

# 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
```

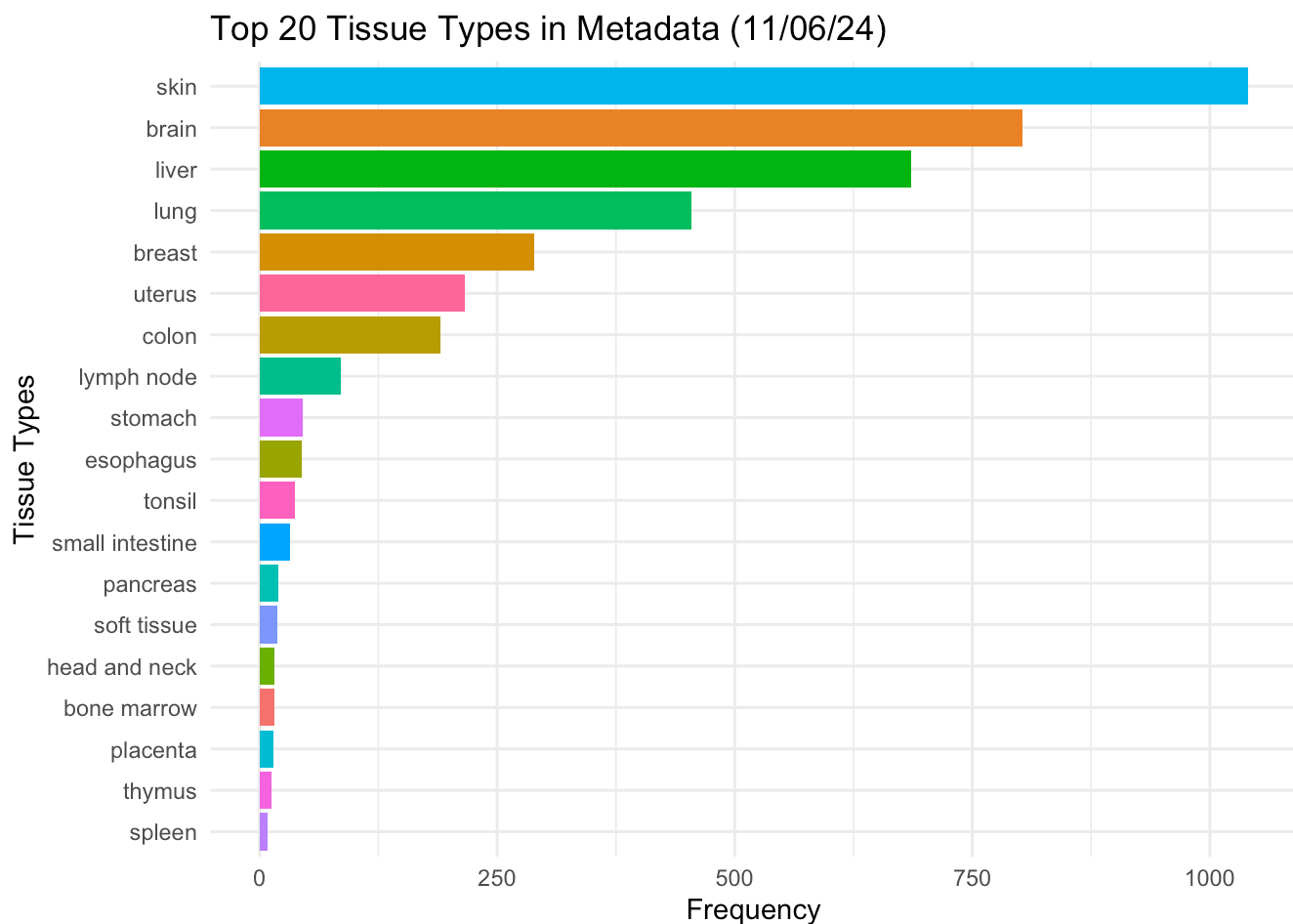
```
library(RColorBrewer)
library(viridisLite)

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)
  )

