

# Data exploratory analysis

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-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-p-r0.3.20.so; LAPACK vers
##
## locale:
## [1] LC_CTYPE=en_US.UTF-8 LC_NUMERIC=C
## [3] LC_TIME=en_US.UTF-8 LC_COLLATE=en_US.UTF-8
## [5] LC_MONETARY=en_US.UTF-8 LC_MESSAGES=en_US.UTF-8
## [7] LC_PAPER=en_US.UTF-8 LC_NAME=C
## [9] LC_ADDRESS=C LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=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] yaml_2.3.10 tinytex_0.54
## [3] lubridate_1.9.3 dplyr_1.1.4
## [5] readr_2.1.5 tidyr_1.3.1
## [7] tibble_3.2.1 tidyverse_2.0.0
## [9] tidytext_0.4.2 stringr_1.5.1
## [11] SoupX_1.6.2 shiny_1.9.1
## [13] SeuratObject_5.0.2 Seurat_4.4.0
```

```

## [15] R.utils_2.12.3          R.oo_1.27.0
## [17] R.methodsS3_1.8.2       rlist_0.4.6.2
## [19] rliqer_2.1.0            reshape2_1.4.4
## [21] RColorBrewer_1.1-3      purrr_1.0.2
## [23] patchwork_1.3.0         optparse_1.7.5
## [25] leiden_0.4.3.1          knitr_1.49
## [27] irlba_2.3.5.1           igraph_2.1.1
## [29] hdf5r_1.3.11            harmony_1.2.3
## [31] Rcpp_1.0.13-1           ggthemes_5.1.0
## [33] ggrepel_0.9.6           ggpmisc_0.6.1
## [35] ggpp_0.5.8-1            ggh4x_0.2.8
## [37] GGally_2.2.1            future_1.34.0
## [39] fs_1.6.5                forcats_1.0.0
## [41] flextable_0.9.7         flexmix_2.3-19
## [43] lattice_0.22-6          data.table_1.16.2
## [45] cowplot_1.1.3           clustree_0.5.1
## [47] ggraph_2.2.1            numbat_1.4.2
## [49] Matrix_1.7-0            RcppPlanc_1.0.0
## [51] scooter_0.0.0.9004       infercnv_1.22.0
## [53] SingleR_2.8.0           celldex_1.16.0
## [55] scDblFinder_1.20.0      scater_1.34.0
## [57] ggplot2_3.5.1           scuttle_1.16.0
## [59] SingleCellExperiment_1.28.1 SummarizedExperiment_1.36.0
## [61] Biobase_2.66.0          GenomicRanges_1.58.0
## [63] GenomeInfoDb_1.42.1     IRanges_2.40.0
## [65] S4Vectors_0.44.0        BiocGenerics_0.52.0
## [67] MatrixGenerics_1.18.0   matrixStats_1.4.1
## [69] miQC_1.14.0             remotes_2.5.0
## [71] devtools_2.4.5          usethis_3.1.0
## [73] 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                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_2.2.2
## [17] goftest_1.2-3            textshaping_0.4.0
## [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_6.0.1              mime_0.12
## [27] evaluate_1.0.1           tidytree_0.4.6
## [29] coin_1.4-3               stringi_1.8.4
## [31] rjags_4-16               parallelDist_0.2.6
## [33] XML_3.99-0.17           httpuv_1.6.15
## [35] AnnotationDbi_1.68.0     magrittr_2.0.3
## [37] rappdirs_0.3.3          splines_4.4.0

```

## [39]	getopt_1.20.4	logger_0.4.0
## [41]	sctransform_0.4.1	ggbeeswarm_0.7.2
## [43]	sessioninfo_1.2.2	DBI_1.2.3
## [45]	HDF5Array_1.34.0	jquerylib_0.1.4
## [47]	withr_3.0.2	systemfonts_1.1.0
## [49]	rprojroot_2.0.4	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_1.6.0
## [57]	reticulate_1.40.0	zoo_1.8-12
## [59]	XVector_0.46.0	hahmmr_1.0.0
## [61]	UCSC.utils_1.2.0	RhpcBLASctl_0.23-42
## [63]	timechange_0.3.0	foreach_1.5.2
## [65]	fansi_1.0.6	caTools_1.18.3
## [67]	ggtree_3.10.1	rhdf5_2.50.0
## [69]	quantreg_5.99.1	janeaustenr_1.0.0
## [71]	