

# 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 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] gg dendro_0.2.0          DT_0.33
## [3] shinyhelper_0.3.2       ShinyCell_2.1.0
## [5] glue_1.8.0              gridExtra_2.3
## [7] reticulate_1.40.0       yaml_2.3.10
## [9] tinytex_0.54            lubridate_1.9.4
## [11] dplyr_1.1.4             readr_2.1.5
## [13] tidyr_1.3.1             tibble_3.2.1
## [15] tidyverse_2.0.0         tidytext_0.4.2
## [17] stringr_1.5.1           SoupX_1.6.2
## [19] Signac_1.14.9002        shiny_1.10.0
## [21] SeuratWrappers_0.2.0    SeuratObject_5.0.2
## [23] Seurat_4.4.0            R.utils_2.12.3
```

```

## [25] R.oo_1.27.0                R.methodsS3_1.8.2
## [27] rlist_0.4.6.2              rligier_2.1.0.9004
## [29] reshape2_1.4.4             RColorBrewer_1.1-3
## [31] purrr_1.0.2                patchwork_1.3.0
## [33] optparse_1.7.5             leiden_0.4.3.1
## [35] knitr_1.49                 irlba_2.3.5.1
## [37] igraph_2.1.4              hdf5r_1.3.12
## [39] harmony_1.2.3              Rcpp_1.0.14
## [41] ggthemes_5.1.0            ggrepel_0.9.6
## [43] ggpmisc_0.6.1             ggpp_0.5.8-1
## [45] ggh4x_0.3.0               GGally_2.2.1
## [47] future_1.34.0             fs_1.6.5
## [49] forcats_1.0.0            flextable_0.9.7
## [51] flexmix_2.3-19            lattice_0.22-6
## [53] data.table_1.16.4         cowplot_1.1.3
## [55] clustree_0.5.1            ggraph_2.2.1
## [57] numbat_1.4.2              Matrix_1.7-2
## [59] RcppPlanc_1.0.0           scooter_0.0.0.9004
## [61] infercnv_1.22.0           SingleR_2.8.0
## [63] celldex_1.16.0           scDblFinder_1.20.0
## [65] scater_1.34.0            ggplot2_3.5.1
## [67] scuttle_1.16.0           SingleCellExperiment_1.28.1
## [69] SummarizedExperiment_1.36.0 Biobase_2.66.0
## [71] GenomicRanges_1.58.0     GenomeInfoDb_1.42.3
## [73] IRanges_2.40.1           S4Vectors_0.44.0
## [75] BiocGenerics_0.52.0      MatrixGenerics_1.18.1
## [77] matrixStats_1.5.0        miQC_1.14.0
## [79] remotes_2.5.0            devtools_2.4.5
## [81] usethis_3.1.0            BiocManager_1.30.25
##
## loaded via a namespace (and not attached):
## [1] ica_1.0-3                  plotly_4.10.4
## [3] zlibbioc_1.52.0           tidyselect_1.2.1
## [5] bit_4.5.0.1               doParallel_1.0.17
## [7] rjson_0.2.23              blob_1.2.4
## [9] urlchecker_1.0.1          S4Arrays_1.6.0
## [11] parallel_4.4.0            png_0.1-8
## [13] cli_3.6.3                 ggplotify_0.1.2
## [15] askpass_1.2.1             openssl_2.3.2
## [17] goftest_1.2-3             textshaping_1.0.0
## [19] BiocIO_1.16.0            bluster_1.16.0
## [21] officer_0.6.7            tokenizers_0.3.0
## [23] BiocNeighbors_2.0.1       uwot_0.2.2
## [25] curl_6.2.0               mime_0.12
## [27] evaluate_1.0.3           tidytree_0.4.6
## [29] coin_1.4-3               stringi_1.8.4
## [31] rjags_4-16               parallelDist_0.2.6
## [33] XML_3.99-0.18            httpuv_1.6.15
## [35] AnnotationDbi_1.68.0     magrittr_2.0.3
## [37] rappdirs_0.3.3           splines_4.4.0
## [39] RcppRoll_0.3.1           getopt_1.20.4

```

