Hickey Lab!

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```
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(networkD3)
```

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

```
tissue_freq <- newmeta |>
  group_by(renamed_tissue) |>
  summarize(Frequency = n()) |>
  arrange(desc(Frequency))

print(tissue_freq)
```

```
## # A tibble: 37 × 2
##    renamed_tissue Frequency
##    <chr>              <int>
##  1 skin                1040
##  2 <NA>                 827
##  3 brain                803
##  4 liver                686
##  5 lung                 454
##  6 breast               289
##  7 uterus               216
##  8 colon                190
##  9 lymph node            85
## 10 stomach               45
## # ℹ 27 more rows
```

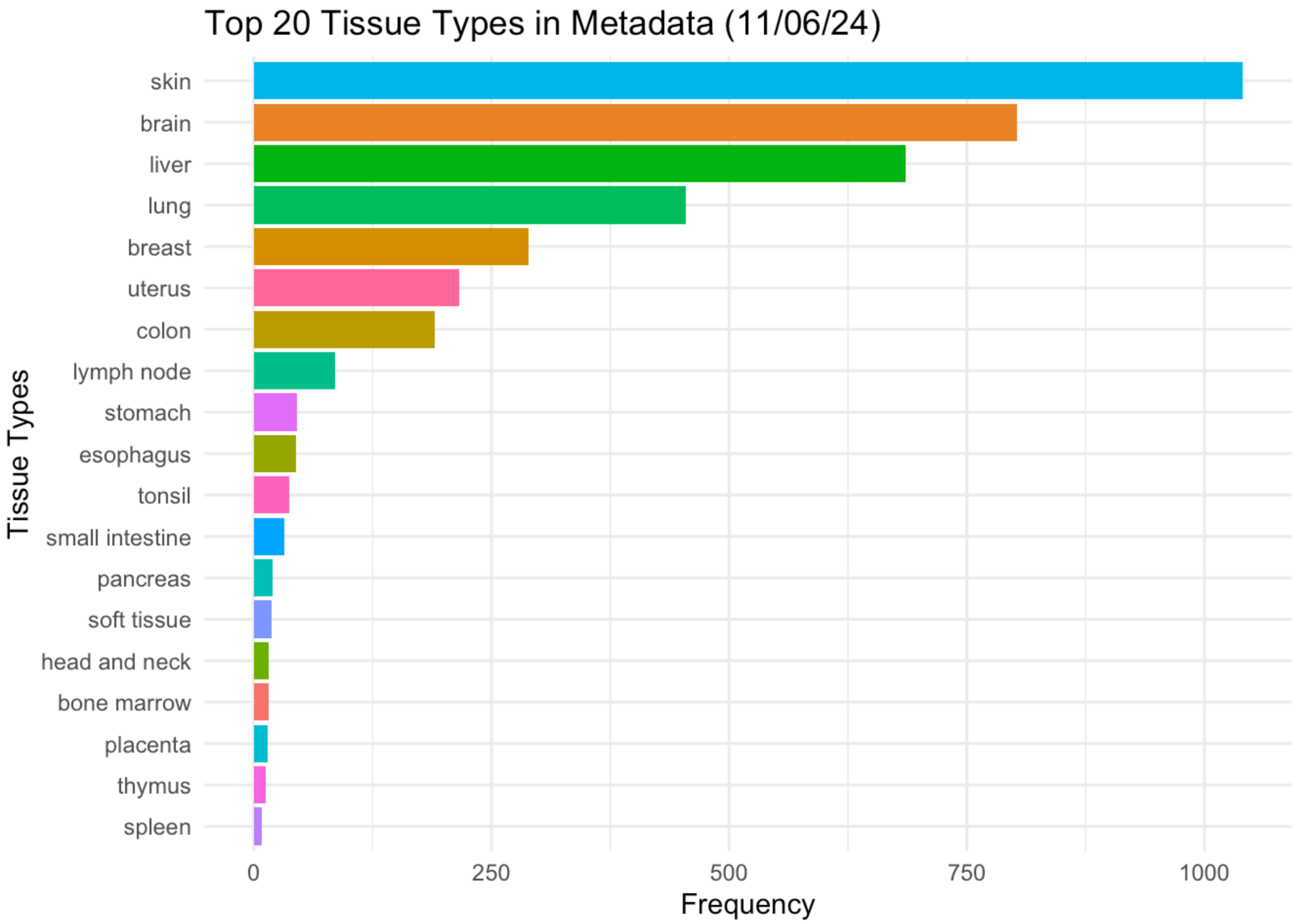
```
tissue_top <- head(tissue_freq, 20)
print(tissue_top)
```

```
## # A tibble: 20 × 2
##    renamed_tissue  Frequency
##    <chr>               <int>
##  1 skin                 1040
##  2 <NA>                  827
##  3 brain                 803
##  4 liver                 686
##  5 lung                  454
##  6 breast                289
##  7 uterus                216
##  8 colon                 190
##  9 lymph node             85
## 10 stomach                45
## 11 esophagus              44
## 12 tonsil                 37
## 13 small intestine        32
## 14 pancreas               20
## 15 soft tissue            19
## 16 bone marrow            16
## 17 head and neck          16
## 18 placenta               15
## 19 thymus                 13
## 20 spleen                  8
```

```
library(RColorBrewer)
library(viridisLite)

renamed_tissues <- table(tissue_top$tissue)
```

```
## Warning: Unknown or uninitialised column: `tissue`.
```

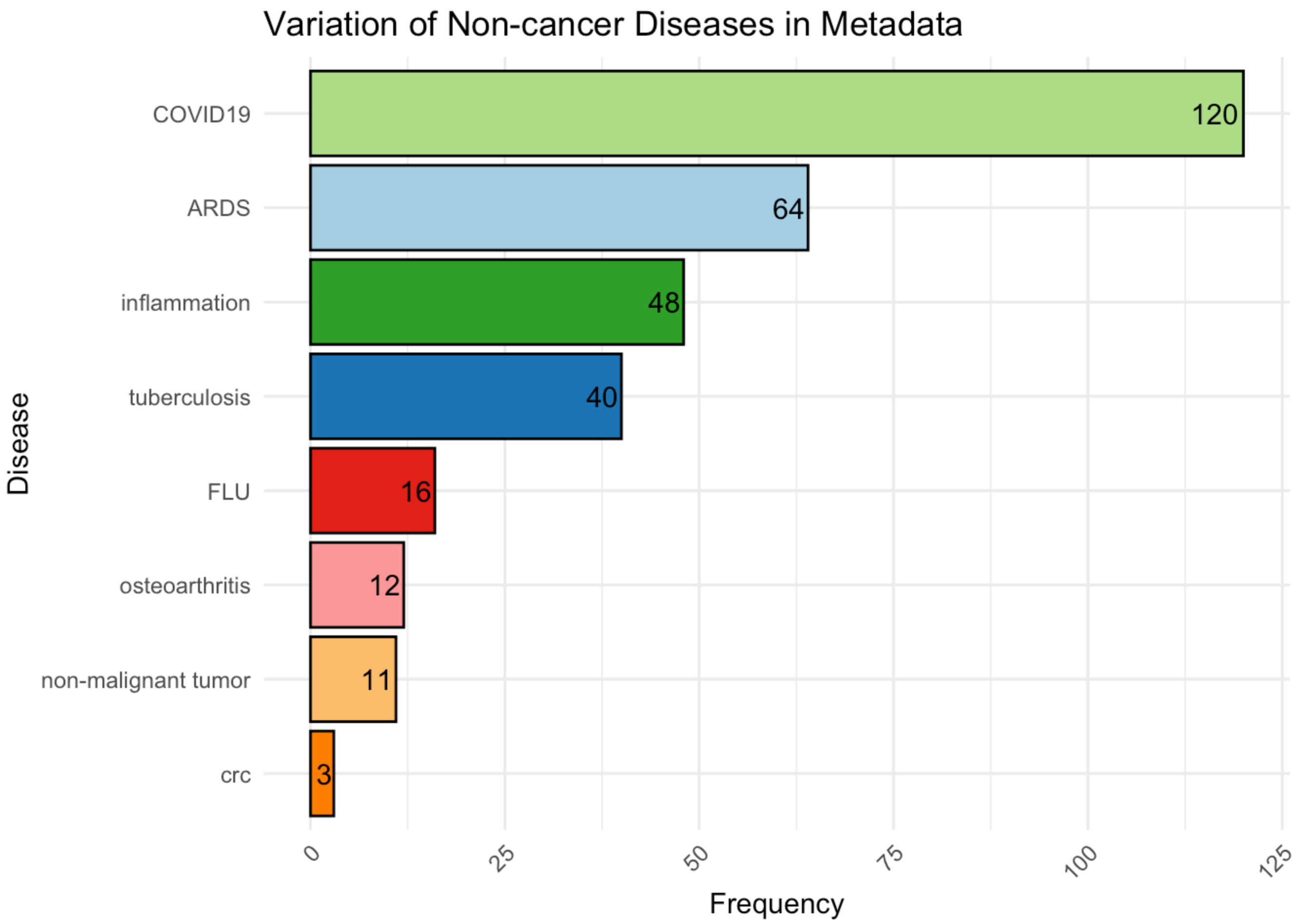
```
#mypalette <- brewer.pal(length(tissues), "Set3")
mypalette <- viridis(19)
#my_palette <- brewer.pal(19, "Set3")

