

hackathon

```
library(RColorBrewer)
library(tidyverse)
```

```
## — Attaching core tidyverse packages — tidyverse 2.0.0 —
## ✓ dplyr      1.1.4      ✓ readr      2.1.5
## ✓ forcats    1.0.0      ✓ stringr    1.5.1
## ✓ ggplot2    3.5.0      ✓ tibble     3.2.1
## ✓ lubridate  1.9.3      ✓ tidyr      1.3.1
## ✓ purrr      1.0.2
## — Conflicts — tidyverse_conflicts() —
## ✖ dplyr::filter() masks stats::filter()
## ✖ dplyr::lag()     masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts
to become errors
```

```
library(dplyr)
library(ggplot2)
library(gganimate)
```

```
## No renderer backend detected. gganimate will default to writing frames to separate fi
les
## Consider installing:
## - the `gifsqi` package for gif output
## - the `av` package for video output
## and restarting the R session
```

for the hackathon, focused on dataset visualizations and cell atlas visualizations

```
metadata = read.csv("/Users/riahcul/Downloads/20241106_allmetadata.csv")
metadata[metadata == ""] <- NA

spatialdata = read.csv("/Users/riahcul/Downloads/locofsatialdata.csv")
spatialdata[spatialdata == ""] <- NA
```

```
colnames(metadata)
```

```
## [1] "dataset_name"      "region_imaged"     "age"
## [4] "sex"               "donor"             "tissue"
## [7] "disease"           "renamed_tissue"    "large_tissue_unit"
```

```
colnames(spatialdata)
```

## [1]	"manuscript"	"title"	"doi"
## [4]	"priority"	"folder_name"	"x_col_name"
## [7]	"y_col_name"	"celltype_col_name"	"uniqueregion_col_name"
## [10]	"metadata_file_added"	"tissue_col_name_md"	"disease_col_name_md"
## [13]	"donor_col_name_md"	"age_col_name"	"sex_col_name"
## [16]	"has_tissue_data"	"donor_col_name_seg"	"donor_col_name_mdd"
## [19]	"associated_md"	"email_reason"	"need_to_email"
## [22]	"need_to_email_md"	"email_drafted"	"emailed"
## [25]	"author_email"	"been_emailed"	"received_data"
## [28]	"singlecell_data_loc"	"image_data_loc"	"priority_2"
## [31]	"species"	"tissue"	"disease"
## [34]	"modality"	"lab"	"added_by"
## [37]	"checked_by"	"person_downloaded"	"not_usable"
## [40]	"rprocessing_notes"	"processed"	

```
unique(metadata$tissue)
```