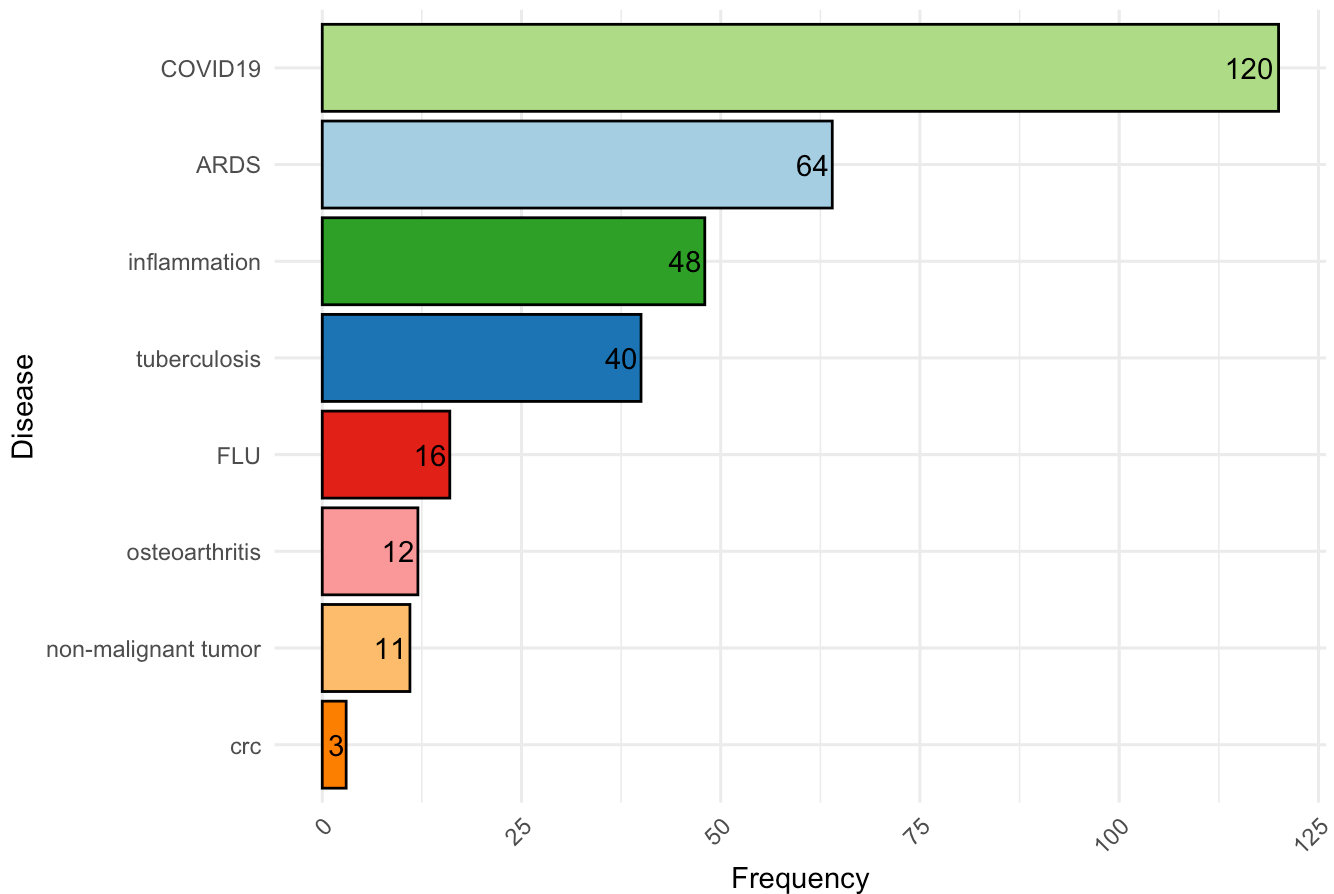
#mypalette <- brewer.pal(length(tissues), "Set3")

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()
```

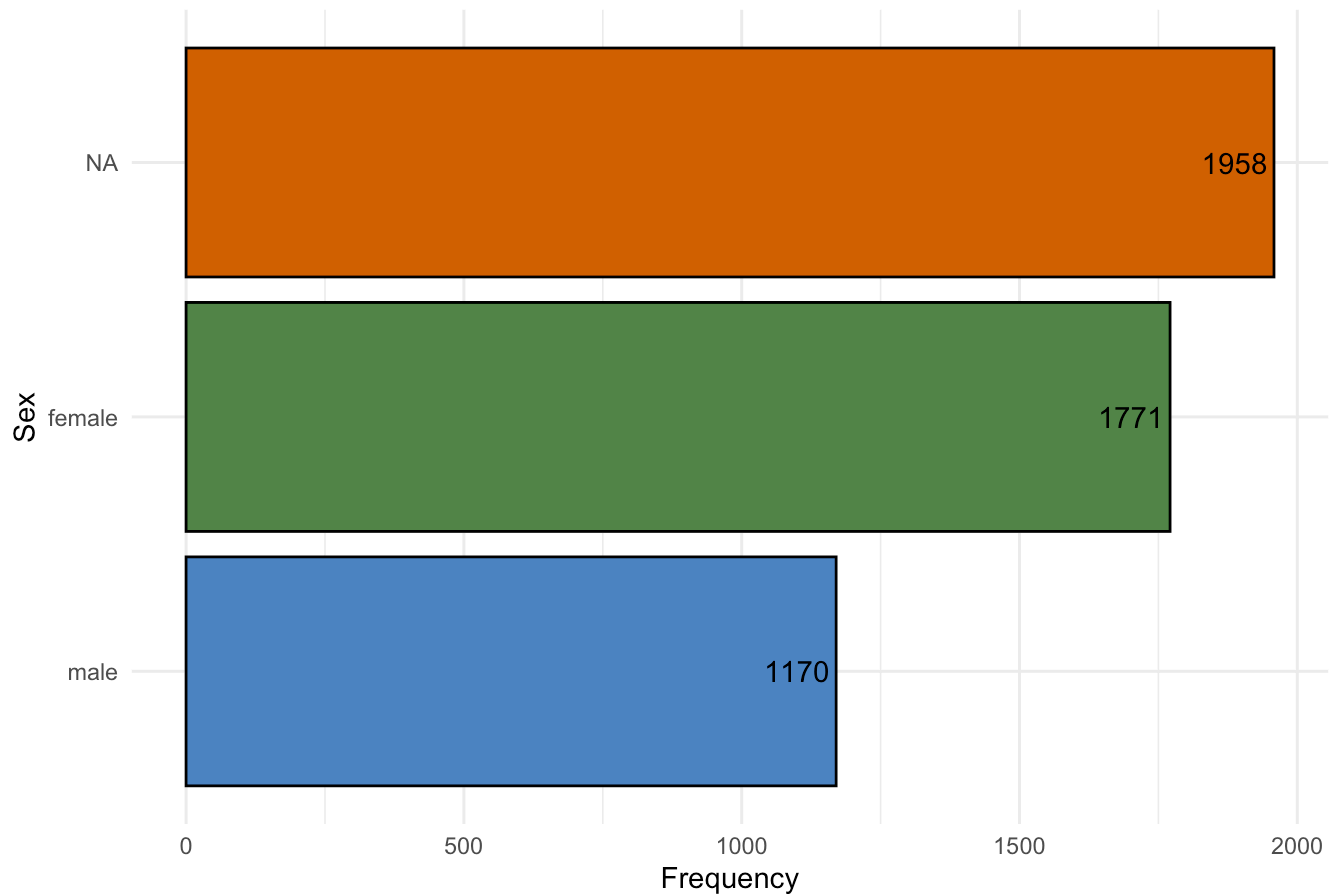
## Variation of Non-cancer Diseases in Metadata



