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)
```

```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)
####################################################
})
```

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] clusterProfiler_4.14.6          biovizBase_1.54.0
##  [3] cicero_1.3.9                    Gviz_1.46.1
##  [5] monocle3_1.4.26                 BSgenome.Hsapiens.UCSC.hg19_1.4.3
##  [7] motifmatchr_1.28.0              BSgenome.Mmusculus.UCSC.mm10_1.4.3
##  [9] BSgenome_1.74.0                 BiocIO_1.16.0
## [11] Biostrings_2.74.1               XVector_0.46.0
## [13] TFBSTools_1.44.0                JASPAR2020_0.99.10
## [15] org.Mm.eg.db_3.20.0             org.Hs.eg.db_3.20.0
## [17] enrichplot_1.26.6               htmlwidgets_1.6.4
## [19] rtracklayer_1.66.0              ensembldb_2.30.0
## [21] AnnotationFilter_1.30.0         GenomicFeatures_1.58.0
## [23] AnnotationDbi_1.68.0            AnnotationHub_3.14.0
## [25] BiocFileCache_2.14.0            dbplyr_2.5.0
## [27] ggdendro_0.2.0                  DT_0.34.0
## [29] shinyhelper_0.3.2               ShinyCell_2.1.0
## [31] glue_1.8.0                      gridExtra_2.3
## [33] R.utils_2.13.0                  R.oo_1.26.0
## [35] R.methodsS3_1.8.2               reticulate_1.37.0
## [37] data.table_1.17.8               SingleR_2.8.0
## [39] celldex_1.16.0                  yaml_2.3.10
## [41] reshape2_1.4.4                  SeuratWrappers_0.2.0
## [43] RcppPlanc_2.0.13                rliger_2.2.1
## [45] harmony_1.2.3                   Rcpp_1.0.12
## [47] ggthemes_5.1.0                  patchwork_1.3.2
## [49] scDblFinder_1.20.2              hdf5r_1.3.10
## [51] tinytex_0.57                    SoupX_1.6.2
## [53] knitr_1.50                      RColorBrewer_1.1-3
## [55] fs_1.6.6                        lubridate_1.9.4
## [57] dplyr_1.1.4                     purrr_1.1.0
## [59] readr_2.1.5                     tidyr_1.3.1
## [61] tibble_3.3.0                    tidyverse_2.0.0
## [63] scooter_0.0.0.9004              irlba_2.3.5.1
## [65] Matrix_1.7-0                    SeuratObject_5.2.0
## [67] Seurat_4.4.0                    scater_1.34.1
## [69] scuttle_1.16.0                  SingleCellExperiment_1.28.1
## [71] SummarizedExperiment_1.36.0     Biobase_2.66.0
## [73] GenomicRanges_1.58.0            GenomeInfoDb_1.42.3
## [75] IRanges_2.40.1                  S4Vectors_0.44.0
## [77] BiocGenerics_0.52.0             MatrixGenerics_1.18.1
## [79] matrixStats_1.5.0               flexmix_2.3-20
## [81] lattice_0.22-6                  miQC_1.14.0
## [83] ggrepel_0.9.6                   ggpmisc_0.6.2
```

```
## [85] ggpp_0.5.9                          stringr_1.5.2
## [87] GGally_2.4.0                         ggplot2_4.0.0
## [89] forcats_1.0.1                        devtools_2.4.5
## [91] usethis_2.2.3                        cowplot_1.2.0
## [93] future_1.67.0
##
## loaded via a namespace (and not attached):
##    [1] igraph_2.1.4                     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
##   [77] limma_3.62.2                    Rsamtools_2.22.0
##   [79] filelock_1.0.3                  foreign_0.8-86
##   [81] pkgconfig_2.0.3                 xml2_1.4.0
##   [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_0.2.1
## [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_1.45.1
## [115] pkgload_1.3.4              statmod_1.5.0
## [117] ScaledMatrix_1.14.0        minqa_1.2.7
## [119] pbapply_1.7-2              httr2_1.2.1
## [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_1.11.1
## [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_0.0.7
## [147] xfun_0.53                  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_1.3.3
## [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_0.2.0
## [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] jsonlite_1.8.8
```