



Create cohort

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

Project: Comprehensive Omics Catalogue for Hartwell

St. Jude Children's Research Hospital BioHackathon Team 1

Date started: 09/04/2024 Date completed: 9/06/2024 Report generated: 12:46:14 CDT
09/11/2024

1 Information about this notebook

This is an exploratory analysis of the data availability in terms of assays in the Comprehensive Omics Catalogue for Hartwell.

For demo purposes, we use dummy data cohort and subset by human brain tumor samples. In addition, we generate random fake SJUID per brain cancer type as this information is not contained in the demo cohort. This cohort will be used for further analysis.

2 Set up

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

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_dir <- file.path(analysis_dir, "input")  
  
# We will first read in metadata file as we need to define sample_name  
metadata_file <- file.path(input_dir, input_file) # metadata input file  
  
source(paste0(analysis_dir, "/util/generate-fake-SJUID.R"))
```

4 Read metadata file

We will subset by human brain tumor samples.

```
# Read metadata  
project_df <- read.csv(metadata_file, stringsAsFactors=FALSE) %>%  
  
# Add cancer_type_brain: Ependymoma, HGG, LGG, Medulloblastoma  
add_column(cancer_type_brain = "other") %>%  
mutate(cancer_type_brain = case_when(grepl("Ependymoma", Disease) ~ "Ependymoma",  
                                     grepl("HGG", Disease) ~ "HGG",  
                                     grepl("LGG", Disease) ~ "LGG",  
                                     grepl("MedulloBlastoma", Disease) ~ "Medulloblastoma"),  
       Assay = Omics.Method) %>%  
mutate(across(where(is.character), ~ na_if(., ""))) %>% # Omics Method for NA  
filter(!cancer_type_brain == "other",  
       !is.na(cancer_type_brain),  
       !is.na(Omics.Method),  
       Source == "Human") %>%  
select(Source, Disease, Assay, Omics.Method.Detail, Site, Sub.Group, cancer_type_brain)
```

4.1 Generate fake SJUID

We will generate random fake SJUID per brain cancer type as this information is not contained in the demo cohort.

```
# Create a smaller set of unique strings, each starting with "SJH"
unique_strings <- paste0("SJH", sapply(1:80, function(x) generate_string(8)))

# Sample from this set to create a vector of 100 strings, allowing duplicates
SJUID <- sample(unique_strings, 100, replace = TRUE)

# Generate vector for `cancer_type_brain`
cancer_type_brain_vec <- c("Ependymoma", "HGG", "LGG", "Medulloblastoma")
n <- 25 # random number
cancer_type_brain <- rep(cancer_type_brain_vec, each=n)

# Assign `SJUID` to `cancer_type_brain`
bind_df <- cbind(SJUID, cancer_type_brain) %>%
  as.data.frame()

# Merge both df
df <- project_df %>%
  left_join(bind_df, by = "cancer_type_brain", relationship = "many-to-many") %>%
  unique() %>%
  mutate(match_id_assay = paste(SJUID, Assay, sep = "_")) %>%
  distinct(match_id_assay, .keep_all = TRUE)

# Save file
write.csv(df, file.path(input_dir, "cohort.csv"), row.names = FALSE)
```

4.2 Generate fake longitudinal data

We will generate random longitudinal data per SJUID and per brain cancer type as this information is not contained in the demo cohort.

```
# Generate vector for `cancer_type_brain`
longitudinal_vec <- c("Diagnosis", "Remission", "Relapse", "Deceased")
n <- length(df$SJUID)
longitudinal <- rep(longitudinal_vec, each=n)

# Assign `longitudinal` TO df
#longitudinal_bind_df <- cbind(df, longitudinal) %>%
# as.data.frame()

longitudinal_df <- cbind(df, longitudinal) %>%
  #left_join(longitudinal_bind_df, by = "SJUID", relationship = "many-to-many") %>%
  unique() %>%
  mutate(match_id_longitudinal_assay = paste(SJUID, longitudinal, Assay, sep = "_")) %>%
  distinct(match_id_longitudinal_assay, .keep_all = TRUE)

# Save file
write.csv(longitudinal_df, file.path(input_dir, "cohort-longitudinal.csv"), row.names = FALSE)
```

5 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:   /research/rgs01/applications/hpcf/authorized_apps/rhel8_apps/lapack/3.10.1/install/lib64/libblas.so.3
## LAPACK: /research/rgs01/applications/hpcf/authorized_apps/rhel8_apps/lapack/3.10.1/install/lib64/liblapack.so.3
##
## 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] lubridate_1.9.3 forcats_1.0.0  stringr_1.5.1  dplyr_1.1.4
## [5] purrr_1.0.2     readr_2.1.5  tidyr_1.3.1    tibble_3.2.1
## [9] ggplot2_3.5.1   tidyverse_2.0.0
##
## loaded via a namespace (and not attached):
## [1] gtable_0.3.5      jsonlite_1.8.8    compiler_4.4.0    tidyselect_1.2.1
## [5] jquerylib_0.1.4   scales_1.3.0      yaml_2.3.10       fastmap_1.2.0
## [9] mime_0.12         R6_2.5.1          generics_0.1.3    knitr_1.48
## [13] munsell_0.5.1     bslib_0.8.0       pillar_1.9.0      tzdb_0.4.0
## [17] rlang_1.1.4       utf8_1.2.4        stringi_1.8.4     cachem_1.1.0
## [21] xfun_0.47         sass_0.4.9        timechange_0.3.0  cli_3.6.3
## [25] withr_3.0.1       magrittr_2.0.3    digest_0.6.37     grid_4.4.0
## [29] hms_1.1.3         lifecycle_1.0.4   vctrs_0.6.5       evaluate_0.24.0
## [33] glue_1.7.0        fansi_1.0.6       colorspace_2.1-1  rmarkdown_2.28
## [37] tools_4.4.0       pkgconfig_2.0.3   htmltools_0.5.8.1
```