```
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"
    )
  )
```

## Sex distribution in Metadata (11/06/2024)



```
#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)))
```

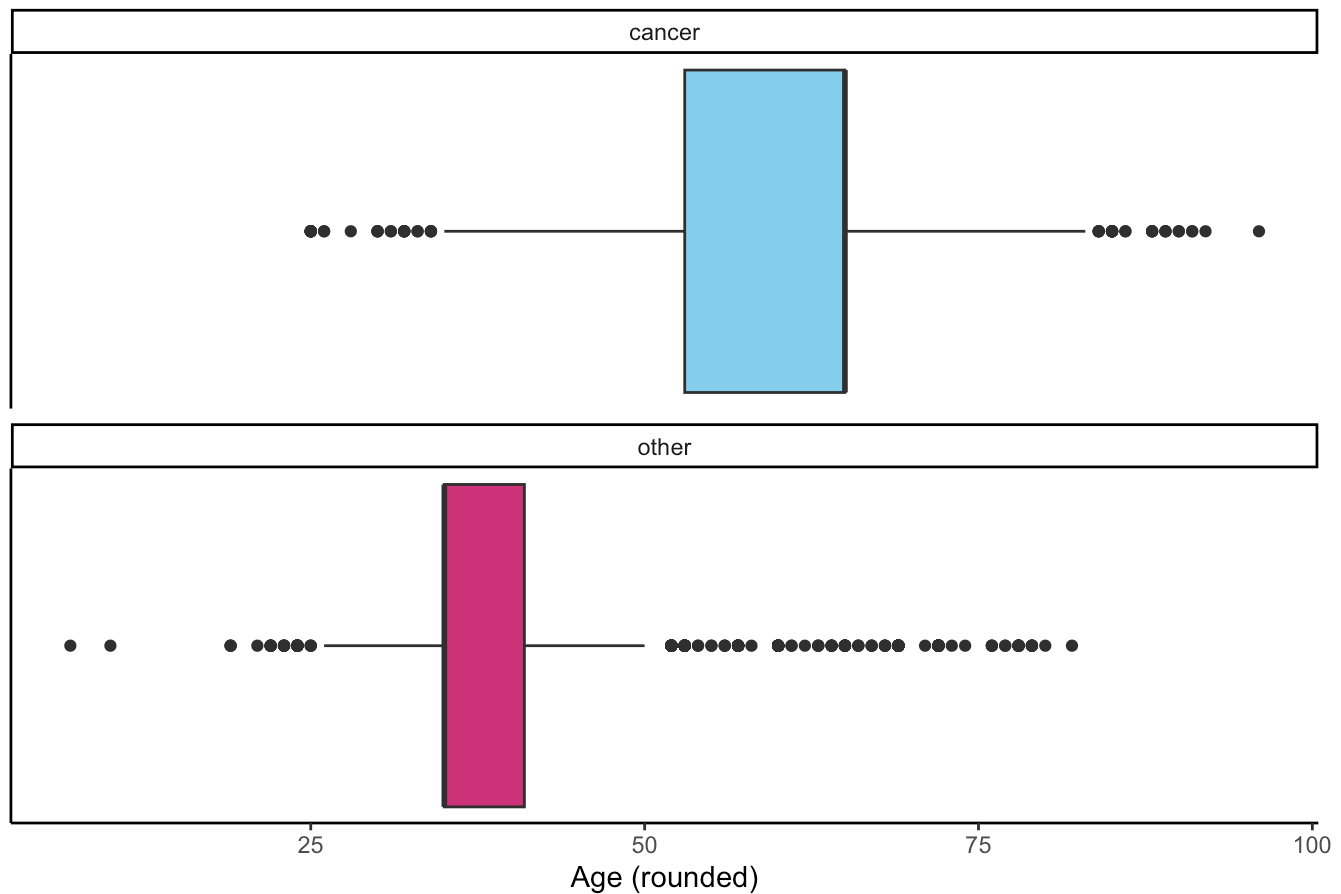
```
## Warning: There was 1 warning in `mutate()`.
## i In argument: `newAge = round(as.numeric(age))`.
## Caused by warning:
## ! NAs introduced by coercion
```

