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(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(JASPAR2020)
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] JASPAR2020_0.99.10                  org.Mm.eg.db_3.20.0
## [19] org.Hs.eg.db_3.20.0                 enrichplot_1.26.6
## [21] htmlwidgets_1.6.4                   rtracklayer_1.66.0
## [23] ensembldb_2.30.0                    AnnotationFilter_1.30.0
## [25] GenomicFeatures_1.58.0              AnnotationDbi_1.68.0
## [27] AnnotationHub_3.14.0                BiocFileCache_2.14.0
## [29] dbplyr_2.5.0                        ggdendro_0.2.0
## [31] DT_0.34.0                           shinyhelper_0.3.2
## [33] ShinyCell_2.1.0                     glue_1.8.0
## [35] gridExtra_2.3                       R.utils_2.13.0
## [37] R.oo_1.26.0                         R.methodsS3_1.8.2
## [39] reticulate_1.37.0                   data.table_1.17.8
## [41] SingleR_2.8.0                       celldex_1.16.0
## [43] yaml_2.3.12                         reshape2_1.4.5
## [45] SeuratWrappers_0.2.0                RcppPlanc_2.0.13
## [47] rliger_2.2.1.9001                   harmony_1.2.4
## [49] Rcpp_1.0.12                         ggthemes_5.2.0
## [51] patchwork_1.3.2                     scDblFinder_1.20.2
## [53] hdf5r_1.3.10                        tinytex_0.58
## [55] SoupX_1.6.2                         knitr_1.50
## [57] RColorBrewer_1.1-3                  fs_1.6.6
## [59] lubridate_1.9.4                     dplyr_1.1.4
## [61] purrr_1.2.0                         readr_2.1.5
## [63] tidyr_1.3.1                         tibble_3.3.0
## [65] tidyverse_2.0.0                     scooter_0.0.0.9004
## [67] irlba_2.3.5.1                       Matrix_1.7-0
## [69] SeuratObject_5.3.0                  Seurat_4.4.0
## [71] scater_1.34.1                       scuttle_1.16.0
## [73] SingleCellExperiment_1.28.1         SummarizedExperiment_1.36.0
```

```
## [75] Biobase_2.66.0                      GenomicRanges_1.58.0
## [77] GenomeInfoDb_1.42.3                 IRanges_2.40.1
## [79] S4Vectors_0.44.0                    BiocGenerics_0.52.0
## [81] MatrixGenerics_1.18.1               matrixStats_1.5.0
## [83] flexmix_2.3-20                      lattice_0.22-6
## [85] miQC_1.14.0                         ggrepel_0.9.6
## [87] ggpmisc_0.6.3                       ggpp_0.5.9
## [89] stringr_1.6.0                       GGally_2.4.0
## [91] ggplot2_4.0.1                       forcats_1.0.1
## [93] devtools_2.4.5                      usethis_2.2.3
## [95] cowplot_1.2.0                       future_1.68.0
##
## 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] jpeg_0.1-10                       sctransform_0.4.1
##   [37] ggbeeswarm_0.7.2                  sessioninfo_1.2.2
##   [39] DBI_1.2.3                         HDF5Array_1.34.0
##   [41] jquerylib_0.1.4                   withr_3.0.2
##   [43] xgboost_1.7.7.1                   lmtest_0.9-40
##   [45] BiocManager_1.30.23              biomaRt_2.62.1
##   [47] SparseArray_1.6.2                annotate_1.84.0
##   [49] VariantAnnotation_1.52.0         zoo_1.8-12
##   [51] UCSC.utils_1.2.0                 TFMPvalue_0.0.9
##   [53] timechange_0.3.0                 caTools_1.18.3
##   [55] ggtree_3.14.0                    rhdf5_2.50.2
##   [57] pwalign_1.2.0                    quantreg_6.1
##   [59] poweRlaw_0.80.0                  alabaster.schemas_1.6.0
##   [61] gridGraphics_0.5-1              ellipsis_0.3.2
##   [63] lazyeval_0.2.2                   survival_3.5-8
##   [65] scattermore_1.2                 BiocVersion_3.20.0
##   [67] crayon_1.5.2                     RcppAnnoy_0.0.22
##   [69] progressr_0.14.0                 later_1.3.2
##   [71] base64enc_0.1-3                  ggridges_0.5.6
##   [73] codetools_0.2-20                profvis_0.3.8
##   [75] KEGGREST_1.46.0                  Rtsne_0.17
```

