Data exploratory analysis

Antonia Chroni for SJCRH DNB_BINF_Core

Contents


```
## The following object is masked _by_ .GlobalEnv:
##
##     root_dir
```

PI: NA
Project: test-dataset
Task: NA
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DNB Bioinformatics Core Pipeline: Standard sc-/sn-ATAC-Seq Analysis in 10X Genomics data

Date started: Dec-16-2024
Date completed: ONGOING
Report generated: 14:37:21 CST 01/09/2025

Reviewed by: _____ Date: _____

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1 Information about this notebook

This is an exploratory analysis of the data available for the testing phase for the `sc-atac-seq` pipeline(s). We are investigating number of samples overall per condition and variables as defined in the `params`. We are looking for cohorts that fit the following criteria as described in the ./analyses/README.md[2]. - Control vs condition (min. 3+3 samples) - Number of cells/sample - size of datasets might determined packages/pipelines to be used - Single cell/Single-nucleus ATAC - Integration of scRNA-seq and scATAC-seq data from the same biological system (multiple modalities) - Pipeline for same samples but not same cells with scRNA-seq and scATAC-seq - Annotate scATAC-seq cells via label transfer by using scRNA data: cell type annotation - Available bulk ATAC-seq data for the same samples (matched) - this could be used for cell type annotation

2 Set up

```
suppressPackageStartupMessages({
  library(tidyverse)
  library(knitr)
  library(readxl)
})
```

3 Directories and paths to file Inputs/Outputs

```
attach(params)
```

```
## The following object is masked _by_ .GlobalEnv:
##
##     root_dir
```

```
analysis_dir <- file.path(root_dir, "analyses", "data-exploratory-analysis")

# input files
data_file <- file.path(metadata_dir, "TestData_10x_2024_12_16.xlsx")
jackie_data_file <- file.path(metadata_dir, "cohorts_10x_rna_atac_testing_phase_JN.xlsx")

# File path to `input` directory
input_dir <- file.path(analysis_dir, "input")
if (!dir.exists(input_dir)) {
  dir.create(input_dir)}

# File path to `plots` directory
plots_dir <- file.path(analysis_dir, "plots")
if (!dir.exists(plots_dir)) {
  dir.create(plots_dir)}

# File path to `results` directory
results_dir <- file.path(analysis_dir, "results")
if (!dir.exists(results_dir)) {
  dir.create(results_dir)}
```

[2] https://github.com/stjude-dnb-binfcore/sc-atac-seq/tree/main/analyses

4 Read raw data file

```
# Read metadata
raw_data_df <- read_excel(data_file) %>%

  # save data under a more descriptive file name
  # all edits will be made on this one and not on the RAW data
  # RAW data were edited manually by Antonia Chroni to add typo of experiment and type of k
  write_tsv(file.path(input_dir, "cohorts_10x_rna_atac_testing_phase_not_processed.tsv"))
```

5 Read processed data file

```
df_processed <- raw_data_df %>%

  # Add metadata
  add_column(seq_unit = "nucleus",
             condition = "unknown",
             species = "mouse") %>%
  tidyr::separate(Kit, c("seq_technology", "assay_drop"), sep = ' ', remove = FALSE) %>%
  tidyr::separate(assay_drop, c("assay", "drop"), sep = ' ', remove = FALSE) %>%
  select(!c(assay_drop, drop)) %>%
  mutate(seq_unit = case_when(grepl("More Retina", experiment) ~ "cell",
                              grepl("Stressed Retina", experiment) ~ "cell",
                              TRUE ~ seq_unit),
         Sample = case_when(grepl("6wk Cerebellum", Sample) ~ "6 week cerebellum",
                            grepl("P0 Cerebellum,", Sample) ~ "P0 cerebellum",
                            grepl("E14.5", Sample) ~ "E14.5 Retina",
                            TRUE ~ Sample),

         # Add condition col
         condition = case_when(grepl("P0 cerebellum|6 week cerebellum|E14.5|P0 Retina|E14.5
                               grepl("Wt1|Wt2|SEKO_21|SEKO_25", Sample) ~ "knock-out",
                               grepl("ATOH HI|ATOH Low", Sample) ~ "treatment",
                               TRUE ~ condition)) %>%

  write_tsv(file.path(results_dir, "cohorts_10x_rna_atac_testing_phase_2024-12-17.tsv"))
```

