Debugging step: Verify installations for LSF

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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)
```

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


####################################################
# sc-epigenie
library(Signac)
library(AnnotationHub)
library(ensembldb)
library(GenomeInfoDb) #translation between chromosome names

library(GenomicRanges)
library(rtracklayer)

library(Matrix)
library(htmlwidgets)

library(enrichplot)

library(org.Hs.eg.db)
library(org.Mm.eg.db) # Mouse gene annotation (use org.Hs.eg.db for human)

# Motif analysis with Signac
library(JASPAR2018)
library(JASPAR2020)
library(JASPAR2022)
library(JASPAR2024)
library(TFBSTools)
library(BSgenome.Mmusculus.UCSC.mm10)

# Transcription factor footprinting
library(motifmatchr)
library(BSgenome.Hsapiens.UCSC.hg19)

library(monocle3)
library(cicero)
library(biovizBase)
library(clusterProfiler)
####################################################

# `motif-footprint-analysis` module
library(BSgenome.Mmusculus.UCSC.mm39)
library(chromVAR)
library(ggseqlogo)
})
```

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] ggseqlogo_0.1                   chromVAR_1.28.0
##    [3] BSgenome.Mmusculus.UCSC.mm39_1.4.3 clusterProfiler_4.14.6
##    [5] biovizBase_1.54.0              cicero_1.3.9
##    [7] Gviz_1.46.1                    monocle3_1.4.26
##    [9] BSgenome.Hsapiens.UCSC.hg19_1.4.3  motifmatchr_1.28.0
##   [11] BSgenome.Mmusculus.UCSC.mm10_1.4.3 BSgenome_1.74.0
##   [13] BiocIO_1.16.0                  Biostrings_2.74.1
##   [15] XVector_0.46.0                 TFBSTools_1.44.0
##   [17] JASPAR2024_0.99.6             JASPAR2022_0.99.8
##   [19] JASPAR2020_0.99.10            JASPAR2018_1.1.1
##   [21] org.Mm.eg.db_3.20.0          org.Hs.eg.db_3.20.0
##   [23] enrichplot_1.26.6            htmlwidgets_1.6.4
##   [25] rtracklayer_1.66.0           ensembldb_2.30.0
##   [27] AnnotationFilter_1.30.0      GenomicFeatures_1.58.0
##   [29] AnnotationDbi_1.68.0         AnnotationHub_3.14.0
##   [31] BiocFileCache_2.14.0         dbplyr_2.5.0
##   [33] Signac_1.16.0                ggdendro_0.2.0
##   [35] DT_0.34.0                    shinyhelper_0.3.2
##   [37] ShinyCell_2.1.0              glue_1.8.0
##   [39] gridExtra_2.3                R.utils_2.13.0
##   [41] R.oo_1.26.0                  R.methodsS3_1.8.2
##   [43] reticulate_1.37.0            data.table_1.18.2.1
##   [45] SingleR_2.8.0                celldex_1.16.0
##   [47] yaml_2.3.12                  reshape2_1.4.5
##   [49] SeuratWrappers_0.2.0         RcppPlanc_2.0.13
##   [51] rliger_2.2.1.9001            harmony_1.2.4
##   [53] Rcpp_1.0.12                  ggthemes_5.2.0
##   [55] patchwork_1.3.2              scDblFinder_1.20.2
##   [57] hdf5r_1.3.10                 tinytex_0.58
##   [59] SoupX_1.6.2                  knitr_1.51
##   [61] RColorBrewer_1.1-3           fs_1.6.6
##   [63] lubridate_1.9.4              dplyr_1.1.4
##   [65] purrr_1.2.1                  readr_2.1.5
```

