GO Sementic analysis

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Contents

Introduction

Gene ontology (GO) analyses also showed that genes upregulated in control BMDM were significantly enriched for terms related to developmental processes including cell-cell differentiation and cell development, while genes upregulated in Mafb-deficient BMDM were associated with terms related to response to stimuli such as cell communication and cell activation, reminiscent of a monocyte phenotype.

Load packages

```
suppressMessages(library(dplyr))
suppressMessages(library(Seurat))
suppressMessages(library(patchwork))
suppressMessages(library(ggplot2))
suppressMessages(library(simplifyEnrichment))
suppressMessages(library(formatR))
suppressMessages(library(simona))
suppressMessages(library(org.Mm.eg.db))
suppressMessages(library(ComplexHeatmap))
```

Create Directed Acyclic Graph (DAG)

```
dag <- create_ontology_DAG_from_GO_db(org_db = "org.Mm.eg.db")
```

GO for Mafb KO macrophage

```
# Load genes up in KO BMDM
DE_results <- read.table("DEG.csv", header = T, sep = ",")
```

```r
DE_results <- DE_results[order(DE_results$log2FoldChange.x, decreasing = T),
    ]

# Convert gene symbol to entrez ID
Gene_entrez <- mapIds(org.Mm.eg.db, keys = DE_results$X[1:438],
    keytype = "SYMBOL", column = "ENTREZID")

# Perform ORA
Gene_entrez <- Gene_entrez[!is.na(Gene_entrez)]

tb = dag_enrich_on_genes(dag, Gene_entrez)
tb = tb[order(tb$p_adjust), ]
top_go_ids = tb$term[1:100]

# Plot the significant GO terms in a DAG
dag_circular_viz(dag, top_go_ids)
```