##	[1]	"breast"	NA	"bone marrow"
##	[4]	"tonsil"	"spleen"	"lymph node"
##	[7]	"head and neck"	"thymus"	"liver"
##	[10]	"biliary system"	"stomach"	"colon"
##	[13]	"pancreas"	"ovary"	"uterus"
##	[16]	"placenta"	"muscle"	"kidney"
##	[19]	"nerve"	"soft tissue"	"tendon"
##	[22]	"bone"	"skin"	"prostate"
##	[25]	"adrenal gland"	"testis"	"brain"
##	[28]	"meninges"	"lung"	"parathyroid"
##	[31]	"thyroid"	"pleura"	"musculoskeletal"
##	[34]	"bladder"	"vertebral body t7"	"decidua"
##	[37]	"small intestine"	"esophagus"	"blood"
##	[40]	"fallopian tube"	"ovary normal"	"ovtp1"
##	[43]	"ovtp10"	"ovtp100"	"ovtp101"
##	[46]	"ovtp102"	"ovtp103"	"ovtp104"
##	[49]	"ovtp105"	"ovtp106"	"ovtp107"
##	[52]	"ovtp108"	"ovtp109"	"ovtp11"
##	[55]	"ovtp110"	"ovtp111"	"ovtp112"
##	[58]	"ovtp113"	"ovtp116"	"ovtp118"
##	[61]	"ovtp119"	"ovtp120"	"ovtp121"
##	[64]	"ovtp122"	"ovtp123"	"ovtp124"
##	[67]	"ovtp125"	"ovtp127"	"ovtp13"
##	[70]	"ovtp15"	"ovtp16"	"ovtp17"
##	[73]	"ovtp18"	"ovtp19"	"ovtp2"
##	[76]	"ovtp20"	"ovtp21"	"ovtp22"
##	[79]	"ovtp24"	"ovtp26"	"ovtp27"
##	[82]	"ovtp28"	"ovtp29"	"ovtp3"
##	[85]	"ovtp30"	"ovtp31"	"ovtp32"
##	[88]	"ovtp33"	"ovtp34"	"ovtp35"
##	[91]	"ovtp36"	"ovtp37"	"ovtp38"
##	[94]	"ovtp39"	"ovtp4"	"ovtp40"
##	[97]	"ovtp41"	"ovtp42"	"ovtp43"
##	[100]	"ovtp44"	"ovtp45"	"ovtp46"
##	[103]	"ovtp47"	"ovtp49"	"ovtp5"
##	[106]	"ovtp50"	"ovtp51"	"ovtp53"
##	[109]	"ovtp54"	"ovtp55"	"ovtp56"
##	[112]	"ovtp58"	"ovtp59"	"ovtp6"
##	[115]	"ovtp60"	"ovtp61"	"ovtp63"
##	[118]	"ovtp64"	"ovtp65"	"ovtp66"
##	[121]	"ovtp67"	"ovtp68"	"ovtp69"
##	[124]	"ovtp7"	"ovtp70"	"ovtp71"
##	[127]	"ovtp72"	"ovtp73"	"ovtp74"
##	[130]	"ovtp75"	"ovtp76"	"ovtp77"
##	[133]	"ovtp78"	"ovtp79"	"ovtp8"
##	[136]	"ovtp80"	"ovtp81"	"ovtp82"
##	[139]	"ovtp83"	"ovtp84"	"ovtp85"
##	[142]	"ovtp87"	"ovtp88"	"ovtp89"
##	[145]	"ovtp9"	"ovtp90"	"ovtp91"
##	[148]	"ovtp92"	"ovtp93"	"ovtp95"

```
## [151] "ovtp96"          "ovtp97"          "ovtp98"
## [154] "ovtp99"
```

```
unique(metadata$disease)
```

```
## [1] "cancer"          NA          "normal"
## [4] "non-malignant tumor" "ARDS"      "COVID19"
## [7] "FLU"             "Healthy"   "inflammation"
## [10] "tuberculosis"    "osteoarthritis" "crc"
```

```
unique(metadata$large_tissue_unit)
```

```
## [1] "Reproductive System" NA          "Musculoskeletal System"
## [4] "Immune System"      "Digestive System"      "Urinary System"
## [7] "Nervous System"     "Integumentary System"  "Endocrine System"
## [10] "Respiratory System" "Circulatory System"
```

```
# newmeta_update <- metadata |>
#   mutate(
#     newAge = round(as.numeric(age)))
#
# newmeta_update <- newmeta_update |>
#   mutate(
#     disease = if_else(disease == "Healthy", "normal", disease)
#   )
#
# meta_select <- metadata[metadata$disease %in% c("cancer", "normal", "COVID19", "ARDS")]
#
# meta_select |>
#   ggplot(
#     aes(x=age, y= )
```

```
disease_freqs <- spatialdata |>
  group_by(disease) |>
  summarize(Frequency = n()) |>
  arrange(desc(Frequency))
```

```
disease_freqs |>
  ggplot(aes(x = disease, y=Frequency)) +
  geom_point(size=3) +
  geom_segment(aes(x= disease, xend=disease, y=0, yend = Frequency)) +
  theme(legend.position = "none") +
  labs(
    title = "Variation in Disease",
    x = "Diseases across Datasets",
  ) + theme_minimal()
```