```
## [67] tidyr_1.3.1                      tibble_3.3.1
## [69] tidyverse_2.0.0                  scooter_0.0.0.9004
## [71] irlba_2.3.7                      Matrix_1.7-0
## [73] SeuratObject_5.2.0               Seurat_4.4.0
## [75] scater_1.34.1                    scuttle_1.16.0
## [77] SingleCellExperiment_1.28.1      SummarizedExperiment_1.36.0
## [79] Biobase_2.66.0                   GenomicRanges_1.58.0
## [81] GenomeInfoDb_1.42.3              IRanges_2.40.1
## [83] S4Vectors_0.44.0                 BiocGenerics_0.52.0
## [85] MatrixGenerics_1.18.1            matrixStats_1.5.0
## [87] flexmix_2.3-20                   lattice_0.22-6
## [89] miQC_1.14.0                      ggrepel_0.9.6
## [91] ggpmisc_0.6.3                    ggpp_0.6.0
## [93] stringr_1.6.0                    GGally_2.4.0
## [95] ggplot2_4.0.1                    forcats_1.0.1
## [97] devtools_2.4.5                   usethis_2.2.3
## [99] cowplot_1.2.0                    future_1.69.0
##
## loaded via a namespace (and not attached):
##    [1] igraph_2.2.1                   Formula_1.2-5
##    [3] ica_1.0-3                      plotly_4.10.4
##    [5] zlibbioc_1.52.0               tidyselect_1.2.1
##    [7] bit_4.0.5                      rjson_0.2.21
##    [9] blob_1.2.4                     urlchecker_1.0.1
##   [11] S4Arrays_1.6.0                 parallel_4.4.0
##   [13] dichromat_2.0-0.1              seqLogo_1.72.0
##   [15] png_0.1-8                      cli_3.6.5
##   [17] ggplotify_0.1.2                ProtGenerics_1.38.0
##   [19] goftest_1.2-3                  bluster_1.16.0
##   [21] BiocNeighbors_2.0.1            uwot_0.2.2
##   [23] curl_7.0.0                     mime_0.12
##   [25] evaluate_0.24.0                tidytree_0.4.6
##   [27] leiden_0.4.3.1                 stringi_1.8.4
##   [29] backports_1.5.0                XML_3.99-0.16.1
##   [31] httpuv_1.6.15                  magrittr_2.0.4
##   [33] rappdirs_0.3.3                 splines_4.4.0
##   [35] RcppRoll_0.3.0                 jpeg_0.1-10
##   [37] sctransform_0.4.1              ggbeeswarm_0.7.2
##   [39] sessioninfo_1.2.2              DBI_1.2.3
##   [41] HDF5Array_1.34.0               jquerylib_0.1.4
##   [43] withr_3.0.2                    xgboost_1.7.7.1
##   [45] lmtest_0.9-40                  BiocManager_1.30.23
##   [47] biomaRt_2.62.1                 SparseArray_1.6.2
##   [49] annotate_1.84.0                VariantAnnotation_1.52.0
##   [51] zoo_1.8-12                     UCSC.utils_1.2.0
##   [53] TFMPvalue_0.0.9                timechange_0.4.0
##   [55] caTools_1.18.2                 ggtree_3.14.0
##   [57] rhdf5_2.50.2                   pwalign_1.2.0
##   [59] poweRlaw_0.80.0                quantreg_6.1
##   [61] alabaster.schemas_1.6.0        gridGraphics_0.5-1
##   [63] ellipsis_0.3.2                 lazyeval_0.2.2
```