```

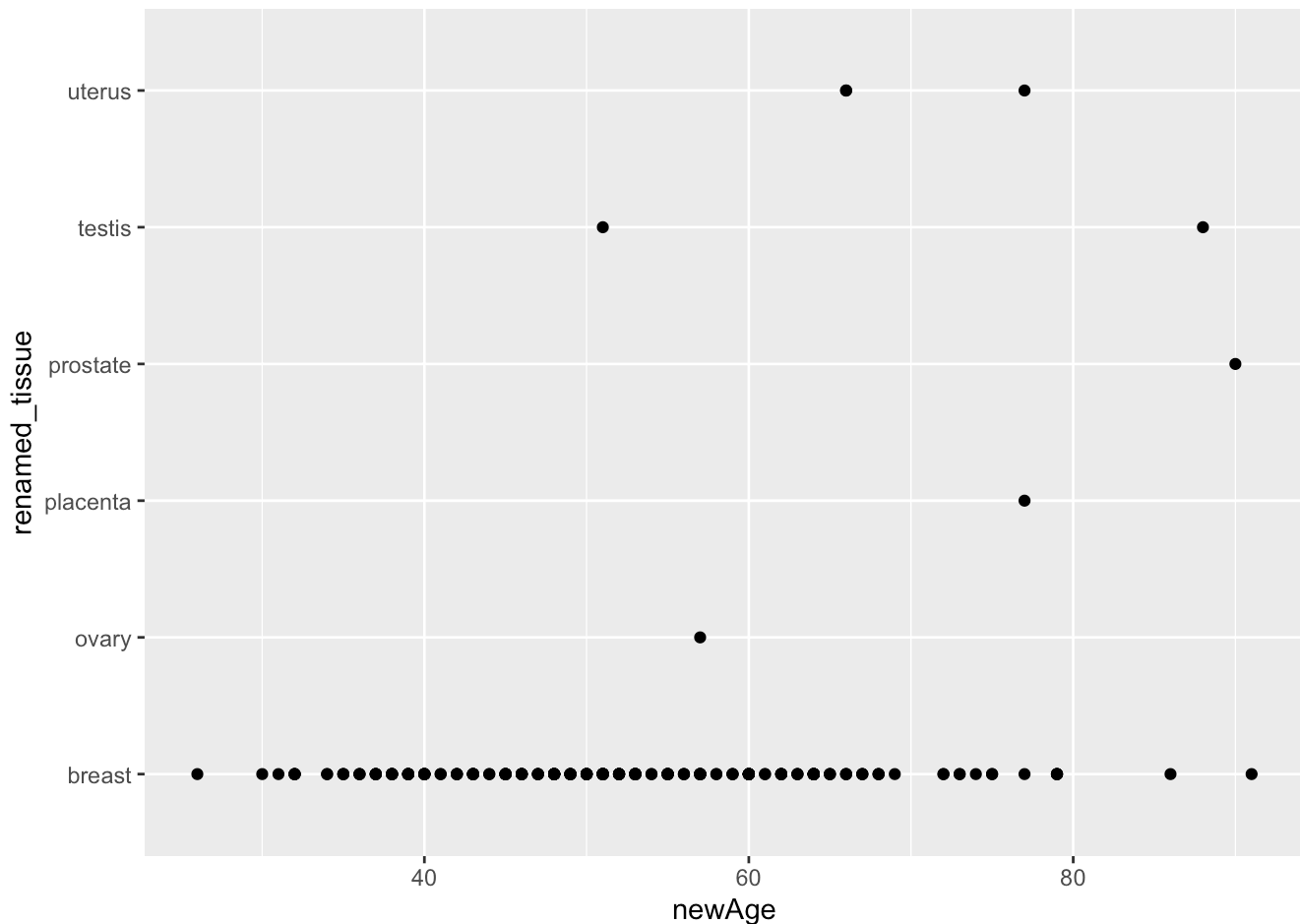
newmeta_update |>
  filter(!is.na(newDisease)) |>
  filter(!is.na(newAge)) |>
  ggplot(
    aes(x = newAge, fill = newDisease)) +
    geom_boxplot() +
    scale_fill_manual(breaks = c("cancer", "other"),
                      values = c("skyblue", "violetred3")) +
    facet_wrap(~newDisease, ncol = 1) +
    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())

```

Age Distribution by Cancer Status (11/06/2024)



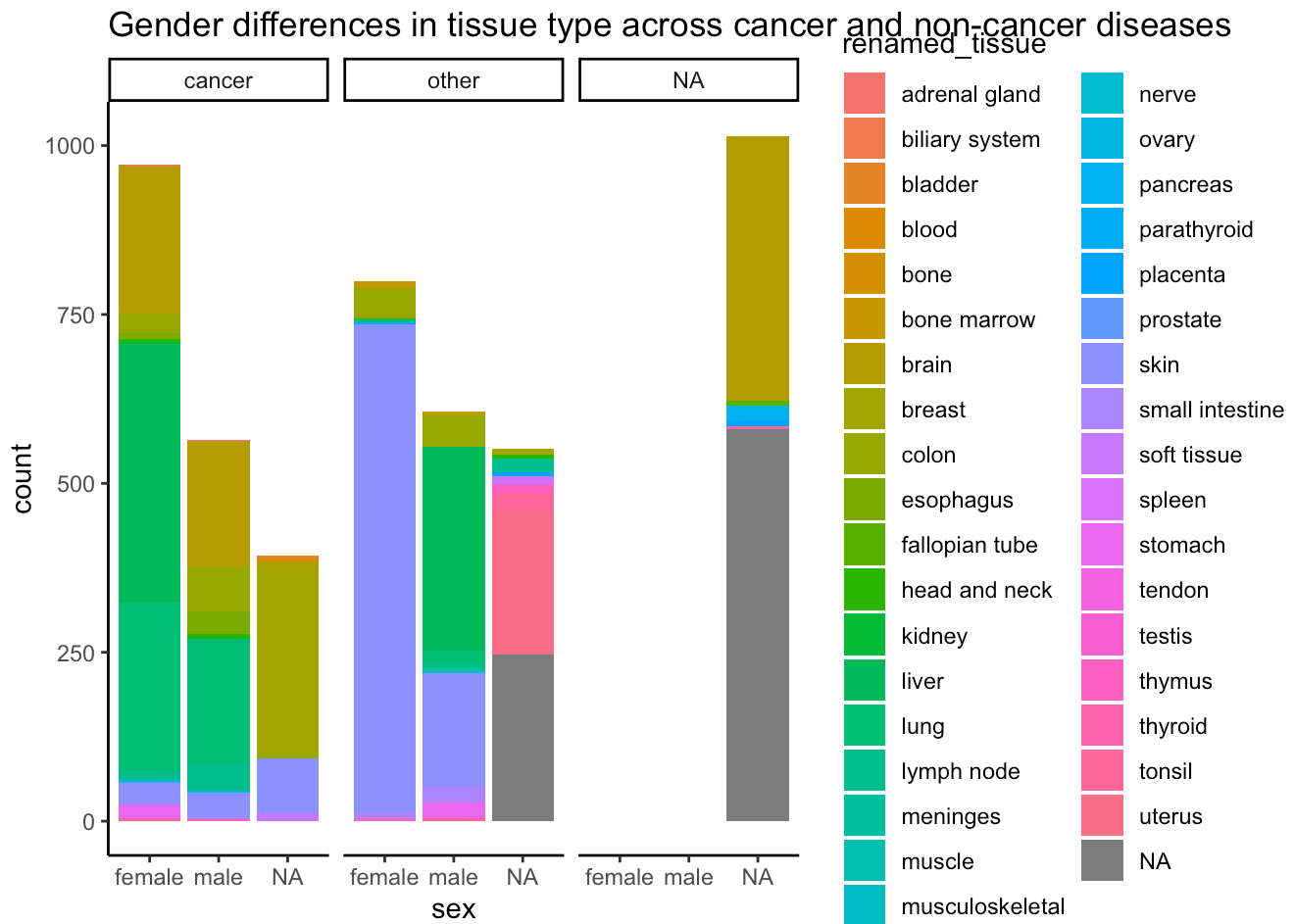
```
newmeta_update |>
  filter(newAge != "NA") |>
  filter(renamed_tissue != "NA") |>
  filter(large_tissue_unit == "Reproductive System") |>
  ggplot(
    aes(x = newAge, y = renamed_tissue)
  ) +
  geom_point()
```



