0.16-1             multcomp_1.4-25
## [71] tools_4.4.0                 ape_5.8
## [73] rlang_1.1.6                  generics_0.1.4
## [75] BiocSingular_1.22.0          ggridges_0.5.6
## [77] evaluate_0.24.0              httr2_1.2.2
## [79] fastcluster_1.2.6            otel_0.2.0
## [81] colorspace_2.1-0             ellipsis_0.3.2
## [83] withr_3.0.2                 RCurl_1.98-1.14
## [85] futile.logger_1.4.3          restfulr_0.0.15
## [87] xtable_1.8-4                alabaster.se_1.6.0
## [89] plyr_1.8.9                  lme4_1.1-35.3
## [91] aplot_0.2.2                 systemfonts_1.3.1
## [93] MatrixModels_0.5-4           httpuv_1.6.15
## [95] rmarkdown_2.27                metapod_1.14.0
## [97] latticeExtra_0.6-30          officer_0.7.2
## [99] MASS_7.3-60.2                dqrng_0.4.1
## [101] deldir_2.0-4                G0.db_3.20.0
## [103] sandwich_3.1-0              rhdf5_2.50.2
## [105] tensor_1.5                  ragg_1.5.0
## [107] vctrs_0.6.5                 lifecycle_1.0.4
## [109] logger_0.3.0                codetools_0.2-20
## [111] nlme_3.1-164                progress_1.2.3

```

```

## [113] pkgload_1.3.4                jquerylib_0.1.4
## [115] rstudioapi_0.16.0             stringi_1.8.4
## [117] VGAM_1.1-11                  hms_1.1.3
## [119] pbapply_1.7-2                 minqa_1.2.7
## [121] cachem_1.1.0                 alabaster.ranges_1.6.0
## [123] janeaustenr_1.0.0            tidytree_0.4.6
## [125] listenv_0.9.1                urlchecker_1.0.1
## [127] plotly_4.10.4                ggtree_3.14.0
## [129] jpeg_0.1-10                 alabaster.base_1.6.1
## [131] ExperimentHub_2.14.0          pkgbuild_1.4.4
## [133] ggfunk_0.2.0                 HDF5Array_1.34.0
## [135] ggsci_3.1.0                  ggtangle_0.0.9
## [137] SparseArray_1.6.2             Formula_1.2-5
## [139] memoise_2.0.1                crayon_1.5.2
## [141] gridGraphics_0.5-1           rappdirs_0.3.3
## [143] S4Arrays_1.6.0               xml2_1.5.1
## [145] filelock_1.0.3              interp_1.1-6
## [147] GOSemSim_2.32.0             UCSC.utils_1.2.0
## [149] png_0.1-8                   progressr_0.14.0
## [151] tzdb_0.4.0                  alabaster.matrix_1.6.1
## [153] fastmap_1.2.0                coda_0.19-4.1
## [155] tidygraph_1.3.1              pkgconfig_2.0.3
## [157] cli_3.6.5                   beeswarm_0.4.0
## [159] alabaster.schemas_1.6.0       DOSE_4.0.1
## [161] ggforce_0.4.2                pwalign_1.2.0
## [163] nnet_7.3-19                 DirichletMultinomial_1.48.0
## [165] lmtest_0.9-40                textshaping_0.4.0
## [167] BiocVersion_3.20.0           RcppAnnoy_0.0.22
## [169] gdtools_0.4.4                argparse_2.2.3
## [171] timechange_0.3.0             viridisLite_0.4.2
## [173] rjags_4-15                  askpass_1.2.0
## [175] scran_1.34.0                foreign_0.8-86
## [177] splines_4.4.0               blob_1.2.4
## [179] annotate_1.84.0              XML_3.99-0.16.1
## [181] VariantAnnotation_1.52.0       globals_0.18.0
## [183] ggbeeswarm_0.7.2             RcppRoll_0.3.0
## [185] ica_1.0-3                  spam_2.10-0
## [187] dichromat_2.0-0.1            compiler_4.4.0
## [189] rjson_0.2.21                RcppParallel_5.1.7
## [191] biomaRt_2.62.1              bit_4.0.5
## [193] BiocNeighbors_2.0.1            sp_2.1-4
## [195] formatR_1.14                 digest_0.6.35
## [197] quadprog_1.5-8                graphlayouts_1.1.1
## [199] fontLiberation_0.1.0          foreach_1.5.2
## [201] seqLogo_1.72.0              fontBitstreamVera_0.1.1
## [203] spatstat.random_3.2-3         SparseM_1.84-2
## [205] zlibbioc_1.52.0              dotCall64_1.1-1
## [207] tweenr_2.0.3                 openssl_2.2.0
## [209] phangorn_2.11.1              statmod_1.5.0
## [211] rsvd_1.0.5                  gson_0.1.0
## [213] nloptr_2.0.3                mvtnorm_1.2-5

```

```
## [215] qvalue_2.38.0           later_1.3.2
## [217] modeltools_0.2-23        backports_1.5.0
## [219] Rsamtools_2.22.0         parallel_4.4.0
## [221] parallelDist_0.2.6       fontquiver_0.2.1
## [223] quantreg_6.1            miniUI_0.1.1.1
## [225] gtable_0.3.6             abind_1.4-5
## [227] xfun_0.55               getopt_1.20.4
## [229] curl_7.0.0               doParallel_1.0.17
## [231] KernSmooth_2.23-22       futile.options_1.0.1
## [233] gypsum_1.2.0             survival_3.5-8
## [235] jsonlite_1.8.8           magrittr_2.0.4
## [237] coin_1.4-3               base64enc_0.1-3
## [239] iterators_1.0.14          TH.data_1.1-2
## [241] RhpcBLASctl_0.23-42      fastmatch_1.1-4
## [243] checkmate_2.3.1           gtools_3.9.5
## [245] SnowballC_0.7.1           htmlTable_2.4.2
## [247] spatstat.sparse_3.0-3     RANN_2.6.1
## [249] bluster_1.16.0            phyclus_0.1-34
## [251] spatstat.explore_3.2-7    polynom_1.4-1
## [253] bit64_4.0.5               cluster_2.1.6
## [255] farver_2.1.2              zip_2.3.1
## [257] hahmmr_1.0.0              gplots_3.1.3.1
```