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##  [77] limma_3.62.2                    Rsamtools_2.22.0
##  [79] filelock_1.0.3                  foreign_0.8-86
##  [81] pkgconfig_2.0.3                 xml2_1.5.1
##  [83] GenomicAlignments_1.42.0        aplot_0.2.2
##  [85] spatstat.sparse_3.0-3           alabaster.base_1.6.1
##  [87] ape_5.8                         viridisLite_0.4.2
##  [89] xtable_1.8-4                    interp_1.1-6
##  [91] plyr_1.8.9                      httr_1.4.7
##  [93] tools_4.4.0                     globals_0.18.0
##  [95] pkgbuild_1.4.4                  checkmate_2.3.1
##  [97] htmlTable_2.4.2                 beeswarm_0.4.0
##  [99] nlme_3.1-164                    ExperimentHub_2.14.0
## [101] MatrixModels_0.5-4              lme4_1.1-35.3
## [103] digest_0.6.35                   farver_2.1.2
## [105] tzdb_0.4.0                      yulab.utils_0.2.3
## [107] viridis_0.6.5                   rpart_4.1.23
## [109] DirichletMultinomial_1.48.0     cachem_1.1.0
## [111] polyclip_1.10-6                 Hmisc_5.1-3
## [113] generics_0.1.4                  parallelly_1.46.0
## [115] pkgload_1.3.4                   statmod_1.5.0
## [117] ScaledMatrix_1.14.0             minqa_1.2.7
## [119] pbapply_1.7-2                   httr2_1.2.2
## [121] spam_2.10-0                     gson_0.1.0
## [123] dqrng_0.4.1                     gtools_3.9.5
## [125] alabaster.se_1.6.0              shiny_1.12.1
## [127] GenomeInfoDbData_1.2.13         rhdf5filters_1.18.1
## [129] RCurl_1.98-1.14                 memoise_2.0.1
## [131] rmarkdown_2.27                  scales_1.4.0
## [133] gypsum_1.2.0                    RANN_2.6.1
## [135] rstudioapi_0.16.0               spatstat.data_3.0-4
## [137] cluster_2.1.6                   spatstat.utils_3.0-4
## [139] hms_1.1.3                       fitdistrplus_1.1-11
## [141] colorspace_2.1-0                rlang_1.1.6
## [143] DelayedMatrixStats_1.28.1       sparseMatrixStats_1.18.0
## [145] dotCall64_1.1-1                 ggtangle_0.0.9
## [147] xfun_0.55                       alabaster.matrix_1.6.1
## [149] CNEr_1.42.0                     remotes_2.5.0
## [151] modeltools_0.2-23               abind_1.4-5
## [153] GOSemSim_2.32.0                 treeio_1.30.0
## [155] ggsci_3.1.0                     Rhdf5lib_1.28.0
## [157] bitops_1.0-7                    promises_1.5.0
## [159] RSQLite_2.3.7                   qvalue_2.38.0
## [161] fgsea_1.32.4                    DelayedArray_0.32.0
## [163] GO.db_3.20.0                    compiler_4.4.0
## [165] prettyunits_1.2.0               alabaster.ranges_1.6.0
## [167] boot_1.3-30                     beachmat_2.22.0
## [169] SparseM_1.84-2                  polynom_1.4-1
## [171] listenv_0.9.1                   edgeR_4.4.2
## [173] BiocSingular_1.22.0             tensor_1.5
## [175] progress_1.2.3                  MASS_7.3-60.2
## [177] BiocParallel_1.40.2             spatstat.random_3.2-3
```

```
## [179] R6_2.6.1                    fastmap_1.2.0
## [181] fastmatch_1.1-4             vipor_0.4.7
## [183] ROCR_1.0-11                 ggstats_0.11.0
## [185] rsvd_1.0.5                  nnet_7.3-19
## [187] gtable_0.3.6                KernSmooth_2.23-22
## [189] latticeExtra_0.6-30         miniUI_0.1.1.1
## [191] deldir_2.0-4                htmltools_0.5.8.1
## [193] bit64_4.0.5                 spatstat.explore_3.2-7
## [195] lifecycle_1.0.4             S7_0.2.1
## [197] nloptr_2.0.3                restfulr_0.0.15
## [199] sass_0.4.9                  vctrs_0.6.5
## [201] VGAM_1.1-11                 spatstat.geom_3.2-9
## [203] DOSE_4.0.1                  scran_1.34.0
## [205] ggfun_0.2.0                 sp_2.1-4
## [207] future.apply_1.11.2         pracma_2.4.4
## [209] bslib_0.7.0                 pillar_1.11.1
## [211] metapod_1.14.0              locfit_1.5-9.9
## [213] otel_0.2.0                  jsonlite_1.8.8
```