```
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()
```

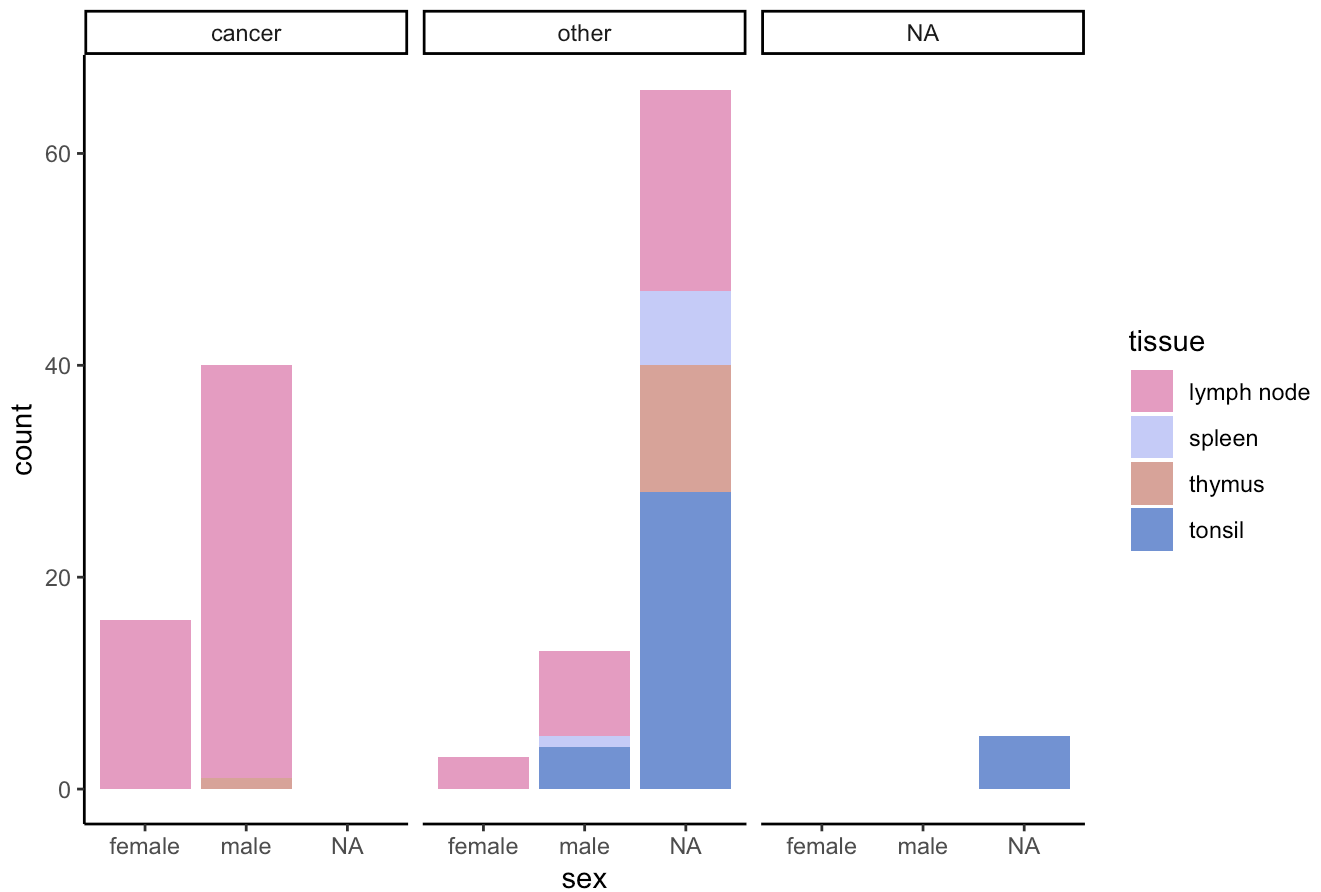




