WGCNA Analysis of scRNA-seq Data

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2025-06-05

Contents

1. Read the merged Data

```
## [1] 885    4
```

```
## Allowing multi-threading with up to 8 threads.
```

```
## pickSoftThreshold: will use block size 885.
##  pickSoftThreshold: calculating connectivity for given powers...
##     ..working on genes 1 through 885 of 885
```

```
##    Power SFT.R.sq   slope truncated.R.sq mean.k. median.k. max.k.
## 1      1 0.914000  4.0800          0.913   511.0     527.0  614.0
## 2      2 0.875000  2.0700          0.876   371.0     383.0  494.0
## 3      3 0.837000  1.3300          0.829   295.0     304.0  421.0
## 4      4 0.741000  0.9390          0.702   247.0     251.0  372.0
## 5      5 0.730000  0.6950          0.702   213.0     213.0  335.0
## 6      6 0.626000  0.5380          0.595   187.0     185.0  306.0
## 7      7 0.509000  0.4180          0.468   168.0     164.0  283.0
## 8      8 0.405000  0.3280          0.358   152.0     146.0  264.0
## 9      9 0.316000  0.2590          0.320   139.0     132.0  247.0
## 10    10 0.222000  0.2060          0.228   128.0     120.0  233.0
## 11    12 0.111000  0.1240          0.262   111.0     102.0  209.0
## 12    14 0.029000  0.0576          0.273    98.2      89.3  190.0
## 13    16 0.000998  0.0101          0.357    88.0      79.2  175.0
## 14    18 0.020200 -0.0452          0.439    79.8      71.8  162.0
## 15    20 0.052800 -0.0763          0.474    73.0      65.6  151.0
## 16    22 0.099700 -0.1030          0.567    67.3      60.7  141.0
## 17    24 0.122000 -0.1190          0.619    62.5      56.4  133.0
## 18    26 0.182000 -0.1450          0.657    58.3      52.3  126.0
## 19    28 0.239000 -0.1760          0.629    54.6      48.7  119.0
## 20    30 0.279000 -0.1950          0.672    51.4      45.8  114.0
## 21    32 0.296000 -0.2160          0.650    48.6      43.2  108.0
## 22    34 0.331000 -0.2290          0.707    46.0      40.9  104.0
## 23    36 0.349000 -0.2390          0.726    43.7      38.8   99.2
## 24    38 0.373000 -0.2570          0.722    41.7      36.8   95.2
## 25    40 0.396000 -0.2690          0.752    39.8      35.1   91.6
## 26    42 0.390000 -0.2750          