

Debugging step: Verify installations for LSF

Antonia Chroni for SJCRH DNB_BINF_Core

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1 Set up

```
suppressPackageStartupMessages({  
  # 01A_run_seurat_qc.Rmd  
  library(future)  
  library(cowplot)  
  library(devtools)  
  library(forcats)  
  library(GGally)  
  library(stringr)  
  library(ggpmisc)  
  library(ggrepel)  
  library(miQC)  
  library(flexmix) # to estimate mixtureModel for miQC  
  library(scater)  
  library(Seurat)  
  library(SingleCellExperiment)  
  library(irlba) # this solves the issue with RunUMAP code chunk  
  library(scooter)  
  library(tidyverse)  
  library(fs) #file system  
  library(RColorBrewer)  
  
  # 02_run_SoupX.Rmd  
  library(future)  
  library(knitr)  
  library(SoupX)  
  library(Seurat)  
  library(stringr)  
  library(tidyverse)  
  library(tinytex)  
  library(hdf5r)  
  
  # 03_run_scDblFinder.Rmd  
  library(scDblFinder)
```

```

library(Seurat)
library(scater)
library(future)
library(tidyverse)
library(grid)
library(knitr)

# 04_run_filter_object.Rmd
library(devtools)
library(future)
library(Seurat)
library(patchwork)
library(tidyverse)
library(ggthemes)
library(scooter)
library(RColorBrewer)
library(knitr)

# 05_run_summary_report.Rmd
library(tidyverse)
library(knitr)
library(patchwork)

# 01-integrative-analysis.Rmd
library(future)
library(tidyverse)
library(patchwork)
library(Seurat)
library(SeuratObject)
library(harmony)
library(rliger)
library(RcppPlanc)
library(SeuratWrappers)
library(scooter)
library(reshape2)
library(RColorBrewer)
library(knitr)

# run-cell-types-annotation.R
library(yaml)
library(tidyverse)
library(celldex)

# 01-cell-types-annotation-SingleR-broad.Rmd
library(tidyverse)
library(Seurat)
library(SingleR)
library(scooter)
library(knitr)

})