```
library(wesanderson)
```

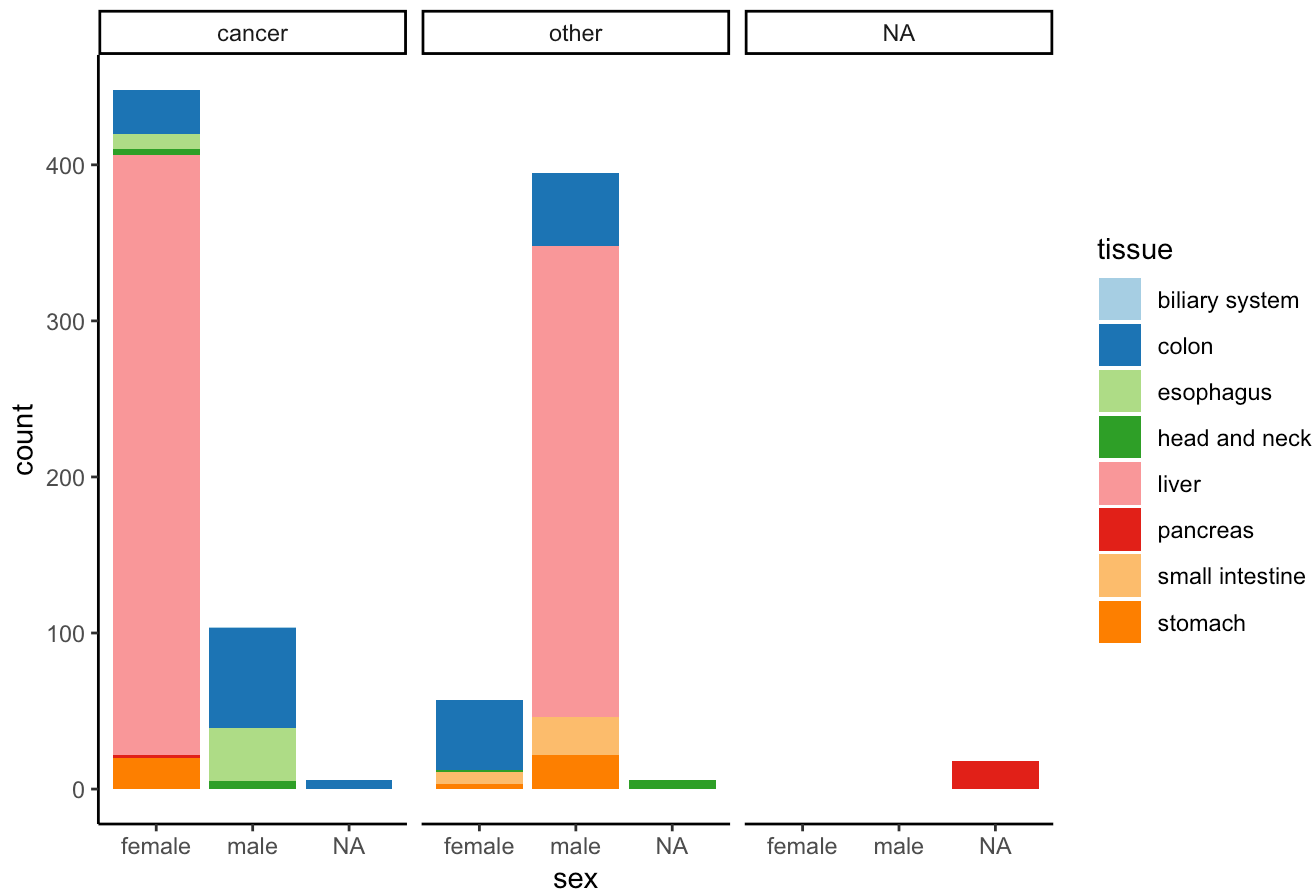
```
newmeta_update |>
  filter(large_tissue_unit == "Immune System") |>
  ggplot(
    aes(x = sex, fill = tissue)) +
  geom_bar(position = "stack") +
  scale_fill_manual(values = wes_palette("GrandBudapest2", n = 4)) +
  facet_wrap(~newDisease) +
  labs(
    title = "Gender differences in the immune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

