

Debugging step: Verify installations for LSF

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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)

```

```
library(ShinyCell)
library(shinyhelper)
library(DT)
library(ggdendro)
})
```

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-p-r0.3.20.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] ggdendro_0.2.0      DT_0.33
## [3] shinyhelper_0.3.2   ShinyCell_2.1.0
## [5] glue_1.8.0          gridExtra_2.3
## [7] R.utils_2.12.3      R.oo_1.27.0
## [9] R.methodsS3_1.8.2   reticulate_1.40.0
## [11] data.table_1.16.4   SingleR_2.8.0
## [13] celldex_1.16.0      yaml_2.3.10
## [15] reshape2_1.4.4      SeuratWrappers_0.2.0
## [17] RcppPlanc_1.0.0     rliqer_2.1.0.9004
## [19] harmony_1.2.3       Rcpp_1.0.14
## [21] ggthemes_5.1.0      patchwork_1.3.0
## [23] scDblFinder_1.20.0  hdf5r_1.3.12
## [25] tinytex_0.54        SoupX_1.6.2
## [27] knitr_1.49          RColorBrewer_1.1-3
## [29] fs_1.6.5            lubridate_1.9.4
## [31] dplyr_1.1.4         purrr_1.0.2
## [33] readr_2.1.5         tidyr_1.3.1
## [35] tibble_3.2.1        tidyverse_2.0.0
## [37] scooter_0.0.0.9004   irlba_2.3.5.1
## [39] Matrix_1.7-2        SeuratObject_5.0.2
## [41] Seurat_4.4.0        scater_1.34.0
## [43] scuttle_1.16.0      SingleCellExperiment_1.28.1
## [45] SummarizedExperiment_1.36.0 Biobase_2.66.0
```

```

## [47] GenomicRanges_1.58.0      GenomeInfoDb_1.42.3
## [49] IRanges_2.40.1            S4Vectors_0.44.0
## [51] BiocGenerics_0.52.0       MatrixGenerics_1.18.1
## [53] matrixStats_1.5.0        flexmix_2.3-19
## [55] lattice_0.22-6           miQC_1.14.0
## [57] ggrepel_0.9.6            ggpmisc_0.6.1
## [59] ggpp_0.5.8-1             stringr_1.5.1
## [61] GGally_2.2.1             ggplot2_3.5.1
## [63] forcats_1.0.0           devtools_2.4.5
## [65] usethis_3.1.0           cowplot_1.1.3
## [67] future_1.34.0
##
## loaded via a namespace (and not attached):
## [1] urlchecker_1.0.1         nnet_7.3-20
## [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_1.42.0
## [13] MASS_7.3-64            httpuv_1.6.15
## [15] withr_3.0.2            xfun_0.50
## [17] ellipsis_0.3.2         survival_3.8-3
## [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_1.2-2     rhdf5filters_1.18.0
## [33] rhdf5_2.50.2           UCSC.utils_1.2.0
## [35] miniUI_0.1.1.1         generics_0.1.3
## [37] curl_6.2.0            zlibbioc_1.52.0
## [39] ScaledMatrix_1.14.0    polyclip_1.10-7
## [41] GenomeInfoDbData_1.2.13 ExperimentHub_2.14.0
## [43] SparseArray_1.6.1      xtable_1.8-4
## [45] evaluate_1.0.3         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] spatstat.data_3.1-4    magrittr_2.0.3
## [55] lmtest_0.9-40         later_1.4.1
## [57] viridis_0.6.5         modeltools_0.2-23
## [59] spatstat.geom_3.3-5    future.apply_1.11.3
## [61] SparseM_1.84-2         scattermore_1.2
## [63] XML_3.99-0.18         RcppAnnoy_0.0.22
## [65] pillar_1.10.1         nlme_3.1-167
## [67] compiler_4.4.0        beachmat_2.22.0
## [69] stringi_1.8.4         tensor_1.5
## [71] GenomicAlignments_1.42.0 plyr_1.8.9
## [73] crayon_1.5.3          abind_1.4-8
## [75] BiocIO_1.16.0         locfit_1.5-9.11

```

## [77] sp_2.2-0	bit_4.5.0.1
## [79] codetools_0.2-20	BiocSingular_1.22.0
## [81] bslib_0.9.0	alabaster.ranges_1.6.0
## [83] plotly_4.10.4	mime_0.12
## [85] splines_4.4.0	quantreg_6.00
## [87] dbplyr_2.5.0	sparseMatrixStats_1.18.0
## [89] blob_1.2.4	BiocVersion_3.20.0
## [91] listenv_0.9.1	DelayedMatrixStats_1.28.1
## [93] pkgbuild_1.4.6	statmod_1.5.0
## [95] tzdb_0.4.0	pkgconfig_2.0.3
## [97] tools_4.4.0	cachem_1.1.0
## [99] RSQLite_2.3.9	viridisLite_0.4.2
## [101] DBI_1.2.3	fastmap_1.2.0
## [103] rmarkdown_2.29	scales_1.3.0
## [105] ica_1.0-3	Rsamtools_2.22.0
## [107] AnnotationHub_3.14.0	sass_0.4.9
## [109] BiocManager_1.30.25	ggstats_0.8.0
## [111] dotCall64_1.2	RANN_2.6.2
## [113] alabaster.schemas_1.6.0	farver_2.1.2
## [115] rtracklayer_1.66.0	cli_3.6.3
## [117] leiden_0.4.3.1	lifecycle_1.0.4
## [119] uwot_0.2.2	bluster_1.16.0
## [121] sessioninfo_1.2.2	BiocParallel_1.40.0
## [123] timechange_0.3.0	gtable_0.3.6
## [125] rjson_0.2.23	ggribes_0.5.6
## [127] progressr_0.15.1	parallel_4.4.0
## [129] limma_3.62.2	jsonlite_1.8.9
## [131] edgeR_4.4.2	bitops_1.0-9
## [133] bit64_4.6.0-1	xgboost_1.7.8.1
## [135] Rtsne_0.17	alabaster.matrix_1.6.1
## [137] spatstat.utils_3.1-2	BiocNeighbors_2.0.1
## [139] alabaster.se_1.6.0	jquerylib_0.1.4
## [141] metapod_1.14.0	dqrng_0.4.1
## [143] spatstat.univar_3.1-1	lazyeval_0.2.2
## [145] alabaster.base_1.6.1	shiny_1.10.0
## [147] htmltools_0.5.8.1	sctransform_0.4.1
## [149] rappdirs_0.3.3	spam_2.11-1
## [151] httr2_1.1.0	XVector_0.46.0
## [153] RCurl_1.98-1.16	scran_1.34.0
## [155] igraph_2.1.4	R6_2.5.1
## [157] cluster_2.1.8	pkgload_1.4.0
## [159] Rhdf5lib_1.28.0	DelayedArray_0.32.0
## [161] tidyselect_1.2.1	vipor_0.4.7
## [163] AnnotationDbi_1.68.0	rsvd_1.0.5
## [165] munsell_0.5.1	KernSmooth_2.23-26
## [167] htmlwidgets_1.6.4	rlang_1.1.5
## [169] spatstat.sparse_3.1-0	spatstat.explore_3.3-4
## [171] remotes_2.5.0	beeswarm_0.4.0