Debugging step: Verify installations for LSF

Antonia Chroni for SJCRH DNB_BINF_Core

Contents

1 Set up

```r
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)
```

```r
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/libopenblasp-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] yaml_2.3.10                reshape2_1.4.4
## [15] SeuratWrappers_0.2.0       RcppPlanc_1.0.0
## [17] rliger_2.1.0               harmony_1.2.3
## [19] Rcpp_1.0.14                ggthemes_5.1.0
## [21] patchwork_1.3.0            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
```

```
## [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              miQC_1.14.0
## [55] ggrepel_0.9.6               ggpmisc_0.6.1
## [57] ggpp_0.5.8-1                stringr_1.5.1
## [59] GGally_2.2.1                ggplot2_3.5.1
## [61] forcats_1.0.0               devtools_2.4.5
## [63] usethis_3.1.0               cowplot_1.1.3
## [65] future_1.34.0
##
## loaded via a namespace (and not attached):
##   [1] spatstat.sparse_3.1-0     httr_1.4.7
##   [3] ggsci_3.2.0               profvis_0.4.0
##   [5] tools_4.4.0               sctransform_0.4.1
##   [7] R6_2.5.1                  lazyeval_0.2.2
##   [9] uwot_0.2.2                urlchecker_1.0.1
##  [11] withr_3.0.2               sp_2.2-0
##  [13] progressr_0.15.1          quantreg_6.00
##  [15] cli_3.6.3                 spatstat.explore_3.3-4
##  [17] sass_0.4.9                spatstat.data_3.1-4
##  [19] ggridges_0.5.6            pbapply_1.7-2
##  [21] parallelly_1.42.0         sessioninfo_1.2.2
##  [23] generics_0.1.3            ica_1.0-3
##  [25] spatstat.random_3.3-2     ggbeeswarm_0.7.2
##  [27] abind_1.4-8               lifecycle_1.0.4
##  [29] SparseArray_1.6.1         Rtsne_0.17
##  [31] promises_1.3.2            crayon_1.5.3
##  [33] miniUI_0.1.1.1            beachmat_2.22.0
##  [35] pillar_1.10.1             future.apply_1.11.3
##  [37] codetools_0.2-20          leiden_0.4.3.1
##  [39] spatstat.univar_3.1-1     remotes_2.5.0
##  [41] vctrs_0.6.5               png_0.1-8
##  [43] spam_2.11-1               gtable_0.3.6
##  [45] cachem_1.1.0              xfun_0.50
##  [47] S4Arrays_1.6.0            mime_0.12
##  [49] survival_3.5-8            ellipsis_0.3.2
##  [51] fitdistrplus_1.2-2        ROCR_1.0-11
##  [53] nlme_3.1-164              bit64_4.6.0-1
##  [55] RcppAnnoy_0.0.22          bslib_0.9.0
##  [57] vipor_0.4.7               KernSmooth_2.23-22
##  [59] colorspace_2.1-1          nnet_7.3-19
##  [61] tidyselect_1.2.1          bit_4.5.0.1
##  [63] compiler_4.4.0            BiocNeighbors_2.0.1
##  [65] SparseM_1.84-2            DelayedArray_0.32.0
##  [67] plotly_4.10.4             scales_1.3.0
##  [69] lmtest_0.9-40             digest_0.6.37
##  [71] goftest_1.2-3             spatstat.utils_3.1-2
##  [73] rmarkdown_2.29            XVector_0.46.0
##  [75] htmltools_0.5.8.1         pkgconfig_2.0.3
##  [77] sparseMatrixStats_1.18.0  fastmap_1.2.0
```

```
##  [79] rlang_1.1.5              htmlwidgets_1.6.4
##  [81] UCSC.utils_1.2.0         shiny_1.10.0
##  [83] DelayedMatrixStats_1.28.1 farver_2.1.2
##  [85] jquerylib_0.1.4          zoo_1.8-12
##  [87] jsonlite_1.8.9           BiocParallel_1.40.0
##  [89] BiocSingular_1.22.0      magrittr_2.0.3
##  [91] polynom_1.4-1            modeltools_0.2-23
##  [93] GenomeInfoDbData_1.2.13  dotCall64_1.2
##  [95] munsell_0.5.1            viridis_0.6.5
##  [97] stringi_1.8.4            zlibbioc_1.52.0
##  [99] MASS_7.3-60.2            plyr_1.8.9
## [101] pkgbuild_1.4.6           ggstats_0.8.0
## [103] parallel_4.4.0           listenv_0.9.1
## [105] deldir_2.0-4             splines_4.4.0
## [107] tensor_1.5               hms_1.1.3
## [109] igraph_2.1.4             spatstat.geom_3.3-5
## [111] ScaledMatrix_1.14.0      pkgload_1.4.0
## [113] evaluate_1.0.3           BiocManager_1.30.25
## [115] tzdb_0.4.0               httpuv_1.6.15
## [117] MatrixModels_0.5-3       RANN_2.6.2
## [119] polyclip_1.10-7          scattermore_1.2
## [121] rsvd_1.0.5               xtable_1.8-4
## [123] later_1.4.1              viridisLite_0.4.2
## [125] memoise_2.0.1            beeswarm_0.4.0
## [127] cluster_2.1.6            timechange_0.3.0
## [129] globals_0.16.3
```