6 Update processed data file per our conversation with Jackie Norrie

This is the `cohorts_10x_rna_atac_testing_phase_2024-12-17.tsv` file updated per our conversation with Jackie Norrie to fix empty cells and/or inconsistencies.

```
df_processed_select <- df_processed %>%
  select(!c(SRM_id, SRM_Sample_id, seq_unit, condition))

# Read and process data
df_processed <- read_excel(jackie_data_file) %>%
  select(DYE, SRM_id, SRM_Sample_id, seq_unit, condition) %>%
  right_join(df_processed_select, by = join_by(DYE)) %>%
```

```
  mutate(seq_technology = case_when(grepl("RNA", assay) ~ "10Xv3",
                                    grepl("ATAC", assay) ~ "10Xv2"),
         seq_technology = case_when(grepl("yes", multiome_10x) ~ "10X",
                                    TRUE ~ seq_technology),
         seq_technology_assay = paste(seq_technology, assay, sep = "_")) %>%
  select(experiment, everything()) %>%

  # Add tissue/location information
  mutate(tissue = case_when(grepl("Retina", experiment) ~ "Retina",
                            grepl("Cerebellum", experiment) ~ "Cerebellum",
                            grepl("Victoria Knockout", experiment) ~ "Retina"),
         matched_sample_info = case_when(grepl("Cerebellum", experiment) ~ "same-mouse-same-
                                         grepl("Multiome Retina", experiment) ~ "same-mouse-
                                         grepl("More Retina", experiment) ~ "different-mouse
                                         grepl("Victoria Knockout", experiment) ~ "same-mous
                                         grepl("Stressed Retina", experiment) ~ "same-mouse-
         wet_lab_info = case_when(grepl("DYE_4687", DYE) ~ "done later, not enough high qual
         #unique_ID = row_number(),
         matched_sample_id = paste(Sample, assay, sep = "_")) %>%
    arrange(experiment, condition, Sample, assay) %>%
  # save data
  write_tsv(file.path(results_dir, glue::glue("cohorts_10x_rna_atac_testing_phase_{Sys.Date
```

```
## New names:
## * `` -> `...12`
```

7 10x matched scRNA-seq and scATAC-seq cohort

We will filter based on matched samples and paired assays. The `Sample` column indicates the unique sample used for sequencing.

```
df <- df_processed %>%
  filter(multiome_10x == "no",

         # we will keep experiments that assays were performed at the same animal and tissu
         matched_sample_info == "same-mouse-same-tissue")
```

7.1 Type of sequencing assay and unit

We should investigate if there are samples from different sequencing technologies and unit.

```
# Was nucleus or whole cell used for the sequencing?
seq_unit_samples <- unique(df$seq_unit)

# What type of assay was used?
assay_samples <- unique(df$assay)

# What type of seq_technology was used?
seq_technology_assay_samples <- unique(df$seq_technology_assay)
```

Single cell sequencing was done by using nucleus, cell and there are 10Xv2_ATAC, 10Xv3_RNA sequencing technologies and assays in the database. Cohort is formed and processed accordingly.

7.2 Number of samples per experiment

Table 1: Summary of samples per experiment

experiment	n
Cerebellum	9
Stressed Retina	3
Victoria Knockout	8

7.3 Number of samples per seq_technology_assay

Here, we investigate the number of libraries per assay, i.e., `seq_technology_assay` and per `Sample`.

