

# 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)

#####
# sc-epigenie
library(AnnotationHub)
library(ensembladb)
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/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] 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] scDbfFinder_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

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## [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          tidysselect_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] palign_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

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## [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	vctr_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	