GO for Mafb WT macrophage

```r
# Load genes up in WT BMDM
DE_results <- read.table("DEG.csv", header = T, sep = ",")
DE_results <- DE_results[order(DE_results$log2FoldChange.x, decreasing = T),
    ]

# Convert gene symbol to entrez ID
Gene_entrez <- mapIds(org.Mm.eg.db, keys = DE_results$X[439:808],
    keytype = "SYMBOL", column = "ENTREZID")

# Perform ORA
Gene_entrez <- Gene_entrez[!is.na(Gene_entrez)]

tb = dag_enrich_on_genes(dag, Gene_entrez)
tb = tb[order(tb$p_adjust), ]
top_go_ids = tb$term[1:100]

# Plot the significant GO terms in a DAG
dag_circular_viz(dag, top_go_ids)
```

```r
sessionInfo()
```

```
## R version 4.3.3 (2024-02-29)
## Platform: x86_64-pc-linux-gnu (64-bit)
## 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 version 3.10.0
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=fr_BE.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=fr_BE.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=fr_BE.UTF-8       LC_NAME=C
```

```
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=fr_BE.UTF-8 LC_IDENTIFICATION=C
##
## time zone: Europe/Brussels
## tzcode source: system (glibc)
##
## attached base packages:
## [1] stats4    grid      stats     graphics  grDevices utils     datasets
## [8] methods   base
##
## other attached packages:
##  [1] ComplexHeatmap_2.16.0   org.Mm.eg.db_3.17.0
##  [3] AnnotationDbi_1.62.1    IRanges_2.34.0
##  [5] S4Vectors_0.38.1        Biobase_2.60.0
##  [7] simona_1.1.5            formatR_1.14
##  [9] simplifyEnrichment_1.10.0 BiocGenerics_0.46.0
## [11] ggplot2_3.4.2           patchwork_1.1.2
## [13] SeuratObject_4.1.3      Seurat_4.3.0
## [15] dplyr_1.1.2
##
## loaded via a namespace (and not attached):
##   [1] RcppAnnoy_0.0.21        splines_4.3.3           later_1.3.1
##   [4] bitops_1.0-7            tibble_3.2.1            polyclip_1.10-4
##   [7] lifecycle_1.0.3         doParallel_1.0.17       globals_0.16.2
##  [10] NLP_0.2-1               lattice_0.22-5          MASS_7.3-60.0.1
##  [13] magrittr_2.0.3          plotly_4.10.2           rmarkdown_2.23
##  [16] yaml_2.3.7              httpuv_1.6.11           sctransform_0.3.5
##  [19] spam_2.9-1              sp_2.0-0                spatstat.sparse_3.0-2
##  [22] reticulate_1.30         cowplot_1.1.1           pbapply_1.7-2
##  [25] DBI_1.1.3               RColorBrewer_1.1-3      abind_1.4-5
##  [28] zlibbioc_1.46.0         Rtsne_0.16              purrr_1.0.1
##  [31] RCurl_1.98-1.12         circlize_0.4.15         GenomeInfoDbData_1.2.10
##  [34] tm_0.7-11               ggrepel_0.9.3           irlba_2.3.5.1
##  [37] listenv_0.9.0           spatstat.utils_3.0-3    goftest_1.2-3
##  [40] spatstat.random_3.1-5   fitdistrplus_1.1-11     parallelly_1.36.0
##  [43] leiden_0.4.3            codetools_0.2-19        xml2_1.3.4
##  [46] tidyselect_1.2.0        shape_1.4.6             matrixStats_1.0.0
##  [49] spatstat.explore_3.2-1  jsonlite_1.8.7          GetoptLong_1.0.5
##  [52] ellipsis_0.3.2          progressr_0.13.0        ggridges_0.5.4
##  [55] survival_3.5-8          iterators_1.0.14        foreach_1.5.2
##  [58] tools_4.3.3             ica_1.0-3               Rcpp_1.0.11
##  [61] glue_1.6.2              gridExtra_2.3           xfun_0.39
##  [64] GenomeInfoDb_1.36.0     withr_2.5.0             fastmap_1.1.1
##  [67] fansi_1.0.4             digest_0.6.33           R6_2.5.1
##  [70] mime_0.12               colorspace_2.1-0        scattermore_1.2
##  [73] GO.db_3.17.0            tensor_1.5              spatstat.data_3.0-1
##  [76] RSQLite_2.3.1           utf8_1.2.3              tidyr_1.3.0
##  [79] generics_0.1.3          data.table_1.14.8       httr_1.4.6
##  [82] htmlwidgets_1.6.2       scatterplot3d_0.3-44    uwot_0.1.16
##  [85] pkgconfig_2.0.3         gtable_0.3.3            blob_1.2.4
##  [88] lmtest_0.9-40           XVector_0.40.0          htmltools_0.5.5
##  [91] dotCall64_1.0-2         clue_0.3-64             scales_1.2.1
##  [94] png_0.1-8               knitr_1.43              rstudioapi_0.14
##  [97] reshape2_1.4.4          rjson_0.2.21            nlme_3.1-164
```

```
## [100] org.Hs.eg.db_3.17.0     zoo_1.8-12              cachem_1.0.8
## [103] GlobalOptions_0.1.2      Polychrome_1.5.1        stringr_1.5.0
## [106] KernSmooth_2.23-22       parallel_4.3.3          miniUI_0.1.1.1
## [109] proxyC_0.3.4             pillar_1.9.0            vctrs_0.6.3
## [112] RANN_2.6.1               slam_0.1-50             promises_1.2.0.1
## [115] xtable_1.8-4             cluster_2.1.6           evaluate_0.21
## [118] cli_3.6.1                compiler_4.3.3          rlang_1.1.1
## [121] crayon_1.5.2             future.apply_1.11.0     plyr_1.8.8
## [124] stringi_1.7.12           viridisLite_0.4.2       deldir_1.0-9
## [127] munsell_0.5.0            Biostrings_2.68.1       lazyeval_0.2.2
## [130] spatstat.geom_3.2-4      GOSemSim_2.26.1         Matrix_1.6-1
## [133] bit64_4.0.5              future_1.33.0           KEGGREST_1.40.0
## [136] shiny_1.7.4.1            ROCR_1.0-11             igraph_1.5.0.1
## [139] memoise_2.0.1            RcppParallel_5.1.7      bit_4.0.5
```