tissue_top |>
  filter(renamed_tissue != "NA")|>
  ggplot(
    aes(x= reorder(renamed_tissue, Frequency), y = Frequency, fill = renamed_tissue)
  ) + geom_bar(stat= "identity") + coord_flip() +
  theme_minimal() +
  theme(legend.position = "none") +
  labs(
    title = "Top 20 Tissue Types in Metadata (11/06/24)",
    x = "Tissue Types"
  )
```



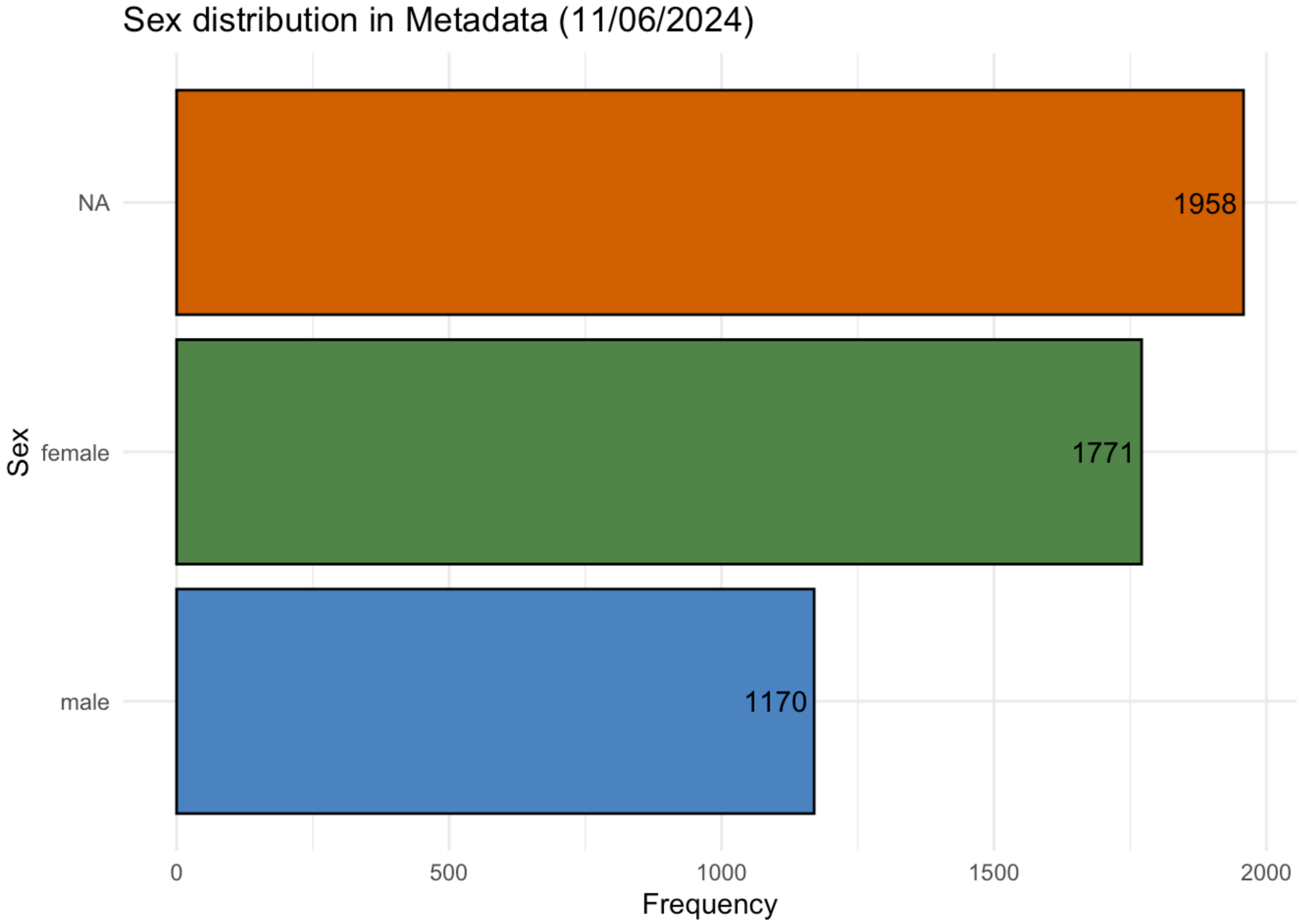
```
disease_freqs <- newmeta |>
  group_by(disease) |>
  summarize(Frequency = n()) |>
  arrange(desc(Frequency))

print(disease_freqs)
```

```
## # A tibble: 12 × 2
##    disease             Frequency
##    <chr>                   <int>
##  1 cancer                   1929
##  2 normal                   1605
##  3 <NA>                     1014
##  4 COVID19                   120
##  5 ARDS                       64
##  6 inflammation               48
##  7 tuberculosis               40
##  8 Healthy                    37
##  9 FLU                        16
## 10 osteoarthritis             12
## 11 non-malignant tumor        11
## 12 crc                         3
```

```
disease_freqs <- disease_freqs |>
  mutate(
    disease = if_else(disease == "Healthy", "normal", disease)
  )

#mypalette <- brewer.pal(length(tissues), "Set3")

library(ggplot2)
library(dplyr)
library(viridis)

mypalette <- brewer.pal(8, "Paired")