0.739    38.1      33.5   88.2
## 27    44 0.419000 -0.2850          0.800    36.5      31.9   85.1
## 28    46 0.448000 -0.2990          0.812    35.1      30.5   82.2
## 29    48 0.437000 -0.2990          0.828    33.7      29.4   79.5
## 30    50 0.446000 -0.3030          0.842    32.5      28.3   77.0
## 31    52 0.464000 -0.3110          0.863    31.4      27.3   74.6
## 32    54 0.466000 -0.3140          0.860    30.3      26.2   72.4
## 33    56 0.476000 -0.3260          0.824    29.3      25.3   70.3
## 34    58 0.491000 -0.3340          0.841    28.4      24.6   68.3
## 35    60 0.521000 -0.3510          0.852    27.5      23.8   66.4
## 36    62 0.537000 -0.3560          0.845    26.7      23.2   64.6
## 37    64 0.548000 -0.3630          0.838    25.9      22.4   63.0
## 38    66 0.551000 -0.3640          0.841    25.2      21.8   61.4
## 39    68 0.548000 -0.3710          0.819    24.5      21.2   59.8
## 40    70 0.563000 -0.3770          0.821    23.8      20.6   58.4
## 41    72 0.572000 -0.3820          0.816    23.2      20.0   57.0
## 42    74 0.579000 -0.3850          0.819    22.7      19.5   55.7
## 43    76 0.581000 -0.3950          0.800    22.1      19.1   54.4
## 44    78 0.572000 -0.4000          0.775    21.6      18.7   53.2
## 45    80 0.567000 -0.4010          0.760    21.1      18.3   52.0
```

```
## 46      82 0.571000 -0.4020              0.757   20.6     17.9    50.9
## 47      84 0.569000 -0.4060              0.743   20.1     17.5    49.9
## 48      86 0.564000 -0.4080              0.725   19.7     17.2    48.8
## 49      88 0.574000 -0.4090              0.733   19.3     16.8    47.9
## 50      90 0.584000 -0.4120              0.743   18.9     16.5    46.9
## 51      92 0.596000 -0.4180              0.745   18.5     16.2    46.1
## 52      94 0.602000 -0.4170              0.750   18.1     15.8    45.2
## 53      96 0.600000 -0.4190              0.745   17.8     15.5    44.4
## 54      98 0.608000 -0.4210              0.752   17.4     15.2    43.6
## 55     100 0.617000 -0.4210              0.770   17.1     14.9    42.8
```

Scale independence · **Mean connectivity**
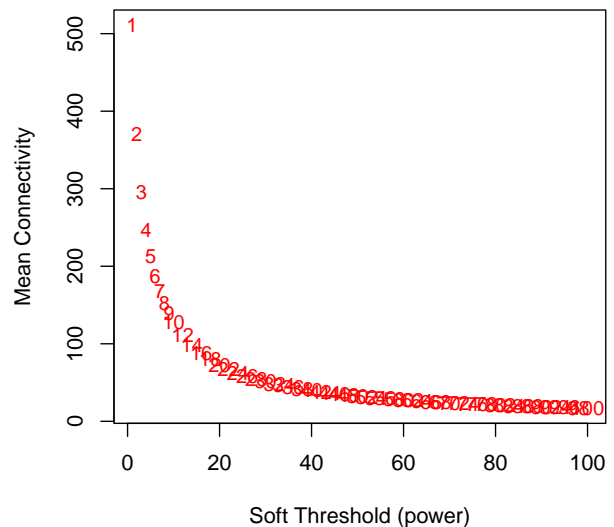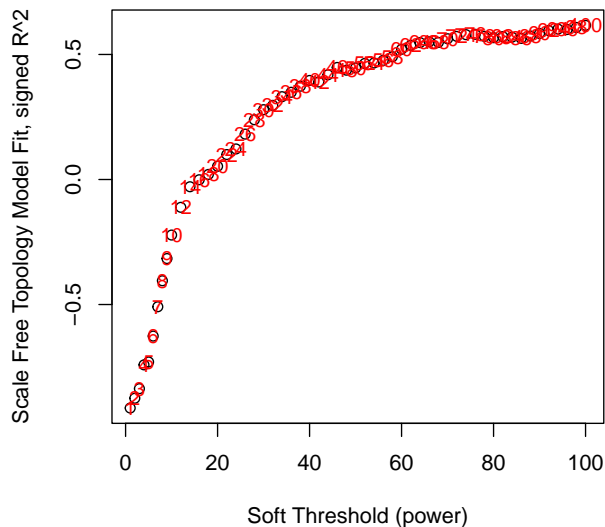