alabaster.schemas_1.6.0	gridGraphics_0.5-1
## [73]	ellipsis_0.3.2	lazyeval_0.2.2
## [75]	phyclust_0.1-34	survival_3.5-8
## [77]	scattermore_1.2	BiocVersion_3.20.0
## [79]	crayon_1.5.3	RcppAnnoy_0.0.22
## [81]	progressr_0.15.1	tweenr_2.0.3
## [83]	scistree_1.2.0	later_1.4.1
## [85]	ggribes_0.5.6	codetools_0.2-20
## [87]	profvis_0.4.0	KEGGREST_1.46.0
## [89]	Rtsne_0.17	limma_3.62.1
## [91]	gdtools_0.4.1	Rsamtools_2.22.0
## [93]	filelock_1.0.3	pkgconfig_2.0.3
## [95]	xml2_1.3.6	spatstat.univar_3.1-1
## [97]	GenomicAlignments_1.42.0	aplot_0.2.3
## [99]	spatstat.sparse_3.1-0	alabaster.base_1.6.1
## [101]	ape_5.8	viridisLite_0.4.2
## [103]	xtable_1.8-4	fastcluster_1.2.6
## [105]	plyr_1.8.9	httr_1.4.7
## [107]	tools_4.4.0	globals_0.16.3
## [109]	pkgbuild_1.4.5	beeswarm_0.4.0
## [111]	nlme_3.1-164	futile.logger_1.4.3
## [113]	lambda.r_1.2.4	dbplyr_2.5.0
## [115]	ExperimentHub_2.14.0	MatrixModels_0.5-3
## [117]	digest_0.6.37	farver_2.1.2
## [119]	tzdb_0.4.0	SnowballC_0.7.1
## [121]	yulab.utils_0.1.8	viridis_0.6.5
## [123]	glue_1.8.0	cachem_1.1.0
## [125]	BiocFileCache_2.14.0	polycip_1.10-7
## [127]	generics_0.1.3	Biostrings_2.74.0
## [129]	mvtnorm_1.3-2	parallelly_1.39.0
## [131]	pkgload_1.4.0	statmod_1.5.0
## [133]	here_1.0.1	ragg_1.3.3
## [135]	ScaledMatrix_1.14.0	fontBitstreamVera_0.1.1
## [137]	pbapply_1.7-2	httr2_1.0.7
## [139]	spam_2.11-0	dqrng_0.4.1

## [141]	utf8_1.2.4	graphlayouts_1.2.1
## [143]	gtools_3.9.5	alabaster.se_1.6.0
## [145]	gridExtra_2.3	GenomeInfoDbData_1.2.13
## [147]	rhdf5filters_1.18.0	RCurl_1.98-1.16
## [149]	memoise_2.0.1	rmarkdown_2.29
## [151]	scales_1.3.0	gypsum_1.2.0
## [153]	RANN_2.6.2	fontLiberation_0.1.0
## [155]	spatstat.data_3.1-4	cluster_2.1.6
## [157]	spatstat.utils_3.1-1	hms_1.1.3
## [159]	fitdistrplus_1.2-1	munsell_0.5.1
## [161]	colorspace_2.1-1	rlang_1.1.4
## [163]	quadprog_1.5-8	DelayedMatrixStats_1.28.0
## [165]	sparseMatrixStats_1.18.0	dotCall64_1.2
## [167]	ggforce_0.4.2	xfun_0.49
## [169]	alabaster.matrix_1.6.1	coda_0.19-4.1
## [171]	TH.data_1.1-2	iterators_1.0.14
## [173]	modeltools_0.2-23	abind_1.4-8
## [175]	libcoin_1.0-10	treeio_1.26.0
## [177]	ggsci_3.2.0	Rhdf5lib_1.28.0
## [179]	futile.options_1.0.1	bitops_1.0-9
## [181]	promises_1.3.2	RSQLite_2.3.8
## [183]	sandwich_3.1-1	DelayedArray_0.32.0
## [185]	compiler_4.4.0	alabaster.ranges_1.6.0
## [187]	beachmat_2.22.0	SparseM_1.84-2
## [189]	polynom_1.4-1	listenv_0.9.1
## [191]	fontquiver_0.2.1	edgeR_4.4.0
## [193]	AnnotationHub_3.14.0	BiocSingular_1.22.0
## [195]	tensor_1.5	MASS_7.3-60.2
## [197]	uuid_1.2-1	BiocParallel_1.40.0
## [199]	spatstat.random_3.3-2	R6_2.5.1
## [201]	fastmap_1.2.0	multcomp_1.4-26
## [203]	fastmatch_1.1-4	vipor_0.4.7
## [205]	ROCR_1.0-11	ggstats_0.7.0
## [207]	rsvd_1.0.5	nnet_7.3-19
## [209]	gtable_0.3.6	phangorn_2.12.1
## [211]	KernSmooth_2.23-22	miniUI_0.1.1.1
## [213]	deldir_2.0-4	htmltools_0.5.8.1
## [215]	RcppParallel_5.1.9	bit64_4.5.2
## [217]	spatstat.explore_3.3-3	lifecycle_1.0.4
## [219]	zip_2.3.1	restfulr_0.0.15
## [221]	sass_0.4.9	vctrs_0.6.5
## [223]	spatstat.geom_3.3-4	scraper_1.34.0
## [225]	ggfun_0.1.7	sp_2.1-4
## [227]	future.apply_1.11.3	bslib_0.8.0
## [229]	pillar_1.9.0	gplots_3.2.0
## [231]	metapod_1.14.0	locfit_1.5-9.10
## [233]	jsonlite_1.8.9	argparse_2.2.4