```

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] SingleR_2.8.0             celldex_1.16.0
##  [3] yaml_2.3.10              reshape2_1.4.4
##  [5] SeuratWrappers_0.2.0      RcppPlanc_1.0.0
##  [7] rlgier_2.1.0             harmony_1.2.3
##  [9] Rcpp_1.0.13-1            ggthemes_5.1.0
## [11] patchwork_1.3.0          scDblFinder_1.20.0
## [13] hdf5r_1.3.11            tinytex_0.54
## [15] SoupX_1.6.2              knitr_1.49
## [17] RColorBrewer_1.1-3       fs_1.6.5
## [19] lubridate_1.9.4          dplyr_1.1.4
## [21] purrr_1.0.2             readr_2.1.5
## [23] tidyr_1.3.1             tibble_3.2.1
## [25] tidyverse_2.0.0          scooter_0.0.0.9004
## [27] irlba_2.3.5.1           Matrix_1.7-0
## [29] SeuratObject_5.0.2       Seurat_4.4.0
## [31] scater_1.34.0            scuttle_1.16.0
## [33] SingleCellExperiment_1.28.1 SummarizedExperiment_1.36.0
## [35] Biobase_2.66.0          GenomicRanges_1.58.0
## [37] GenomeInfoDb_1.42.1     IRanges_2.40.1
## [39] S4Vectors_0.44.0        BiocGenerics_0.52.0
## [41] MatrixGenerics_1.18.0    matrixStats_1.4.1
## [43] flexmix_2.3-19          lattice_0.22-6
## [45] miQC_1.14.0             ggrepel_0.9.6
## [47] ggpmisc_0.6.1           ggpp_0.5.8-1
## [49] stringr_1.5.1           GGally_2.2.1
## [51] ggplot2_3.5.1           forcats_1.0.0
## [53] devtools_2.4.5          usethis_3.1.0
## [55] cowplot_1.1.3           future_1.34.0
##
## loaded via a namespace (and not attached):
```

## [1] urlchecker_1.0.1	nnet_7.3-19
## [3] goftest_1.2-3	HDF5Array_1.34.0
## [5] Biostrings_2.74.1	vctrs_0.6.5
## [7] spatstat.random_3.3-2	digest_0.6.37
## [9] png_0.1-8	gypsum_1.2.0
## [11] deldir_2.0-4	parallelly_1.41.0
## [13] MASS_7.3-60.2	httpuv_1.6.15
## [15] withr_3.0.2	xfun_0.49
## [17] ellipsis_0.3.2	survival_3.5-8
## [19] memoise_2.0.1	ggbeeswarm_0.7.2
## [21] MatrixModels_0.5-3	profvis_0.4.0
## [23] ggsci_3.2.0	zoo_1.8-12
## [25] pbapply_1.7-2	KEGGREST_1.46.0
## [27] promises_1.3.2	httr_1.4.7
## [29] restfulr_0.0.15	globals_0.16.3
## [31] fitdistrplus_1.2-1	rhdf5filters_1.18.0
## [33] rhdf5_2.50.1	UCSC.utils_1.2.0
## [35] miniUI_0.1.1.1	generics_0.1.3
## [37] curl_6.0.1	zlibbioc_1.52.0
## [39] ScaledMatrix_1.14.0	polyclip_1.10-7
## [41] GenomeInfoDbData_1.2.13	ExperimentHub_2.14.0
## [43] SparseArray_1.6.0	xtable_1.8-4
## [45] evaluate_1.0.1	S4Arrays_1.6.0
## [47] BiocFileCache_2.14.0	hms_1.1.3
## [49] colorspace_2.1-1	filelock_1.0.3
## [51] polynom_1.4-1	ROCR_1.0-11
## [53] reticulate_1.40.0	spatstat.data_3.1-4
## [55] magrittr_2.0.3	lmtest_0.9-40
## [57] later_1.4.1	viridis_0.6.5
## [59] modeltools_0.2-23	spatstat.geom_3.3-4
## [61] future.apply_1.11.3	SparseM_1.84-2
## [63] scattermore_1.2	XML_3.99-0.17
## [65] RcppAnnoy_0.0.22	pillar_1.10.0
## [67] nlme_3.1-164	compiler_4.4.0
## [69] beachmat_2.22.0	stringi_1.8.4
## [71] tensor_1.5	GenomicAlignments_1.42.0
## [73] plyr_1.8.9	crayon_1.5.3
## [75] abind_1.4-8	BiocIO_1.16.0
## [77] locfit_1.5-9.10	sp_2.1-4
## [79] bit_4.5.0.1	codetools_0.2-20
## [81] BiocSingular_1.22.0	bslib_0.8.0
## [83] alabaster.ranges_1.6.0	plotly_4.10.4
## [85] mime_0.12	splines_4.4.0
## [87] quantreg_5.99.1	dbplyr_2.5.0
## [89] sparseMatrixStats_1.18.0	blob_1.2.4
## [91] BiocVersion_3.20.0	listenv_0.9.1
## [93] DelayedMatrixStats_1.28.0	pkgbuild_1.4.5
## [95] statmod_1.5.0	tzdb_0.4.0
## [97] pkgconfig_2.0.3	tools_4.4.0
## [99] cachem_1.1.0	RSQLite_2.3.9
## [101] viridisLite_0.4.2	DBI_1.2.3

## [103] fastmap_1.2.0	rmarkdown_2.29
## [105] scales_1.3.0	ica_1.0-3
## [107] Rsamtools_2.22.0	AnnotationHub_3.14.0
## [109] sass_0.4.9	BiocManager_1.30.25
## [111] ggstats_0.7.0	dotCall64_1.2
## [113] RANN_2.6.2	alabaster.schemas_1.6.0
## [115] farver_2.1.2	rtracklayer_1.66.0
## [117] cli_3.6.3	leiden_0.4.3.1
## [119] lifecycle_1.0.4	uwot_0.2.2
## [121] bluster_1.16.0	sessioninfo_1.2.2
## [123] BiocParallel_1.40.0	timechange_0.3.0
## [125] gtable_0.3.6	rjson_0.2.23
## [127] ggribes_0.5.6	progressr_0.15.1
## [129] parallel_4.4.0	limma_3.62.1
## [131] jsonlite_1.8.9	edgeR_4.4.1
## [133] bitops_1.0-9	bit64_4.5.2
## [135] xgboost_1.7.8.1	Rtsne_0.17
## [137] alabaster.matrix_1.6.1	spatstat.utils_3.1-1
## [139] BiocNeighbors_2.0.1	alabaster.se_1.6.0
## [141] jquerylib_0.1.4	metapod_1.14.0
## [143] dqrng_0.4.1	spatstat.univar_3.1-1
## [145] lazyeval_0.2.2	alabaster.base_1.6.1
## [147] shiny_1.10.0	htmltools_0.5.8.1
## [149] sctransform_0.4.1	rappdirs_0.3.3
## [151] glue_1.8.0	spam_2.11-0
## [153] httr2_1.0.7	XVector_0.46.0
## [155] RCurl_1.98-1.16	scraper_1.34.0
## [157] gridExtra_2.3	igraph_2.1.2
## [159] R6_2.5.1	cluster_2.1.6
## [161] pkgload_1.4.0	Rhdf5lib_1.28.0
## [163] DelayedArray_0.32.0	tidyselect_1.2.1
## [165] vipor_0.4.7	AnnotationDbi_1.68.0
## [167] rsvd_1.0.5	munsell_0.5.1
## [169] KernSmooth_2.23-22	data.table_1.16.4
## [171] htmlwidgets_1.6.4	rlang_1.1.4
## [173] spatstat.sparse_3.1-0	spatstat.explore_3.3-3
## [175] remotes_2.5.0	beeswarm_0.4.0