# Filtering out 'cancer' before passing to ggplot
disease_freqs |>
  filter(disease != "cancer") |>
  filter(disease != "normal") |>
  ggplot(aes(x = reorder(disease, Frequency), y = Frequency, fill = mypalette)) +
  geom_bar(stat = "identity", color = "black") +
  scale_fill_manual(values = mypalette) +
  theme_minimal() +
  theme(legend.position = "none") +
  theme(axis.text.x = element_text(angle = 45, vjust = 1, hjust = 1)) +
  geom_text(aes(label = Frequency), position = position_dodge(width=.9), hjust=1.1) +
  labs(
    title = "Variation of Non-cancer Diseases in Metadata",
    x = "Disease"
  ) +
  coord_flip()
```



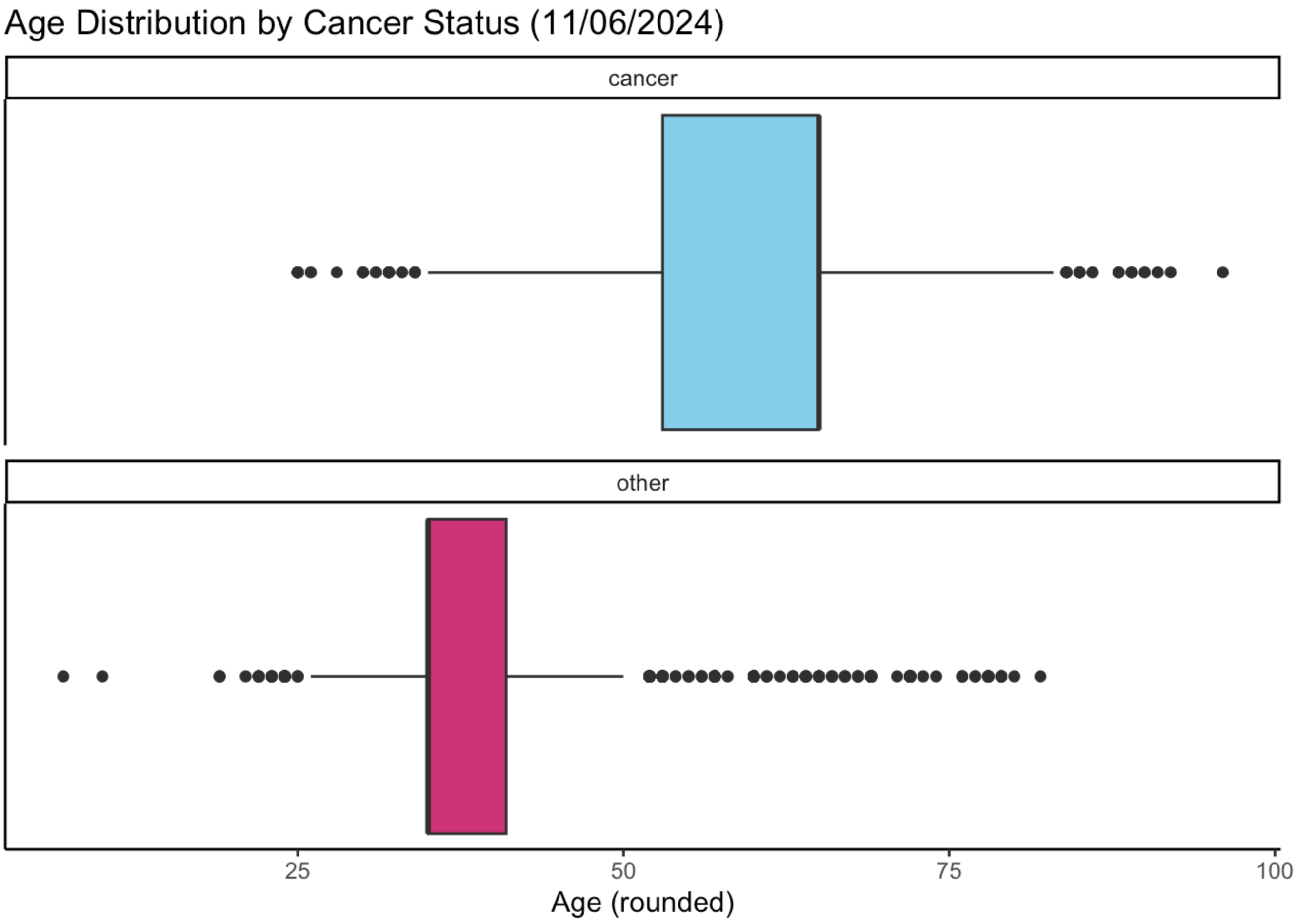
```
sex_freq <- newmeta |>
  group_by(sex) |>
  mutate(
    sex = if_else(sex == "unknown", NA_character_, sex)
    ) |>
  summarize(Frequency = n()) |>
  arrange(desc(Frequency))

sex_freq |>
  ggplot(
    aes(x= reorder(sex, Frequency), y = Frequency, fill = sex)
  ) + geom_bar(stat= "identity", color = "black") +
    scale_fill_manual(breaks = c("female", "male"),
                     values = c("#52854C", "#4E84C4"), na.value = "#D16103") +
   geom_text(aes(label = Frequency), position = position_dodge(width=.9), hjust=1.1) +
  theme_minimal() +
  theme(legend.position = "none") + coord_flip() +
  labs(
    title = "Sex distribution in Metadata (11/06/2024)",
    x = "Sex"
  )
```



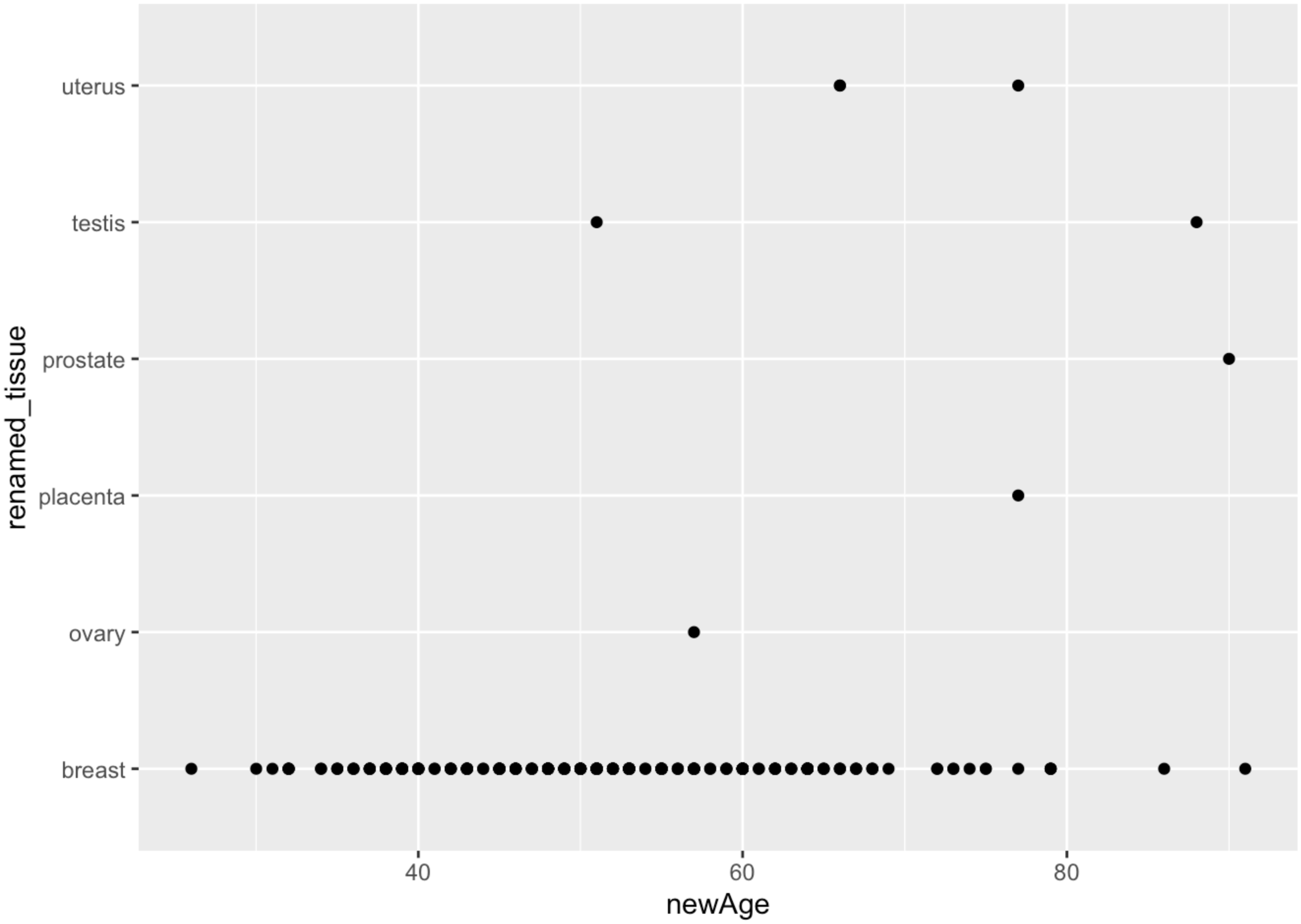
```
#newmetaupdate represents cancer or other and standardizes age
newmeta_update <- newmeta |>
  mutate(
    newDisease = if_else(disease == "cancer", "cancer", "other"))

newmeta_update <- newmeta_update |>
  mutate(
    newAge = round(as.numeric(age)))
```