```
##  [65] survival_3.5-8              scattermore_1.2
##  [67] BiocVersion_3.20.0          crayon_1.5.2
##  [69] RcppAnnoy_0.0.22            progressr_0.14.0
##  [71] later_1.3.2                 base64enc_0.1-3
##  [73] ggridges_0.5.6              codetools_0.2-20
##  [75] profvis_0.3.8               KEGGREST_1.46.0
##  [77] Rtsne_0.17                  limma_3.62.2
##  [79] Rsamtools_2.22.0            filelock_1.0.3
##  [81] foreign_0.8-86              pkgconfig_2.0.3
##  [83] xml2_1.5.2                  GenomicAlignments_1.42.0
##  [85] aplot_0.2.2                 spatstat.sparse_3.0-3
##  [87] alabaster.base_1.6.1        ape_5.8
##  [89] viridisLite_0.4.2           xtable_1.8-4
##  [91] interp_1.1-6                plyr_1.8.9
##  [93] httr_1.4.7                  tools_4.4.0
##  [95] globals_0.19.0              pkgbuild_1.4.4
##  [97] checkmate_2.3.1             htmlTable_2.4.2
##  [99] beeswarm_0.4.0              nlme_3.1-164
## [101] ExperimentHub_2.14.0        MatrixModels_0.5-4
## [103] lme4_1.1-35.3               digest_0.6.35
## [105] farver_2.1.2                tzdb_0.4.0
## [107] yulab.utils_0.2.3           viridis_0.6.5
## [109] rpart_4.1.23                DirichletMultinomial_1.48.0
## [111] cachem_1.1.0                polyclip_1.10-6
## [113] Hmisc_5.1-3                 generics_0.1.4
## [115] parallelly_1.46.1           pkgload_1.3.4
## [117] statmod_1.5.0               ScaledMatrix_1.14.0
## [119] minqa_1.2.7                 pbapply_1.7-2
## [121] httr2_1.2.2                 spam_2.10-0
## [123] gson_0.1.0                  dqrng_0.4.1
## [125] gtools_3.9.5                alabaster.se_1.6.0
## [127] shiny_1.12.1                GenomeInfoDbData_1.2.13
## [129] rhdf5filters_1.18.1         RCurl_1.98-1.14
## [131] memoise_2.0.1               rmarkdown_2.27
## [133] scales_1.4.0                gypsum_1.2.0
## [135] RANN_2.6.1                  rstudioapi_0.16.0
## [137] spatstat.data_3.0-4         cluster_2.1.6
## [139] spatstat.utils_3.0-4        hms_1.1.3
## [141] fitdistrplus_1.1-11         colorspace_2.1-0
## [143] rlang_1.1.7                 DelayedMatrixStats_1.28.1
## [145] sparseMatrixStats_1.18.0    dotCall64_1.1-1
## [147] ggtangle_0.1.1              xfun_0.56
## [149] alabaster.matrix_1.6.1      CNEr_1.42.0
## [151] remotes_2.5.0               modeltools_0.2-23
## [153] abind_1.4-5                 GOSemSim_2.32.0
## [155] treeio_1.30.0               ggsci_3.1.0
## [157] Rhdf5lib_1.28.0             bitops_1.0-7
## [159] promises_1.5.0              RSQLite_2.3.7
## [161] qvalue_2.38.0               fgsea_1.32.4
## [163] DelayedArray_0.32.0         GO.db_3.20.0
## [165] compiler_4.4.0              prettyunits_1.2.0
```

```
## [167] alabaster.ranges_1.6.0        boot_1.3-30
## [169] beachmat_2.22.0               SparseM_1.84-2
## [171] polynom_1.4-1                 listenv_0.9.1
## [173] edgeR_4.4.2                   BiocSingular_1.22.0
## [175] tensor_1.5                    progress_1.2.3
## [177] MASS_7.3-60.2                 BiocParallel_1.40.2
## [179] spatstat.random_3.2-3         R6_2.6.1
## [181] fastmap_1.2.0                 fastmatch_1.1-4
## [183] vipor_0.4.7                   ROCR_1.0-11
## [185] ggstats_0.12.0                rsvd_1.0.5
## [187] nnet_7.3-19                   gtable_0.3.6
## [189] KernSmooth_2.23-22            latticeExtra_0.6-30
## [191] miniUI_0.1.1.1                deldir_2.0-4
## [193] htmltools_0.5.8.1             bit64_4.0.5
## [195] spatstat.explore_3.2-7        lifecycle_1.0.5
## [197] S7_0.2.1                      nloptr_2.0.3
## [199] restfulr_0.0.15               sass_0.4.9
## [201] vctrs_0.7.1                   VGAM_1.1-11
## [203] spatstat.geom_3.2-9           DOSE_4.0.1
## [205] scran_1.34.0                  ggfun_0.2.0
## [207] sp_2.1-4                      pracma_2.4.4
## [209] future.apply_1.11.2           bslib_0.7.0
## [211] pillar_1.11.1                 metapod_1.14.0
## [213] locfit_1.5-9.9                otel_0.2.0
## [215] jsonlite_1.8.8
```