Table 2: Number of samples per seq_technology_assay

experiment	tissue	condition	Sample	seq_unit	seq_technology_assay	n
Cerebellum	Cerebellum	age	6 week cerebellum	cell	10Xv3_RNA	1
Cerebellum	Cerebellum	age	6 week cerebellum	nucleus	10Xv2_ATAC	2
Cerebellum	Cerebellum	age	P0 cerebellum	cell	10Xv3_RNA	1
Cerebellum	Cerebellum	age	P0 cerebellum	nucleus	10Xv2_ATAC	1
Cerebellum	Cerebellum	sorted	ATOH HI	cell	10Xv3_RNA	1
Cerebellum	Cerebellum	sorted	ATOH HI	nucleus	10Xv2_ATAC	1
Cerebellum	Cerebellum	sorted	ATOH Low	cell	10Xv3_RNA	1
Cerebellum	Cerebellum	sorted	ATOH Low	nucleus	10Xv2_ATAC	1
Stressed Retina	Retina	LPS Injection	LPS	cell	10Xv3_RNA	1
Stressed Retina	Retina	LPS Injection	LPS_ATAC	nucleus	10Xv2_ATAC	1
Stressed Retina	Retina	PBS Injection	PBS	cell	10Xv3_RNA	1
Victoria Knockout	Retina	knock-out	SEKO_21	cell	10Xv3_RNA	1
Victoria Knockout	Retina	knock-out	SEKO_21	nucleus	10Xv2_ATAC	1
Victoria Knockout	Retina	knock-out	SEKO_25	cell	10Xv3_RNA	1
Victoria Knockout	Retina	knock-out	SEKO_25	nucleus	10Xv2_ATAC	1
Victoria Knockout	Retina	wt	Wt1	cell	10Xv3_RNA	1
Victoria Knockout	Retina	wt	Wt1	nucleus	10Xv2_ATAC	1
Victoria Knockout	Retina	wt	Wt2	cell	10Xv3_RNA	1
Victoria Knockout	Retina	wt	Wt2	nucleus	10Xv2_ATAC	1

7.4 Summary of samples

Table 3: Summary of samples

experiment	tissue	condition	Sample	seq_unit	seq_technology_assay
Cerebellum	Cerebellum	age	6 week cerebellum	nucleus	10Xv2_ATAC
Cerebellum	Cerebellum	age	6 week cerebellum	nucleus	10Xv2_ATAC
Cerebellum	Cerebellum	age	6 week cerebellum	cell	10Xv3_RNA
Cerebellum	Cerebellum	age	P0 cerebellum	nucleus	10Xv2_ATAC
Cerebellum	Cerebellum	age	P0 cerebellum	cell	10Xv3_RNA
Cerebellum	Cerebellum	sorted	ATOH HI	nucleus	10Xv2_ATAC
Cerebellum	Cerebellum	sorted	ATOH HI	cell	10Xv3_RNA
Cerebellum	Cerebellum	sorted	ATOH Low	nucleus	10Xv2_ATAC
Cerebellum	Cerebellum	sorted	ATOH Low	cell	10Xv3_RNA
Stressed Retina	Retina	LPS Injection	LPS	cell	10Xv3_RNA
Stressed Retina	Retina	LPS Injection	LPS_ATAC	nucleus	10Xv2_ATAC
Stressed Retina	Retina	PBS Injection	PBS	cell	10Xv3_RNA
Victoria Knockout	Retina	knock-out	SEKO_21	nucleus	10Xv2_ATAC
Victoria Knockout	Retina	knock-out	SEKO_21	cell	10Xv3_RNA
Victoria Knockout	Retina	knock-out	SEKO_25	nucleus	10Xv2_ATAC
Victoria Knockout	Retina	knock-out	SEKO_25	cell	10Xv3_RNA
Victoria Knockout	Retina	wt	Wt1	nucleus	10Xv2_ATAC
Victoria Knockout	Retina	wt	Wt1	cell	10Xv3_RNA
Victoria Knockout	Retina	wt	Wt2	nucleus	10Xv2_ATAC
Victoria Knockout	Retina	wt	Wt2	cell	10Xv3_RNA

8 10x Genomics Multiome cohort

```
df <- df_processed %>%
  filter(multiome_10x == "yes")
```

8.1 Type of sequencing assay and seq_unit

We should investigate if there are samples from two different sequencing technologies and unit.

```
# Was nucleus or whole cell used for the sequencing?
seq_unit_samples <- unique(df$seq_unit)

# What type of assay was used?
assay_samples <- unique(df$assay)

# What type of seq_technology was used?
seq_technology_assay_samples <- unique(df$seq_technology_assay)
```

Single cell sequencing was done by using nucleus and there are 10X_ATAC, 10X_RNA sequencing technologies and assays in the database. Cohort is formed and processed accordingly.

8.2 Number of samples per experiment

Table 4: Summary of samples per experiment

experiment	n
Multiome Retina	6

8.3 Number of samples per seq_technology_assay

Here, we investigate the number of libraries per assay, i.e., `seq_technology_assay` and per `Sample`.