```
## Warning: There was 1 warning in `mutate()`.
## ℹ In argument: `newAge = round(as.numeric(age))`.
## Caused by warning:
## ! NAs introduced by coercion
```

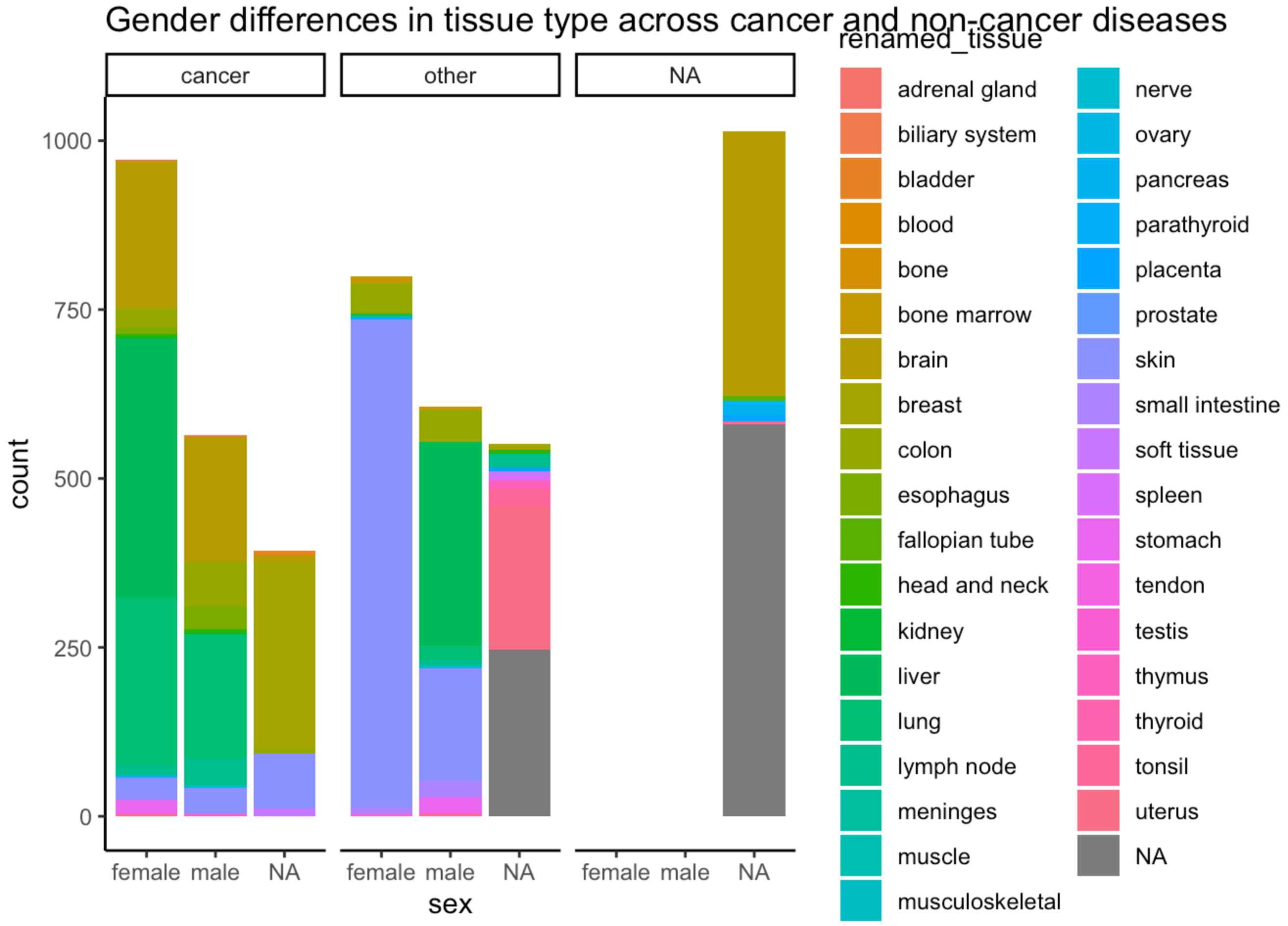
```
newmeta_update |>
  filter(!is.na(newDisease)) |>
  filter(!is.na(newAge)) |>
  ggplot(
    aes(x = newAge, fill = newDisease)) +
    geom_boxplot() +
  scale_fill_manual(breaks = c("cancer", "other"),
                    values = c("skyblue", "violetred3")) +
  facet_wrap(~newDisease, ncol =1) +
  labs(
    title = "Age Distribution by Cancer Status (11/06/2024)",
    x = "Age (rounded)"
  ) +
  theme_classic() +
  theme(legend.position = "none", axis.ticks.y = element_blank(), axis.text.y = element_blank())
```



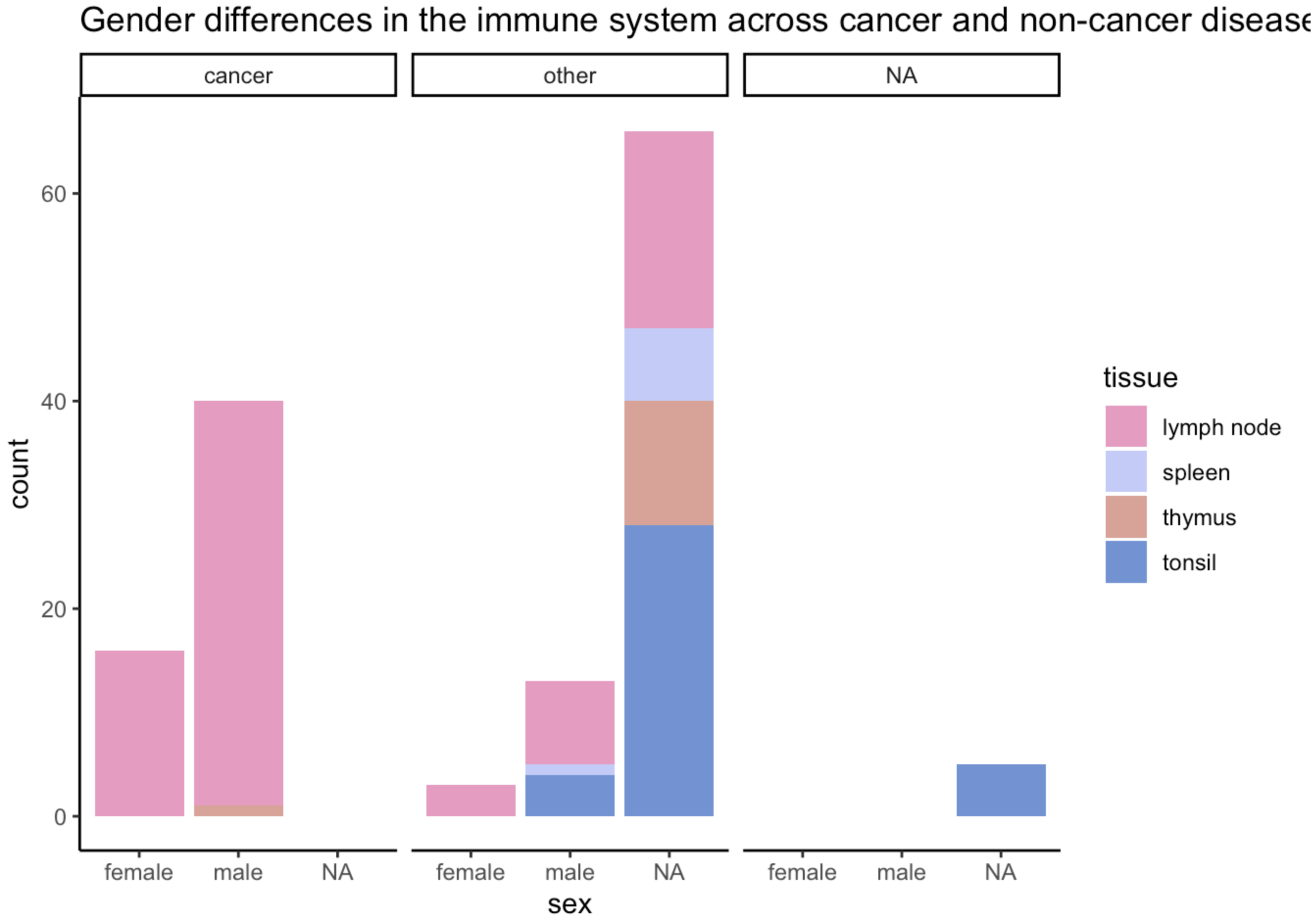
```
newmeta_update |>
  filter(newAge != "NA") |>
  filter(renamed_tissue != "NA") |>
  filter(large_tissue_unit == "Reproductive System") |>
  ggplot(
    aes(x = newAge, y = renamed_tissue)
  ) +
  geom_point()
```



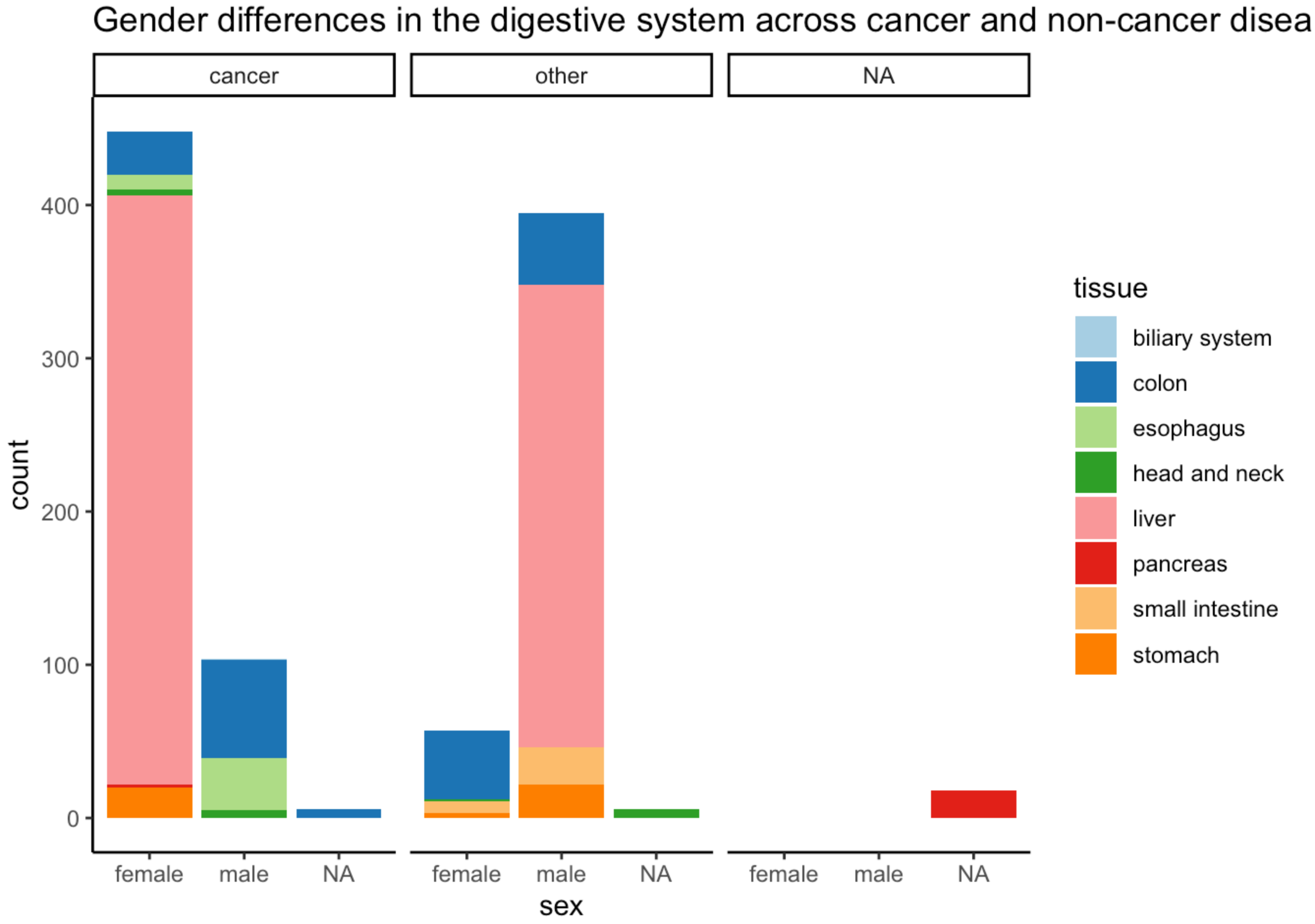
```
newmeta_update <- newmeta_update |>
   mutate(
    sex = if_else(sex == "unknown", NA_character_, sex)
    )

