

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-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] rliger_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                gg dendro_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                 tidyr_1.3.1
## [49] tibble_3.3.1                tidyverse_2.0.0
## [51] tidytext_0.4.3             stringr_1.6.0
## [53] SoupX_1.6.2                 Signac_1.16.0
## [55] shiny_1.12.1                SeuratWrappers_0.2.0
## [57] SeuratObject_5.2.0          Seurat_4.4.0
## [59] R.utils_2.13.0              R.oo_1.26.0
## [61] R.methodsS3_1.8.2           rlist_0.4.6.2
## [63] reshape2_1.4.5              RColorBrewer_1.1-3
## [65] purrr_1.2.1                 patchwork_1.3.2
## [67] optparse_1.7.5              leiden_0.4.3.1
## [69] knitr_1.51                   irlba_2.3.7
## [71] igraph_2.2.1                hdf5r_1.3.10
## [73] harmony_1.2.4               Rcpp_1.0.12
## [75] ggthemes_5.2.0              ggrepel_0.9.6
## [77] ggpmisc_0.6.3               ggpp_0.6.0
## [79] ggh4x_0.3.1                 GGally_2.4.0
## [81] future_1.69.0               fs_1.6.6
## [83] forcats_1.0.1               flexmix_2.3-20
## [85] lattice_0.22-6              data.table_1.18.2.1
## [87] cowplot_1.2.0               clustree_0.5.1
## [89] ggraph_2.2.1                numbat_1.4.0
## [91] Matrix_1.7-0                scooter_0.0.0.9004
## [93] infercnv_1.22.0             SingleR_2.8.0
## [95] cellDex_1.16.0              scDblFinder_1.20.2
## [97] scatter_1.34.1              ggplot2_4.0.1
## [99] scuttle_1.16.0              SingleCellExperiment_1.28.1
## [101] SummarizedExperiment_1.36.0 Biobase_2.66.0
## [103] GenomicRanges_1.58.0        GenomeInfoDb_1.42.3
## [105] IRanges_2.40.1              S4Vectors_0.44.0
## [107] BiocGenerics_0.52.0         MatrixGenerics_1.18.1
## [109] matrixStats_1.5.0           miQC_1.14.0
## [111] remotes_2.5.0               devtools_2.4.5
## [113] 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_0.2.3            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	uuid_1.2-2
## [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_0.12.0	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	scistree_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	aplot_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

## [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	scraper_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] rsvd_1.0.5	nloptr_2.0.3

## [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] phyclust_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	