## Gender differences in the immune system across cancer and non-cancer disease



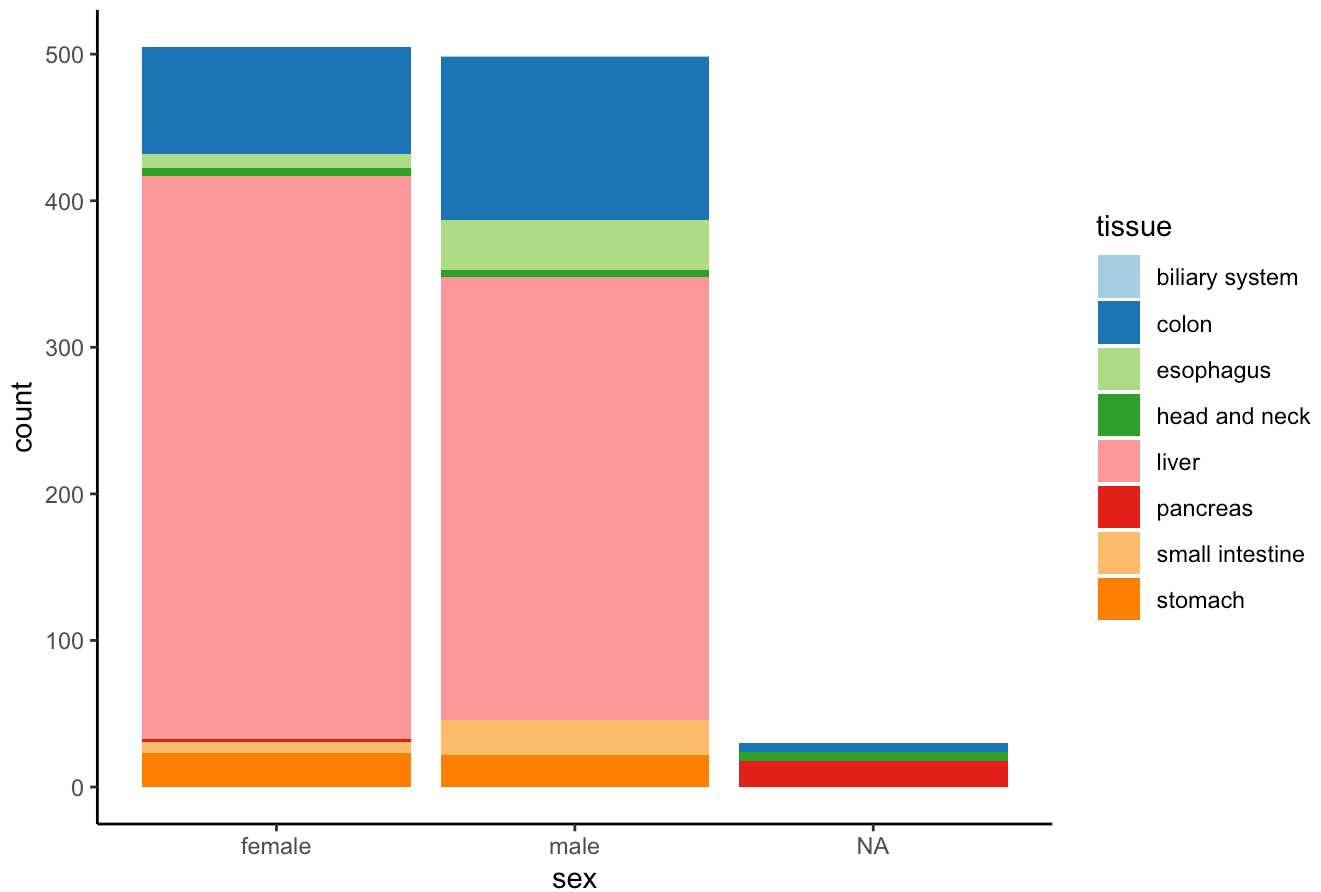
```
newmeta_update |>
  filter(large_tissue_unit == "Digestive System") |>
  ggplot(
    aes(x = sex, fill = tissue)) +
  geom_bar(position = "stack") +
  scale_fill_manual(values = brewer.pal(8, "Paired")) +
  facet_wrap(~newDisease) +
  labs(
    title = "Gender differences in the digestive system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

## Gender differences in the digestive system across cancer and non-cancer disea



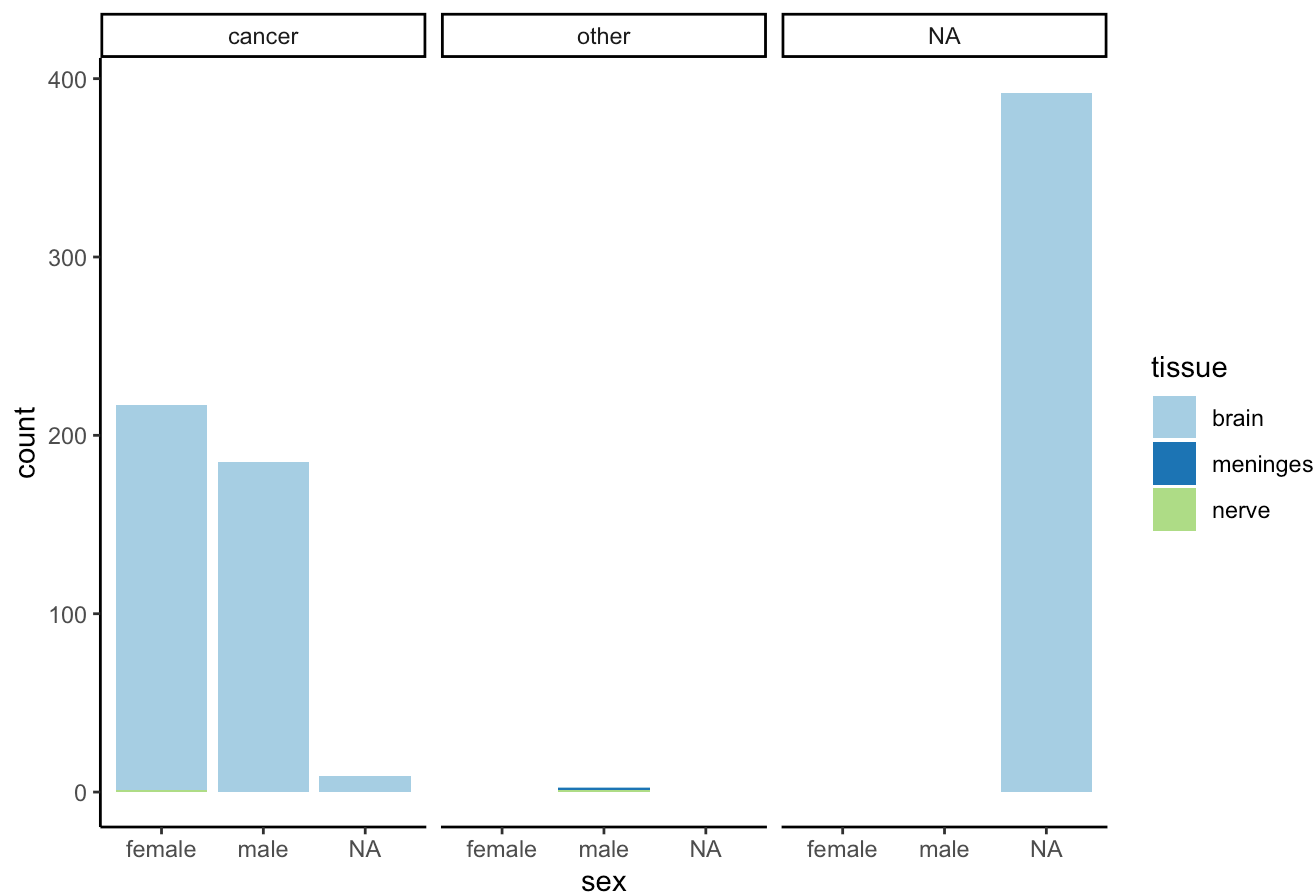
```
newmeta_update |>
  filter(large_tissue_unit == "Digestive System") |>
  ggplot(
    aes(x = sex, fill = tissue)) +
  geom_bar() +
  scale_fill_manual(values = brewer.pal(8, "Paired")) +
  labs(
    title = "Gender differences in tissue types within the digestive system"
  ) +
  theme_classic()
```

## Gender differences in tissue types within the digestive system



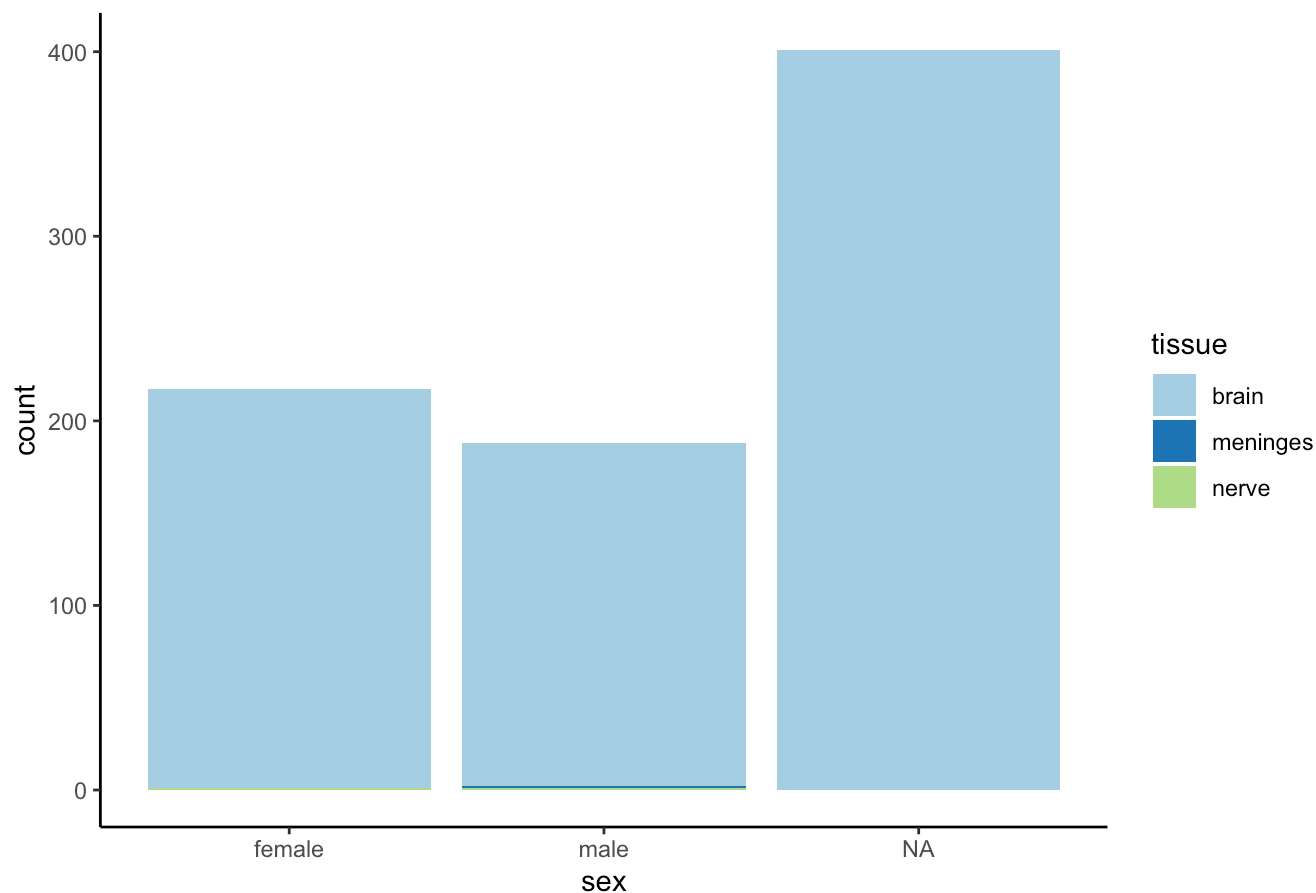
```
newmeta_update |>
  filter(large_tissue_unit == "Nervous System") |>
  ggplot(
    aes(x = sex, fill = tissue)) +
  geom_bar(position = "stack") +
  scale_fill_manual(values = brewer.pal(8, "Paired")) +
  facet_wrap(~newDisease) +
  labs(
    title = "Gender differences in the nervous system across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