newmeta_update |>
  ggplot(
    aes(x = sex, fill = renamed_tissue)) +
  geom_bar(position = "stack") +
  facet_wrap(~newDisease) +
  labs(
    title = "Gender differences in tissue type across cancer and non-cancer diseases"
  ) +
  theme_classic()
```



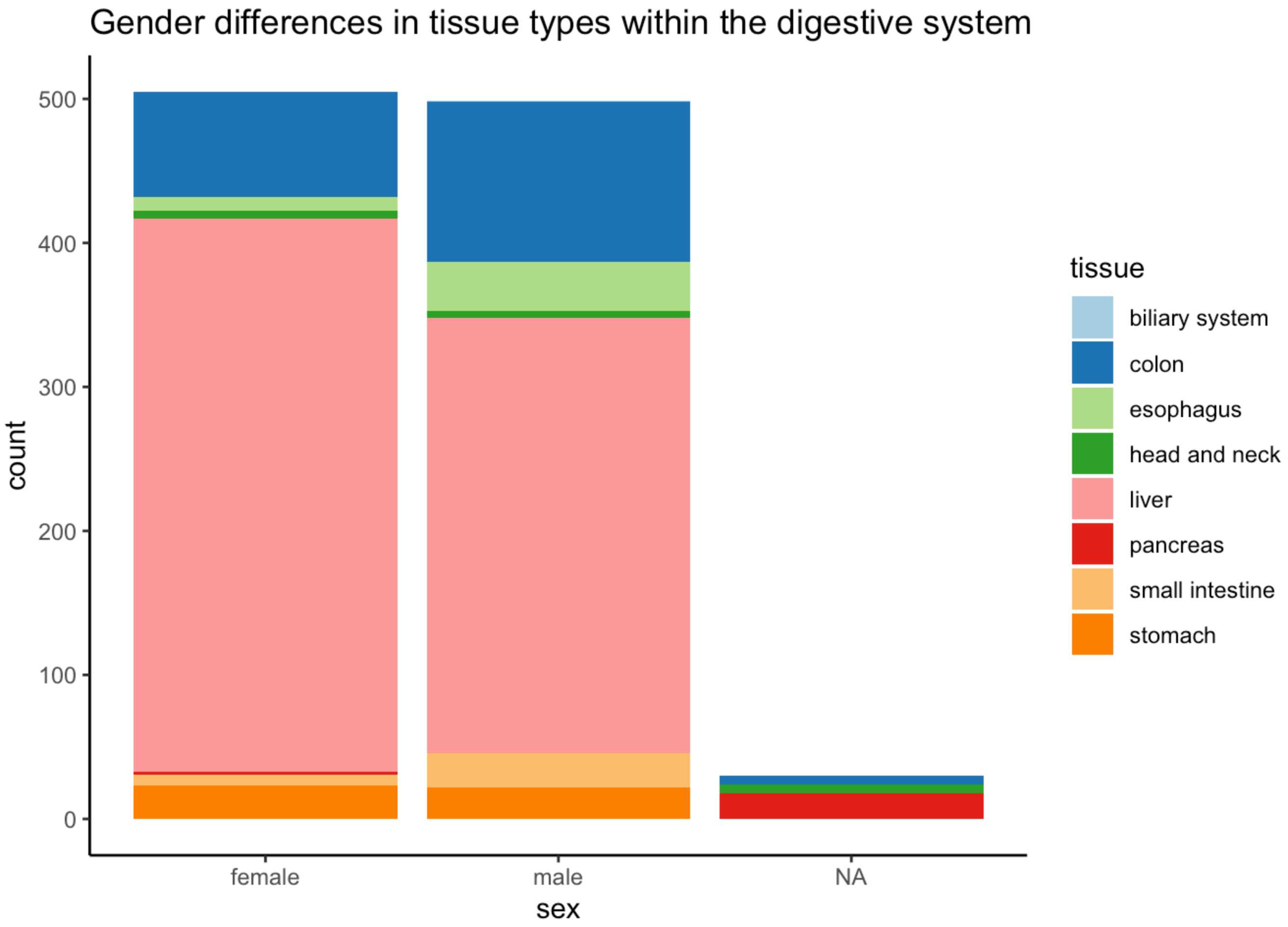
```r
library(wesanderson)

