

# 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] motifmatchr_1.28.0 enrichplot_1.26.6
## [3] RcppPlanc_2.0.13 rligier_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                gg dendro_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_1.16.0
## [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] scatter_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	scistree_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_1.3.1
## [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	G0.db_3.20.0
## [101] sandwich_3.1-0	rhdf5_2.50.2
## [103] tensor_1.5	ragg_1.5.0
## [105] vctr_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

## [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	pwalgn_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_0.4.4	argparse_2.2.3
## [169] timechange_0.3.0	viridisLite_0.4.2
## [171] rjags_4-15	askpass_1.2.0
## [173] scan_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

## [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