```
##  Calculating module eigengenes block-wise from all genes
##    Flagging genes and samples with too many missing values...
##      ..step 1
##  ..Working on block 1 .
##     TOM calculation: adjacency..
##     ..will use 8 parallel threads.
##     Fraction of slow calculations: 0.000000
##     ..connectivity..
##     ..matrix multiplication (system BLAS)..
##     ..normalization..
##     ..done.
##     ..saving TOM for block 1 into file ER-block.1.RData
##  ....clustering..
##  ....detecting modules..
##  ....calculating module eigengenes..
##  ....checking kME in modules..
##      ..removing 1 genes from module 3 because their KME is too low.
##      ..removing 3 genes from module 4 because their KME is too low.
##      ..removing 1 genes from module 9 because their KME is too low.
##  ..merging modules that are too close..
##      mergeCloseModules: Merging modules whose distance is less than 0.15
##         Calculating new MEs...

## mergedColors
##     black     blue     brown     green     grey      red turquoise    yellow
```
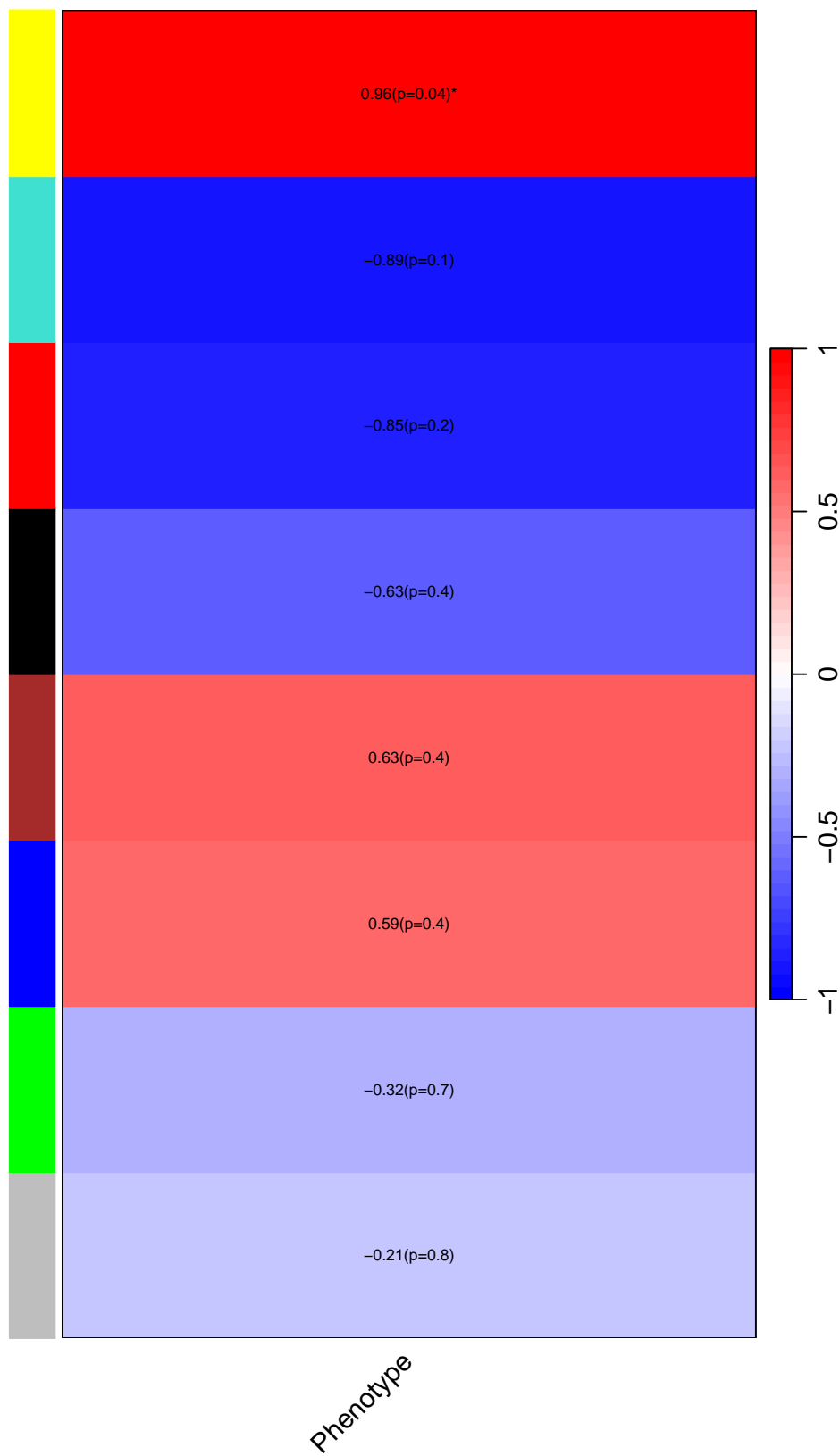
```
##              75            114            103             81              5             76            345             86
## pdf
##   2

## pdf
##   2

## mergedColors
##     black       blue      brown      green       grey        red  turquoise     yellow
##        75        114        103         81          5         76        345         86

## [1] 8
```

Module−Trait Correlations
(cor, p−value, stars)

```
## pdf
##   2
```

```
## pdf
##   2
```

```
## [1] "Processing module: MEyellow"
```

```
## [1] "Processing module: MEturquoise"
```

Session Information

```
## R version 4.4.0 (2024-04-24)
## Platform: aarch64-apple-darwin20
## Running under: macOS 15.5
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.4-arm64/Resources/lib/libRlapack.dylib;  LAPACK v
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## time zone: America/New_York
## tzcode source: internal
##
## attached base packages:
## [1] stats4    stats     graphics  grDevices utils     datasets  methods
## [8] base
##
## other attached packages:
##  [1] extrafont_0.19          gprofiler2_0.2.3
##  [3] WGCNA_1.73              fastcluster_1.3.0
##  [5] dynamicTreeCut_1.63-1   kableExtra_1.4.0
##  [7] patchwork_1.3.0         pheatmap_1.0.12
##  [9] data.table_1.17.4       harmony_1.2.3
## [11] Rcpp_1.0.14             conflicted_1.2.0
## [13] openxlsx_4.2.8          Seurat_5.3.0