newmeta_update |>
  filter(large_tissue_unit == "Immune System") |>
  ggplot(
    aes(x = sex, fill = tissue)) +
  geom_bar(position = "stack") +
    scale_fill_manual(values = wes_palette("GrandBudapest2", n = 4)) +
  facet_wrap(~newDisease) +
  labs(
    title = "Gender differences in the immune system across cancer and non-cancer diseas
es"
  ) +
  theme_classic()
```



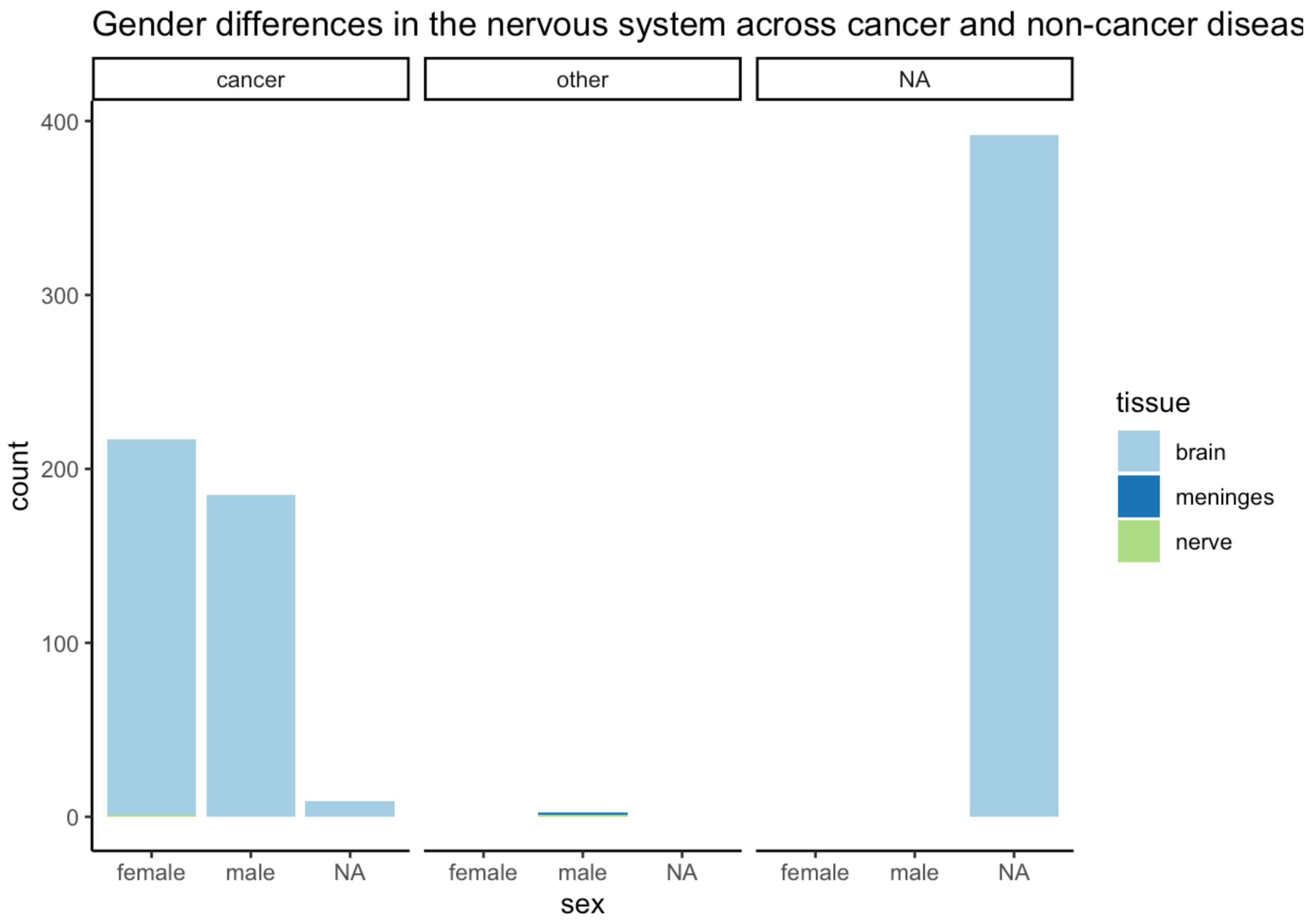
```
newmeta_update |>
  filter(large_tissue_unit == "Digestive System") |>
  ggplot(
    aes(x = sex, fill = tissue)) +
  geom_bar(position = "stack") +
  scale_fill_manual(values = brewer.pal(8, "Paired")) +
    facet_wrap(~newDisease) +
  labs(
    title = "Gender differences in the digestive system across cancer and non-cancer dis
eases"
  ) +
  theme_classic()
```



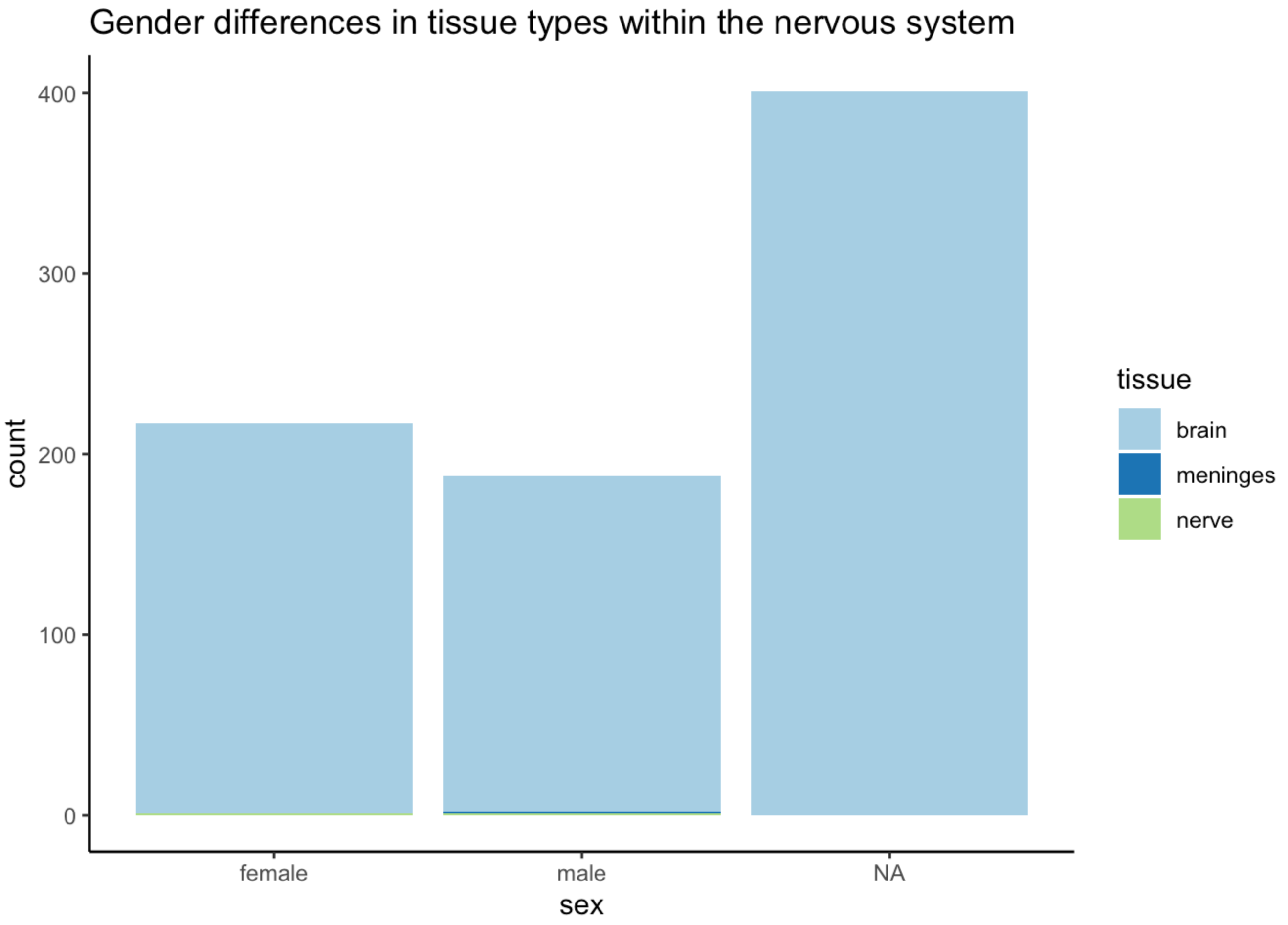
```
newmeta_update |>
  filter(large_tissue_unit == "Digestive System") |>
  ggplot(
    aes(x = sex, fill = tissue)) +
  geom_bar() +
  scale_fill_manual(values =brewer.pal(8, "Paired")) +
  labs(
    title = "Gender differences in tissue types within the digestive system"
  ) +
  theme_classic()
```



