

Data exploratory analysis

Antonia Chroni for SJCRH DNB_BINF_Core

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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-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
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## [15] R.utils_2.12.3          R.oo_1.27.0
## [17] R.methodsS3_1.8.2       rlist_0.4.6.2
## [19] rliqer_2.1.0.9001       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_0.6.0
## [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_0.9.6         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_0.6.6            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

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## [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_5.98	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]	gfonts_0.2.0	ggridges_0.5.6
## [87]	codetools_0.2-20	profvis_0.4.0
## [89]	KEGGREST_1.46.0	Rtsne_0.17
## [91]	limma_3.62.1	gdtools_0.3.7
## [93]	Rsamtools_2.22.0	filelock_1.0.3
## [95]	pkgconfig_2.0.3	xml2_1.3.6
## [97]	spatstat.univar_3.1-1	GenomicAlignments_1.42.0
## [99]	aplot_0.2.3	spatstat.sparse_3.1-0
## [101]	alabaster.base_1.6.1	ape_5.8
## [103]	viridisLite_0.4.2	xtable_1.8-4
## [105]	fastcluster_1.2.6	plyr_1.8.9
## [107]	httr_1.4.7	tools_4.4.0
## [109]	globals_0.16.3	pkgbuild_1.4.5
## [111]	beeswarm_0.4.0	nlme_3.1-164
## [113]	futile.logger_1.4.3	lambda.r_1.2.4
## [115]	dbplyr_2.5.0	ExperimentHub_2.14.0
## [117]	MatrixModels_0.5-3	digest_0.6.37
## [119]	farver_2.1.2	tzdb_0.4.0
## [121]	SnowballC_0.7.1	yulab.utils_0.1.8
## [123]	viridis_0.6.5	crul_1.5.0
## [125]	glue_1.8.0	cachem_1.1.0
## [127]	BiocFileCache_2.14.0	polycip_1.10-7
## [129]	generics_0.1.3	Biostrings_2.74.0
## [131]	mvtnorm_1.3-2	parallelly_1.39.0
## [133]	pkgload_1.4.0	statmod_1.5.0
## [135]	here_1.0.1	ragg_1.3.3
## [137]	ScaledMatrix_1.14.0	fontBitstreamVera_0.1.1
## [139]	pbapply_1.7-2	httr2_1.0.7

## [141] spam_2.11-0	dqrng_0.4.1
## [143] utf8_1.2.4	graphlayouts_1.2.1
## [145] gtools_3.9.5	alabaster.se_1.6.0
## [147] httpcode_0.3.0	gridExtra_2.3
## [149] GenomeInfoDbData_1.2.13	rhdf5filters_1.18.0
## [151] RCurl_1.98-1.16	memoise_2.0.1
## [153] rmarkdown_2.29	scales_1.3.0
## [155] gypsum_1.2.0	RANN_2.6.2
## [157] fontLiberation_0.1.0	spatstat.data_3.1-4
## [159] cluster_2.1.6	spatstat.utils_3.1-1
## [161] hms_1.1.3	fitdistrplus_1.2-1
## [163] munsell_0.5.1	colorspace_2.1-1
## [165] rlang_1.1.4	quadprog_1.5-8
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## [169] dotCall64_1.2	ggforce_0.4.2
## [171] xfun_0.49	alabaster.matrix_1.6.1
## [173] coda_0.19-4.1	TH.data_1.1-2
## [175] iterators_1.0.14	modeltools_0.2-23
## [177] abind_1.4-8	libcoin_1.0-10
## [179] treeio_1.26.0	ggsci_3.2.0
## [181] Rhdf5lib_1.28.0	futile.options_1.0.1
## [183] bitops_1.0-9	promises_1.3.2
## [185] RSQLite_2.3.8	sandwich_3.1-1
## [187] DelayedArray_0.32.0	compiler_4.4.0
## [189] alabaster.ranges_1.6.0	beachmat_2.22.0
## [191] SparseM_1.84-2	polynom_1.4-1
## [193] listenv_0.9.1	fontquiver_0.2.1
## [195] edgeR_4.4.0	AnnotationHub_3.14.0
## [197] BiocSingular_1.22.0	tensor_1.5
## [199] MASS_7.3-60.2	uuid_1.2-1
## [201] BiocParallel_1.40.0	spatstat.random_3.3-2
## [203] R6_2.5.1	fastmap_1.2.0
## [205] multcomp_1.4-26	fastmatch_1.1-4
## [207] vipor_0.4.7	ROCR_1.0-11
## [209] ggstats_0.6.0	rsvd_1.0.5
## [211] nnet_7.3-19	gtable_0.3.6
## [213] phangorn_2.12.1	KernSmooth_2.23-22
## [215] miniUI_0.1.1.1	deldir_2.0-4
## [217] htmltools_0.5.8.1	RcppParallel_5.1.9
## [219] bit64_4.5.2	spatstat.explore_3.3-3
## [221] lifecycle_1.0.4	zip_2.3.1
## [223] restfulr_0.0.15	sass_0.4.9
## [225] vctrs_0.6.5	spatstat.geom_3.3-4
## [227] scan_1.34.0	ggfun_0.1.7
## [229] sp_2.1-4	future.apply_1.11.3
## [231] bslib_0.8.0	pillar_1.9.0
## [233] gplots_3.2.0	metapod_1.14.0
## [235] locfit_1.5-9.10	jsonlite_1.8.9
## [237] argparse_2.2.4	