## [15] SeuratObject_5.1.0      sp_2.2-0
## [17] AnnotationHub_3.12.0    BiocFileCache_2.12.0
## [19] dbplyr_2.5.0            simspec_0.0.0.9000
## [21] cowplot_1.1.3           EnsDb.Hsapiens.v86_2.99.0
## [23] ensembldb_2.28.1        AnnotationFilter_1.28.0
## [25] GenomicFeatures_1.56.0  AnnotationDbi_1.66.0
## [27] Biobase_2.64.0          Signac_1.14.0
## [29] rtracklayer_1.64.0      GenomicRanges_1.56.2
## [31] GenomeInfoDb_1.40.1     IRanges_2.38.1
## [33] S4Vectors_0.42.1        BiocGenerics_0.50.0
## [35] knitr_1.50              lubridate_1.9.4
## [37] forcats_1.0.0           stringr_1.5.1
## [39] dplyr_1.1.4             purrr_1.0.4
## [41] readr_2.1.5             tidyr_1.3.1
## [43] tibble_3.2.1            ggplot2_3.5.2
## [45] tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
##   [1] ProtGenerics_1.36.0     matrixStats_1.5.0
##   [3] spatstat.sparse_3.1-0   bitops_1.0-9
##   [5] httr_1.4.7              RColorBrewer_1.1-3
##   [7] doParallel_1.0.17       backports_1.5.0
##   [9] tools_4.4.0             sctransform_0.4.2
##  [11] R6_2.6.1                lazyeval_0.2.2
##  [13] uwot_0.2.3              withr_3.0.2
##  [15] gridExtra_2.3           preprocessCore_1.66.0
```

```
##  [17] progressr_0.15.1           cli_3.6.5
##  [19] textshaping_1.0.1          spatstat.explore_3.4-3
##  [21] fastDummies_1.7.5          labeling_0.4.3
##  [23] spatstat.data_3.1-6        ggridges_0.5.6
##  [25] pbapply_1.7-2              Rsamtools_2.20.0
##  [27] systemfonts_1.2.3          foreign_0.8-90
##  [29] svglite_2.2.1              dichromat_2.0-0.1
##  [31] parallelly_1.44.0          impute_1.78.0
##  [33] rstudioapi_0.17.1          RSQLite_2.3.11
##  [35] generics_0.1.4             BiocIO_1.14.0
##  [37] ica_1.0-3                  spatstat.random_3.4-1
##  [39] zip_2.3.2                  GO.db_3.19.1
##  [41] Matrix_1.7-3               abind_1.4-8
##  [43] lifecycle_1.0.4            yaml_2.3.10
##  [45] SummarizedExperiment_1.34.0 SparseArray_1.4.8
##  [47] Rtsne_0.17                 grid_4.4.0
##  [49] blob_1.2.4                 promises_1.3.3
##  [51] crayon_1.5.3               miniUI_0.1.2
##  [53] lattice_0.22-7             KEGGREST_1.44.1
##  [55] pillar_1.10.2              rjson_0.2.23
##  [57] future.apply_1.11.3        codetools_0.2-20
##  [59] fastmatch_1.1-6            glue_1.8.0
##  [61] spatstat.univar_3.1-3      vctrs_0.6.5
##  [63] png_0.1-8                  spam_2.11-1
##  [65] gtable_0.3.6               