```
newmeta_update |>
  filter(large_tissue_unit == "Nervous System") |>
  ggplot(
    aes(x = sex, fill = tissue)) +
  geom_bar(position = "stack") +
  scale_fill_manual(values = brewer.pal(8, "Paired")) +
    facet_wrap(~newDisease) +
  labs(
    title = "Gender differences in the nervous system across cancer and non-cancer disea
ses"
  ) +
  theme_classic()
```



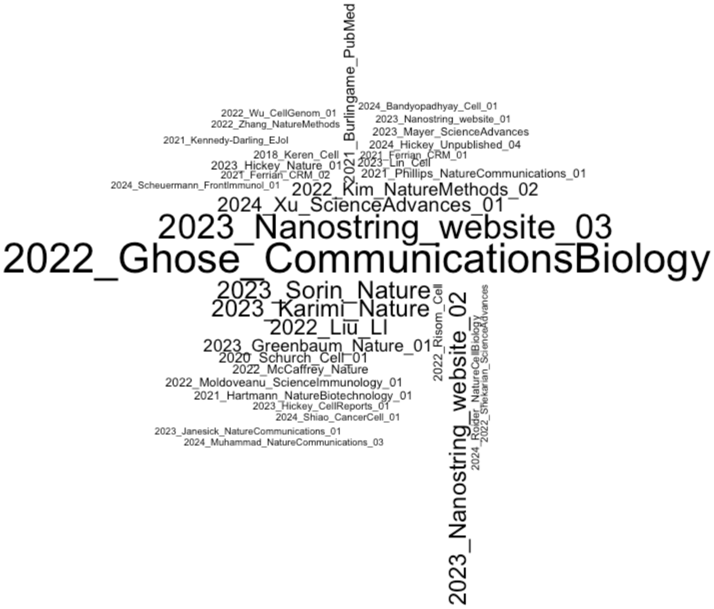
```
newmeta_update |>
  filter(large_tissue_unit == "Nervous System") |>
  ggplot(
    aes(x = sex, fill = tissue)) +
  geom_bar() +
  scale_fill_manual(values = brewer.pal(8, "Paired")) +
  labs(
    title = "Gender differences in tissue types within the nervous system"
  ) +
  theme_classic()
```



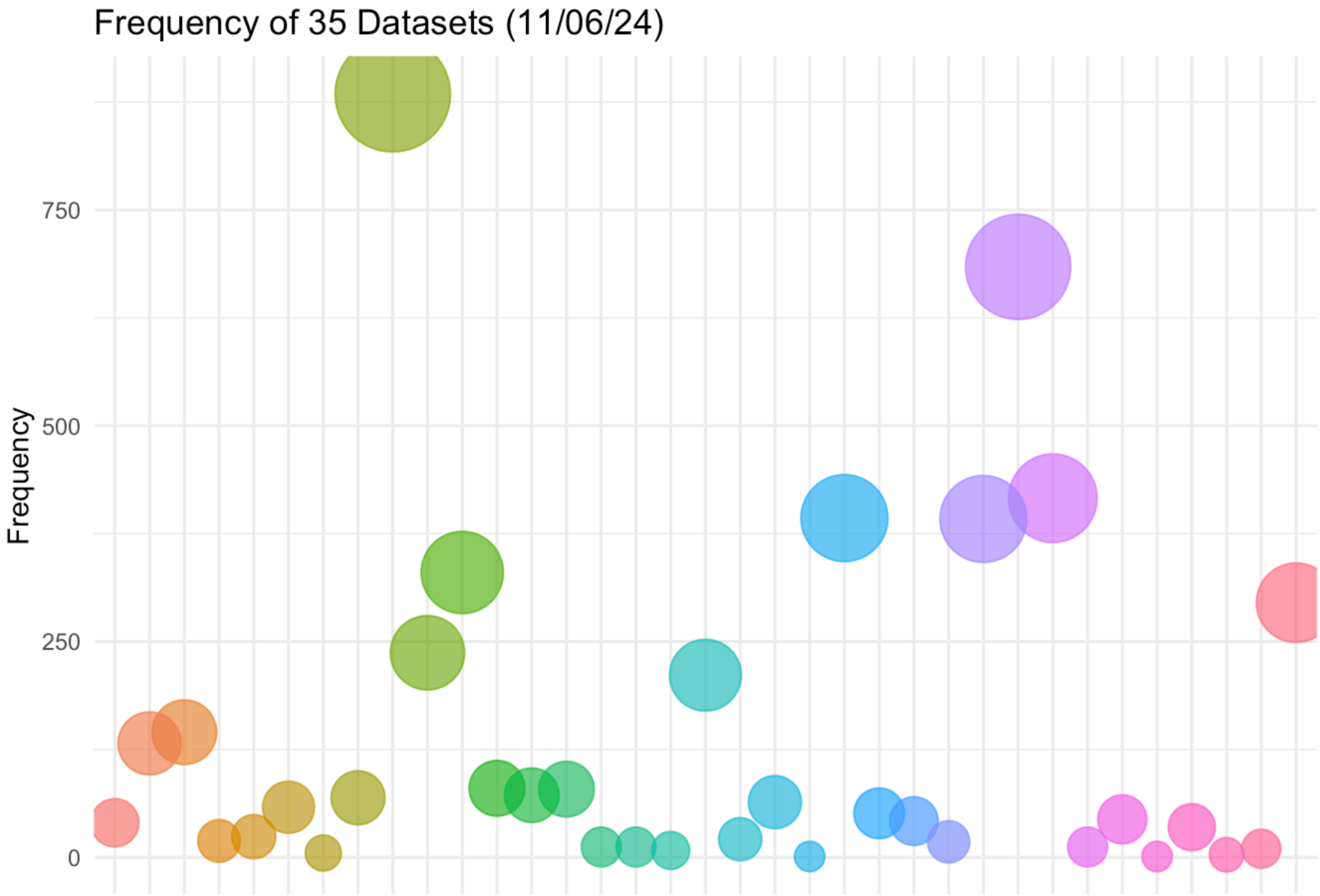
```
library(wordcloud)

