

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-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] 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] yaml_2.3.10          reshape2_1.4.4
## [15] SeuratWrappers_0.2.0 rliqer_2.1.0
## [17] harmony_1.2.3        Rcpp_1.0.14
## [19] ggthemes_5.1.0       patchwork_1.3.0
## [21] scDblFinder_1.20.0   hdf5r_1.3.12
## [23] tinytex_0.54         SoupX_1.6.2
## [25] knitr_1.49           RColorBrewer_1.1-3
## [27] fs_1.6.5             lubridate_1.9.4
## [29] dplyr_1.1.4          purrr_1.0.2
## [31] readr_2.1.5          tidyr_1.3.1
## [33] tibble_3.2.1         tidyverse_2.0.0
## [35] scooter_0.0.0.9004    irlba_2.3.5.1
## [37] Matrix_1.7-0         SeuratObject_5.0.2
## [39] Seurat_4.4.0         scater_1.34.0
## [41] scuttle_1.16.0       SingleCellExperiment_1.28.1
## [43] SummarizedExperiment_1.36.0 Biobase_2.66.0
## [45] GenomicRanges_1.58.0 GenomeInfoDb_1.42.3
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## [47] IRanges_2.40.1          S4Vectors_0.44.0
## [49] BiocGenerics_0.52.0     MatrixGenerics_1.18.1
## [51] matrixStats_1.5.0       flexmix_2.3-19
## [53] lattice_0.22-6          ggrepel_0.9.6
## [55] ggpmisc_0.6.1           ggpp_0.5.8-1
## [57] stringr_1.5.1           GGally_2.2.1
## [59] ggplot2_3.5.1           forcats_1.0.0
## [61] devtools_2.4.5          usethis_3.1.0
## [63] cowplot_1.1.3           future_1.34.0
##
## loaded via a namespace (and not attached):
## [1] spatstat.sparse_3.1-0    bitops_1.0-9
## [3] httr_1.4.7              ggsci_3.2.0
## [5] profvis_0.4.0           tools_4.4.0
## [7] sctransform_0.4.1       R6_2.5.1
## [9] lazyeval_0.2.2          uwot_0.2.2
## [11] urlchecker_1.0.1        withr_3.0.2
## [13] sp_2.1-4                progressr_0.15.1
## [15] quantreg_6.00           cli_3.6.3
## [17] spatstat.explore_3.3-4  sass_0.4.9
## [19] spatstat.data_3.1-4     ggribes_0.5.6
## [21] pbapply_1.7-2           Rsamtools_2.22.0
## [23] parallelly_1.41.0       sessioninfo_1.2.2
## [25] limma_3.62.2            BiocIO_1.16.0
## [27] generics_0.1.3          ica_1.0-3
## [29] spatstat.random_3.3-2   ggbeeswarm_0.7.2
## [31] abind_1.4-8             lifecycle_1.0.4
## [33] edgeR_4.4.2             SparseArray_1.6.1
## [35] Rtsne_0.17             dqrng_0.4.1
## [37] promises_1.3.2          crayon_1.5.3
## [39] miniUI_0.1.1.1          beachmat_2.22.0
## [41] metapod_1.14.0          pillar_1.10.1
## [43] rjson_0.2.23            xgboost_1.7.8.1
## [45] future.apply_1.11.3     codetools_0.2-20
## [47] leiden_0.4.3.1         spatstat.univar_3.1-1
## [49] remotes_2.5.0          vctrs_0.6.5
## [51] png_0.1-8              spam_2.11-1
## [53] gtable_0.3.6           cachem_1.1.0
## [55] xfun_0.50              S4Arrays_1.6.0
## [57] mime_0.12              survival_3.5-8
## [59] statmod_1.5.0          bluster_1.16.0
## [61] ellipsis_0.3.2         fitdistrplus_1.2-2
## [63] ROCR_1.0-11            nlme_3.1-164
## [65] bit64_4.6.0-1          RcppAnnoy_0.0.22
## [67] bslib_0.8.0            vipor_0.4.7
## [69] KernSmooth_2.23-22     colorspace_2.1-1
## [71] nnet_7.3-19            tidyselect_1.2.1
## [73] bit_4.5.0.1            compiler_4.4.0
## [75] curl_6.2.0             BiocNeighbors_2.0.1
## [77] SparseM_1.84-2         DelayedArray_0.32.0
## [79] plotly_4.10.4          rtracklayer_1.66.0

```

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## [81] scales_1.3.0          lmtest_0.9-40
## [83] digest_0.6.37         goftest_1.2-3
## [85] spatstat.utils_3.1-2  rmarkdown_2.29
## [87] XVector_0.46.0        htmltools_0.5.8.1
## [89] pkgconfig_2.0.3       sparseMatrixStats_1.18.0
## [91] fastmap_1.2.0         rlang_1.1.5
## [93] htmlwidgets_1.6.4     UCSC.utils_1.2.0
## [95] DelayedMatrixStats_1.28.1 shiny_1.10.0
## [97] farver_2.1.2          jquerylib_0.1.4
## [99] zoo_1.8-12            jsonlite_1.8.9
## [101] BiocParallel_1.40.0   BiocSingular_1.22.0
## [103] RCurl_1.98-1.16      magrittr_2.0.3
## [105] polynom_1.4-1         modeltools_0.2-23
## [107] GenomeInfoDbData_1.2.13 dotCall64_1.2
## [109] munsell_0.5.1         viridis_0.6.5
## [111] stringi_1.8.4         zlibbioc_1.52.0
## [113] MASS_7.3-60.2         plyr_1.8.9
## [115] pkgbuild_1.4.6        ggstats_0.8.0
## [117] parallel_4.4.0        listenv_0.9.1
## [119] deldir_2.0-4          Biostrings_2.74.1
## [121] splines_4.4.0         tensor_1.5
## [123] hms_1.1.3             locfit_1.5-9.10
## [125] igraph_2.1.4          spatstat.geom_3.3-5
## [127] ScaledMatrix_1.14.0   pkgload_1.4.0
## [129] XML_3.99-0.18         evaluate_1.0.3
## [131] BiocManager_1.30.25   scranner_1.34.0
## [133] tzdb_0.4.0            httpuv_1.6.15
## [135] MatrixModels_0.5-3    RANN_2.6.2
## [137] polyclip_1.10-7       scattermore_1.2
## [139] rsvd_1.0.5            xtable_1.8-4
## [141] restfulr_0.0.15       later_1.4.1
## [143] viridisLite_0.4.2     GenomicAlignments_1.42.0
## [145] memoise_2.0.1         beeswarm_0.4.0
## [147] cluster_2.1.6         timechange_0.3.0
## [149] globals_0.16.3

```