cachem_1.1.0
##  [67] xfun_0.52                  S4Arrays_1.4.1
##  [69] mime_0.13                  survival_3.8-3
##  [71] RcppRoll_0.3.1             iterators_1.0.14
##  [73] tinytex_0.57               fitdistrplus_1.2-2
##  [75] ROCR_1.0-11                nlme_3.1-168
##  [77] bit64_4.6.0-1              filelock_1.0.3
##  [79] RcppAnnoy_0.0.22           rprojroot_2.0.4
##  [81] irlba_2.3.5.1              rpart_4.1.24
##  [83] KernSmooth_2.23-26         colorspace_2.1-1
##  [85] DBI_1.2.3                  Hmisc_5.2-3
##  [87] nnet_7.3-20                tidyselect_1.2.1
##  [89] extrafontdb_1.0            bit_4.6.0
##  [91] compiler_4.4.0             curl_6.2.3
##  [93] htmlTable_2.4.3            xml2_1.3.8
##  [95] DelayedArray_0.30.1        plotly_4.10.4
##  [97] checkmate_2.3.2            scales_1.4.0
##  [99] lmtest_0.9-40              rappdirs_0.3.3
## [101] digest_0.6.37             goftest_1.2-3
## [103] spatstat.utils_3.1-4       rmarkdown_2.29
## [105] XVector_0.44.0             htmltools_0.5.8.1
## [107] pkgconfig_2.0.3            base64enc_0.1-3
## [109] MatrixGenerics_1.16.0      fastmap_1.2.0
## [111] rlang_1.1.6                htmlwidgets_1.6.4
## [113] UCSC.utils_1.0.0           shiny_1.10.0
## [115] farver_2.1.2               zoo_1.8-14
## [117] jsonlite_2.0.0             BiocParallel_1.38.0
## [119] RCurl_1.98-1.17            magrittr_2.0.3
## [121] Formula_1.2-5              GenomeInfoDbData_1.2.12
## [123] dotCall64_1.2              reticulate_1.42.0
```

```
## [125] stringi_1.8.7            zlibbioc_1.50.0
## [127] MASS_7.3-65             plyr_1.8.9
## [129] parallel_4.4.0          listenv_0.9.1
## [131] ggrepel_0.9.6           deldir_2.0-4
## [133] Biostrings_2.72.1       splines_4.4.0
## [135] tensor_1.5              hms_1.1.3
## [137] igraph_2.1.4            spatstat.geom_3.4-1
## [139] RcppHNSW_0.6.0          reshape2_1.4.4
## [141] BiocVersion_3.19.1      XML_3.99-0.18
## [143] evaluate_1.0.3          BiocManager_1.30.25
## [145] tzdb_0.5.0              foreach_1.5.2
## [147] httpuv_1.6.16           Rttf2pt1_1.3.12
## [149] RANN_2.6.2              polyclip_1.10-7
## [151] future_1.49.0           scattermore_1.2
## [153] xtable_1.8-4            restfulr_0.0.15
## [155] RSpectra_0.16-2         later_1.4.2
## [157] ragg_1.4.0              viridisLite_0.4.2
## [159] memoise_2.0.1           GenomicAlignments_1.40.0
## [161] cluster_2.1.8.1         timechange_0.3.0
## [163] globals_0.18.0          here_1.0.1
```