word_freqs <- newmeta_update |>
  #mutate(dataset_name = str_replace(dataset_name, "^([\\d]{4}_[A-Za-z]+)_.*", "\\1")) |
>
  group_by(dataset_name) |>
  summarize(Frequency = n()) |>
  arrange(desc(Frequency))

print(word_freqs)
```

```
## # A tibble: 35 × 2
##    dataset_name                     Frequency
##    <chr>                                <int>
##  1 2022_Ghose_CommunicationsBiology       884
##  2 2023_Nanostring_website_03             684
##  3 2023_Sorin_Nature                      416
##  4 2023_Karimi_Nature                     393
##  5 2023_Nanostring_website_02             392
##  6 2022_Liu_LI                            330
##  7 2024_Xu_ScienceAdvances_01             295
##  8 2022_Kim_NatureMethods_02              237
##  9 2023_Greenbaum_Nature_01               211
## 10 2021_Burlingame_PubMed                 145
## # ℹ 25 more rows
```

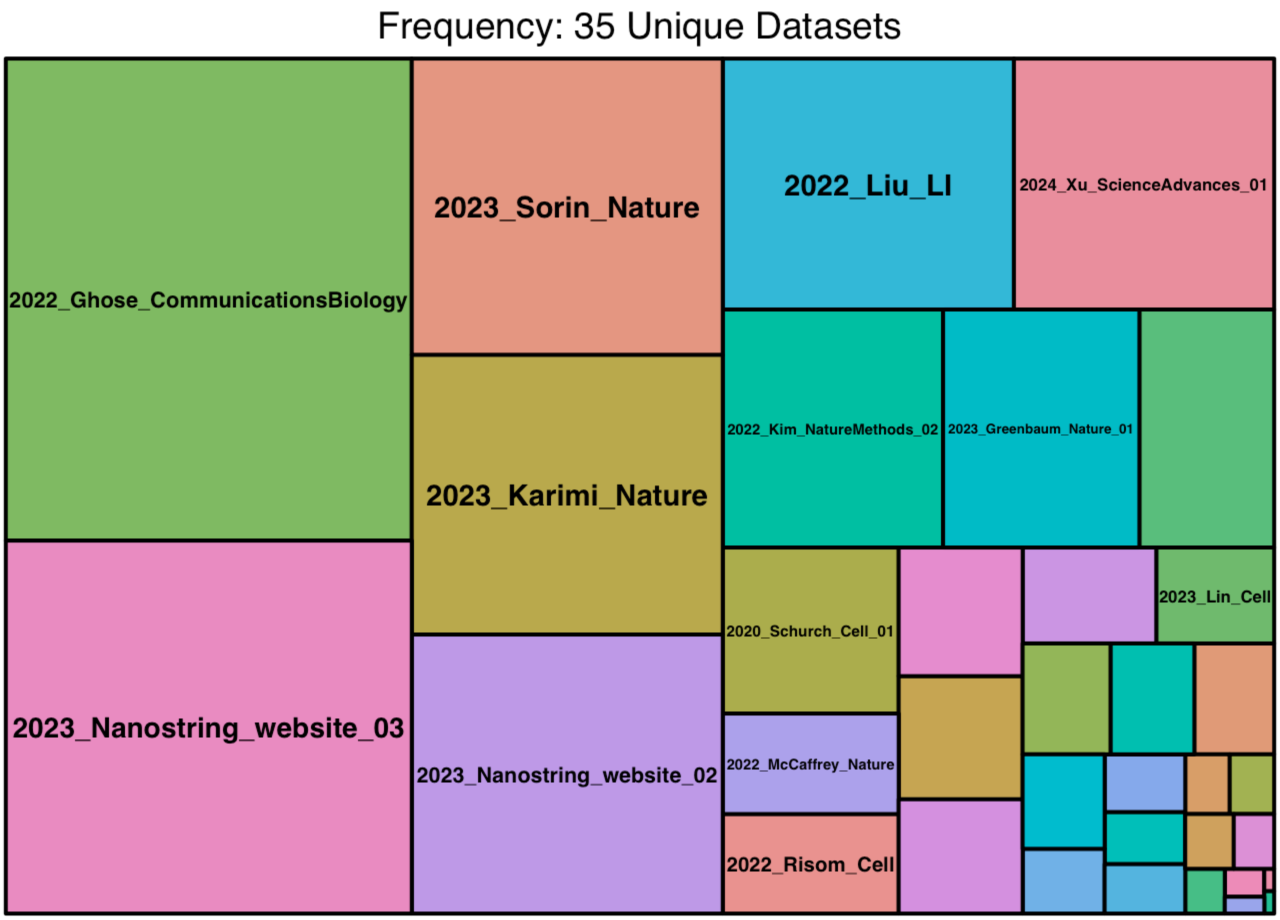
```
wordcloud(words = word_freqs$dataset_name, freq = word_freqs$Frequency, min.freq = 1, sc
ale = c(1.3, 0.3),
          random.order = FALSE, rot.per = .25)
```



```
word_freqs |>
  ggplot(
    aes(x = dataset_name, y = Frequency, size = Frequency, color = dataset_name)) +
      geom_point(alpha =.7) +
      scale_size(range = c(5, 20)) +
      theme_minimal() +
  theme(legend.position = "none",
        axis.text.x = element_blank(),
        axis.ticks.x = element_blank()) +
  labs(
    title = "Frequency of 35 Datasets (11/06/24)",
    x = ""
  )
```



```
library(treemap)

treemap(word_freqs,
        index = c("dataset_name"),
        vSize = "Frequency",
        vColor = "Frequency",
        title = "Frequency: 35 Unique Datasets",
        draw = TRUE)
```



```
print(length(unique(word_freqs$dataset_name)))
```

```
## [1] 35
```