Table 5: Number of samples per seq_technology_assay

experiment	tissue	condition	Sample	seq_unit	seq_technology_assay	n
Multiome Retina	Retina	age	Adult Retina	nucleus	10X_ATAC	1
Multiome Retina	Retina	age	Adult Retina	nucleus	10X_RNA	1
Multiome Retina	Retina	age	E14.5 Retina	nucleus	10X_ATAC	1
Multiome Retina	Retina	age	E14.5 Retina	nucleus	10X_RNA	1
Multiome Retina	Retina	age	P0 Retina	nucleus	10X_ATAC	1
Multiome Retina	Retina	age	P0 Retina	nucleus	10X_RNA	1

8.4 Summary of samples

Table 6: Summary of samples

experiment	tissue	condition	Sample	seq_unit	seq_technology_assay
Multiome Retina	Retina	age	Adult Retina	nucleus	10X_ATAC
Multiome Retina	Retina	age	Adult Retina	nucleus	10X_RNA
Multiome Retina	Retina	age	E14.5 Retina	nucleus	10X_ATAC
Multiome Retina	Retina	age	E14.5 Retina	nucleus	10X_RNA
Multiome Retina	Retina	age	P0 Retina	nucleus	10X_ATAC
Multiome Retina	Retina	age	P0 Retina	nucleus	10X_RNA

9 Notes

I have identified the following datasets that **almost** fit the criteria for the testing phase:

- **10x matched scRNA-seq and scATAC-seq**: `Victoria Knockout` experiment with 1 replicate/knock-out group (4 samples for 10x RNA + 4 samples 10x ATAC). Replicates could be potentially grouped together and have 2 replicates for WT and 2 replicates for knock-out.
- **10x Genomics Multiome**: `Multiome Retina` experiment with 1 replicate/age group (3 samples for 10x RNA (Multiome) + 3 samples for 10x ATAC (multiome).

10 References

- `More Retina` and `Stressed retina` experiments published by Norrie et al., 2025[3].
- `Victoria Knockout` experiment published by Honnell et al., 2022[4].

[3] https://doi.org/10.1016/j.devcel.2024.12.014
[4] https://www.nature.com/articles/s41467-021-27924-y#Sec13

11 Session Info

```
## R version 4.4.0 (2024-04-24)
## Platform: x86_64-pc-linux-gnu
## Running under: Red Hat Enterprise Linux 8.8 (Ootpa)
##
## Matrix products: default
## BLAS:   /usr/lib64/libblas.so.3.8.0
## LAPACK: /usr/lib64/liblapack.so.3.8.0
##
## locale:
##  [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
##  [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
##  [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
##  [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
##  [9] LC_ADDRESS=C               LC_TELEPHONE=C
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
##
## time zone: America/Chicago
## tzcode source: system (glibc)
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
##  [1] readxl_1.4.3    knitr_1.48      lubridate_1.9.3 forcats_1.0.0
##  [5] stringr_1.5.1   dplyr_1.1.4     purrr_1.0.2     readr_2.1.5
##  [9] tidyr_1.3.1     tibble_3.2.1    ggplot2_3.5.1   tidyverse_2.0.0
## [13] yaml_2.3.10
##
## loaded via a namespace (and not attached):
##  [1] bit_4.0.5         gtable_0.3.5      jsonlite_1.8.8    crayon_1.5.3
##  [5] compiler_4.4.0    tidyselect_1.2.1  parallel_4.4.0    jquerylib_0.1.4
##  [9] scales_1.3.0      fastmap_1.2.0     mime_0.12         R6_2.5.1
## [13] generics_0.1.3    munsell_0.5.1     bslib_0.8.0       pillar_1.9.0
## [17] tzdb_0.4.0        rlang_1.1.4       utf8_1.2.4        stringi_1.8.4
## [21] cachem_1.1.0      xfun_0.47         sass_0.4.9        bit64_4.0.5
## [25] timechange_0.3.0  cli_3.6.3         withr_3.0.1       magrittr_2.0.3
## [29] digest_0.6.37     grid_4.4.0        vroom_1.6.5       hms_1.1.3
## [33] lifecycle_1.0.4   vctrs_0.6.5       evaluate_0.24.0   glue_1.7.0
## [37] cellranger_1.1.0  fansi_1.0.6       colorspace_2.1-1  rmarkdown_2.28
## [41] tools_4.4.0       pkgconfig_2.0.3   htmltools_0.5.8.1
```