

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

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## [25] rtracklayer_1.66.0          ensemblldb_2.30.0
## [27] AnnotationFilter_1.30.0     GenomicFeatures_1.58.0
## [29] AnnotationDbi_1.68.0        AnnotationHub_3.14.0
## [31] BiocFileCache_2.14.0        dbplyr_2.5.0
## [33] ggdendro_0.2.0              DT_0.34.0
## [35] shinyhelper_0.3.2           ShinyCell_2.1.0
## [37] glue_1.8.0                  gridExtra_2.3
## [39] reticulate_1.37.0           yaml_2.3.12
## [41] tinytex_0.58                lubridate_1.9.4
## [43] dplyr_1.1.4                 readr_2.1.5
## [45] tidyr_1.3.1                 tibble_3.3.0
## [47] tidyverse_2.0.0             tidytext_0.4.3
## [49] stringr_1.6.0              SoupX_1.6.2
## [51] Signac_1.16.9004           shiny_1.12.1
## [53] SeuratWrappers_0.2.0        SeuratObject_5.3.0
## [55] Seurat_4.4.0                R.utils_2.13.0
## [57] R.oo_1.26.0                 R.methodsS3_1.8.2
## [59] rlist_0.4.6.2              reshape2_1.4.5
## [61] RColorBrewer_1.1-3          purrr_1.2.0
## [63] patchwork_1.3.2            optparse_1.7.5
## [65] leiden_0.4.3.1             knitr_1.50
## [67] irlba_2.3.5.1              igraph_2.2.1
## [69] hdf5r_1.3.10               harmony_1.2.4
## [71] Rcpp_1.0.12                 ggthemes_5.2.0
## [73] ggrepel_0.9.6              ggpmisc_0.6.3
## [75] ggpp_0.5.9                  ggh4x_0.3.1
## [77] GGally_2.4.0                future_1.68.0
## [79] fs_1.6.6                    forcats_1.0.1
## [81] flexmix_2.3-20              lattice_0.22-6
## [83] data.table_1.17.8           cowplot_1.2.0
## [85] clustree_0.5.1              ggraph_2.2.1
## [87] numbat_1.4.0                Matrix_1.7-0
## [89] scooter_0.0.0.9004           infercnv_1.22.0
## [91] SingleR_2.8.0               celldex_1.16.0
## [93] scDbfFinder_1.20.2          scater_1.34.1
## [95] ggplot2_4.0.1              scuttle_1.16.0
## [97] SingleCellExperiment_1.28.1 SummarizedExperiment_1.36.0
## [99] Biobase_2.66.0              GenomicRanges_1.58.0
## [101] GenomeInfoDb_1.42.3         IRanges_2.40.1
## [103] S4Vectors_0.44.0           BiocGenerics_0.52.0
## [105] MatrixGenerics_1.18.1       matrixStats_1.5.0
## [107] miQC_1.14.0                 remotes_2.5.0
## [109] devtools_2.4.5              usethis_2.2.3
## [111] 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
## [9] ggplotify_0.1.2             GenomicAlignments_1.42.0

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## [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	scistree_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	ggribes_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	GO.db_3.20.0
## [103]	sandwich_3.1-0	rhdf5_2.50.2
## [105]	tensor_1.5	ragg_1.5.0
## [107]	vctr_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] ggfun_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] scan_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	phyclust_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