

3.4 Tutorial-4: Multi-modal data integration

This tutorial allows users to combine intra-donor variation value between different modalities like scRNA and scATAC data here. Load CV result from scRNA and scATAC as described above (check output directory for the files). To integrate variability across modalities, please follow following steps.

3.4.1 Load Library

```
#Load Library
library("PALMO")
library("Hmisc")
library("ComplexHeatmap")
library("circlize")
```

3.4.2 Load data

```
#From scRNA analysis obtain the CV data
load("data/result/scrna-CV-allgenes-raw.Rda")
scrna_cv_res <- cv_res

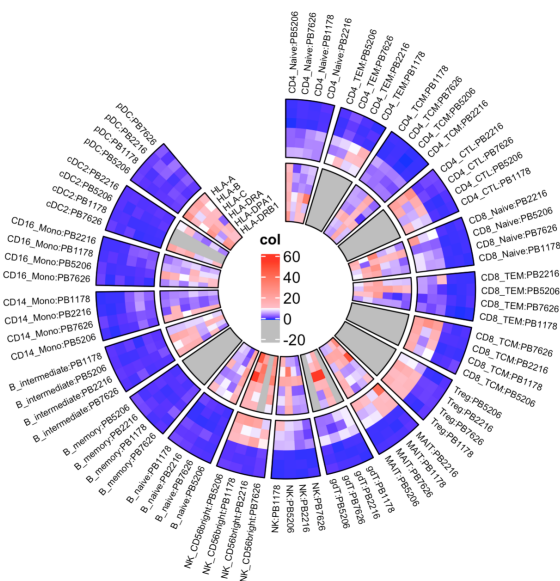
#From scATAC analysis obtain the CV data
load("data/result/scatac-CV-allgenes-raw.Rda")
scatac_cv_res <- cv_res

#Cell type of interest
celltype_oi <- c("CD4_Naive", "CD4_TEM", "CD4_TCM", "CD4_CTL",
                 "CD8_Naive", "CD8_TEM", "CD8_TCM", "Treg",
                 "MAIT", "gdT", "NK", "NK_CD56bright",
                 "B_naive", "B_memory", "B_intermediate",
                 "CD14_Mono", "CD16_Mono",
                 "cDC2", "pDC")

#HLAs
geneList <- c("HLA-A", "HLA-B", "HLA-C", "HLA-DRA", "HLA-DPA1", "HLA-DRB1")
```

3.4.3 Run (Time ~ 10sec)

```
plot <- multimodalView(modality1=scrna_cv_res,
                       modality2=scatac_cv_res,
                       geneList=geneList, group_oi=celltype_oi)
```



6 Session info

```
sessionInfo()
#> R version 4.0.3 (2020-10-10)
#> Platform: x86_64-apple-darwin17.0 (64-bit)
#> Running under: macOS Catalina 10.15.7
#>
#> Matrix products: default
#> BLAS: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
#> LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRlapack.dylib
#>
#> locale:
#> [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
#>
#> attached base packages:
#> [1] grid      stats      graphics  grDevices  utils      datasets  methods
#> [8] base
#>
#> other attached packages:
#> [1] PALMO_0.1.0
#>
#> loaded via a namespace (and not attached):
#> [1] readxl_1.3.1          backports_1.2.0
#> [3] circlize_0.4.11       plyr_1.8.6
#> [5] igraph_1.2.8          lazyeval_0.2.2
#> [7] splines_4.0.3         listenv_0.8.0
#> [9] scattermore_0.7       GenomeInfoDb_1.24.2
#> [11] ggplot2_3.3.5         digest_0.6.28
#> [13] htmltools_0.5.2       fansi_0.5.0
#> [15] magrittr_2.0.1        tensor_1.5
#> [17] cluster_2.1.0         ROCR_1.0-11
#> [19] ComplexHeatmap_2.4.3  globals_0.14.0
#> [21] readr_1.4.0           modelr_0.1.8
#> [23] matrixStats_0.61.0    colorspace_2.0-2
#> [25] rvest_0.3.6           blob_1.2.1
#> [27] ggrepel_0.9.1         haven_2.3.1
#> [29] xfun_0.25             dplyr_1.0.7
#> [31] RCurl_1.98-1.2        crayon_1.4.2
#> [33] jsonlite_1.7.2        lme4_1.1-25
#> [35] spatstat_1.64-1       spatstat.data_2.1-0
#> [37] survival_3.2-7        zoo_1.8-9
#> [39] glue_1.5.0            polyclip_1.10-0
#> [41] gtable_0.3.0          zlibbioc_1.34.0
#> [43] XVector_0.28.0        leiden_0.3.9
#> [45] DelayedArray_0.14.1   GetoptLong_1.0.4
#> [47] SingleCellExperiment_1.10.1 future.apply_1.8.1
#> [49] shape_1.4.5           BiocGenerics_0.34.0
#> [51] abind_1.4-5           scales_1.1.1
#> [53] pheatmap_1.0.12       DBI_1.1.0
#> [55] miniUI_0.1.1.1        Rcpp_1.0.7
#> [57] viridisLite_0.4.0     xtable_1.8-4
#> [59] clue_0.3-57           reticulate_1.22
#> [61] stats4_4.0.3          htmlwidgets_1.5.4
```

```

#> [63] httr_1.4.2
#> [65] ellipsis_0.3.2
#> [67] factoextra_1.0.7.999
#> [69] farver_2.1.0
#> [71] uwot_0.1.10
#> [73] deldir_1.0-6
#> [75] tidyselect_1.1.1
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#> [79] munsell_0.5.0
#> [81] tools_4.0.3
#> [83] broom_0.7.2
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#> [89] goftest_1.2-3
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#> [93] purrr_0.3.4
#> [95] pbapply_1.5-0
#> [97] nlme_3.1-149
#> [99] xml2_1.3.2
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#> [107] statmod_1.4.35
#> [109] forcats_0.5.0
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#> [113] vctrs_0.3.8
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#> [123] GenomicRanges_1.40.0
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#> [135] assertthat_0.2.1
#> [137] MAST_1.14.0
#> [139] SeuratObject_4.0.2
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#> [143] mgcv_1.8-33
#> [145] hms_0.5.3
#> [147] tidyverse_1.3.0
#> [149] minqa_1.2.4
#> [151] Rtsne_0.15
#> [153] Biobase_2.48.0
#> [155] lubridate_1.7.9
RColorBrewer_1.1-2
Seurat_4.0.0
ica_1.0-2
pkgconfig_2.0.3
dbplyr_1.4.4
utf8_1.2.2
rlang_0.4.12
later_1.3.0
cellranger_1.1.0
generics_0.1.1
ggridges_0.5.3
stringr_1.4.0
yaml_2.2.1
knitr_1.30
fitdistrplus_1.1-6
RANN_2.6.1
future_1.23.0
mime_0.12
compiler_4.0.3
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reprex_0.3.0
tibble_3.1.6
stringi_1.7.5
lattice_0.20-41
nloptr_1.2.2.2
pillar_1.6.4
lmtest_0.9-39
RcppAnnoy_0.0.19
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httpuv_1.6.3
R6_2.5.1
KernSmooth_2.23-17
IRanges_2.22.2
codetools_0.2-16
MASS_7.3-53
SummarizedExperiment_1.18.2
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sctransform_0.3.2
S4Vectors_0.26.1
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rpart_4.1-15
tidyr_1.1.4
rmarkdown_2.5
ggforce_0.3.2
shiny_1.7.1

```