## [41]	logger_0.4.0	sctransform_0.4.1
## [43]	ggbeeswarm_0.7.2	sessioninfo_1.2.2
## [45]	DBI_1.2.3	HDF5Array_1.34.0
## [47]	jquerylib_0.1.4	withr_3.0.2
## [49]	systemfonts_1.2.1	xgboost_1.7.8.1
## [51]	lmtest_0.9-40	tidygraph_1.3.1
## [53]	formatR_1.14	rtracklayer_1.66.0
## [55]	htmlwidgets_1.6.4	SparseArray_1.6.1
## [57]	zoo_1.8-12	XVector_0.46.0
## [59]	hahmmr_1.0.0	UCSC.utils_1.2.0
## [61]	RhpcBLASctl_0.23-42	timechange_0.3.0
## [63]	foreach_1.5.2	caTools_1.18.3
## [65]	ggtree_3.15.0	rhdf5_2.50.2
## [67]	quantreg_6.00	janeaustrer_1.0.0
## [69]	alabaster.schemas_1.6.0	gridGraphics_0.5-1
## [71]	ellipsis_0.3.2	lazyeval_0.2.2
## [73]	phyclust_0.1-34	survival_3.8-3
## [75]	scattermore_1.2	BiocVersion_3.20.0
## [77]	crayon_1.5.3	RcppAnnoy_0.0.22
## [79]	progressr_0.15.1	tweenr_2.0.3
## [81]	scistree_1.2.0	later_1.4.1
## [83]	ggridges_0.5.6	codetools_0.2-20
## [85]	profvis_0.4.0	KEGGREST_1.46.0
## [87]	Rtsne_0.17	limma_3.62.2
## [89]	gdtools_0.4.1	Rsamtools_2.22.0
## [91]	filelock_1.0.3	pkgconfig_2.0.3
## [93]	xml2_1.3.6	spatstat.univar_3.1-1
## [95]	GenomicAlignments_1.42.0	aplot_0.2.4
## [97]	spatstat.sparse_3.1-0	alabaster.base_1.6.1
## [99]	ape_5.8-1	viridisLite_0.4.2
## [101]	xtable_1.8-4	fastcluster_1.2.6
## [103]	plyr_1.8.9	httr_1.4.7
## [105]	tools_4.4.0	globals_0.16.3
## [107]	pkgbuild_1.4.6	beeswarm_0.4.0
## [109]	nlme_3.1-167	futile.logger_1.4.3
## [111]	lambda.r_1.2.4	dbplyr_2.5.0
## [113]	ExperimentHub_2.14.0	MatrixModels_0.5-3
## [115]	digest_0.6.37	farver_2.1.2
## [117]	tzdb_0.4.0	SnowballC_0.7.1
## [119]	yulab.utils_0.2.0	viridis_0.6.5
## [121]	cachem_1.1.0	BiocFileCache_2.14.0
## [123]	polyclip_1.10-7	generics_0.1.3
## [125]	Biostrings_2.74.1	mvtnorm_1.3-3
## [127]	parallelly_1.42.0	pkgload_1.4.0
## [129]	statmod_1.5.0	ragg_1.3.3
## [131]	ScaledMatrix_1.14.0	fontBitstreamVera_0.1.1
## [133]	pbapply_1.7-2	httr2_1.1.0
## [135]	spam_2.11-1	dqrng_0.4.1
## [137]	graphlayouts_1.2.2	gtools_3.9.5
## [139]	alabaster.se_1.6.0	GenomeInfoDbData_1.2.13
## [141]	rhdf5filters_1.18.0	RCurl_1.98-1.16

## [143] memoise_2.0.1	rmarkdown_2.29
## [145] scales_1.3.0	gypsum_1.2.0
## [147] RANN_2.6.2	fontLiberation_0.1.0
## [149] spatstat.data_3.1-4	cluster_2.1.8
## [151] spatstat.utils_3.1-2	hms_1.1.3
## [153] fitdistrplus_1.2-2	munsell_0.5.1
## [155] colorspace_2.1-1	rlang_1.1.5
## [157] quadprog_1.5-8	DelayedMatrixStats_1.28.1
## [159] sparseMatrixStats_1.18.0	dotCall64_1.2
## [161] ggforce_0.4.2	xfun_0.50
## [163] alabaster.matrix_1.6.1	coda_0.19-4.1
## [165] TH.data_1.1-3	iterators_1.0.14
## [167] modeltools_0.2-23	abind_1.4-8
## [169] libcoin_1.0-10	treeio_1.30.0
## [171] ggsci_3.2.0	Rhdf5lib_1.28.0
## [173] futile.options_1.0.1	bitops_1.0-9
## [175] promises_1.3.2	RSQLite_2.3.9
## [177] sandwich_3.1-1	DelayedArray_0.32.0
## [179] compiler_4.4.0	alabaster.ranges_1.6.0
## [181] beachmat_2.22.0	SparseM_1.84-2
## [183] polynom_1.4-1	listenv_0.9.1
## [185] fontquiver_0.2.1	edgeR_4.4.2
## [187] AnnotationHub_3.14.0	BiocSingular_1.22.0
## [189] tensor_1.5	MASS_7.3-64
## [191] uuid_1.2-1	BiocParallel_1.40.0
## [193] spatstat.random_3.3-2	R6_2.5.1
## [195] fastmap_1.2.0	multcomp_1.4-28
## [197] fastmatch_1.1-6	vipor_0.4.7
## [199] ROCR_1.0-11	ggstats_0.8.0
## [201] rsvd_1.0.5	nnet_7.3-20
## [203] gtable_0.3.6	phangorn_2.12.1
## [205] KernSmooth_2.23-26	miniUI_0.1.1.1
## [207] deldir_2.0-4	htmltools_0.5.8.1
## [209] RcppParallel_5.1.10	bit64_4.6.0-1
## [211] spatstat.explore_3.3-4	lifecycle_1.0.4
## [213] zip_2.3.2	restfulr_0.0.15
## [215] sass_0.4.9	vctrs_0.6.5
## [217] spatstat.geom_3.3-5	scraper_1.34.0
## [219] ggfun_0.1.8	sp_2.2-0
## [221] future.apply_1.11.3	bslib_0.9.0
## [223] pillar_1.10.1	gplots_3.2.0
## [225] metapod_1.14.0	locfit_1.5-9.11
## [227] jsonlite_1.8.9	argparse_2.2.5