## Gender differences in the nervous system across cancer and non-cancer diseases



```
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()
```

## Gender differences in tissue types within the nervous system



```
library(wordcloud)
```

```
word_freqs <- newmeta_update |>
```

```
  #mutate(dataset_name = str_replace(dataset_name, "^(\\d){4}_[A-Za-z]+_.*", "\\1")) |
```

```
>
```

```
  group_by(dataset_name) |>
```

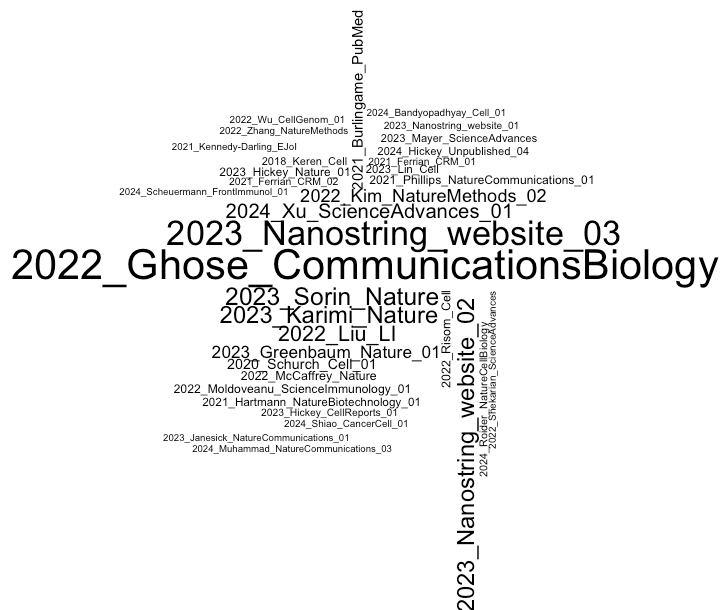
```
  summarize(Frequency = n()) |>
```

```
  arrange(desc(Frequency))
```

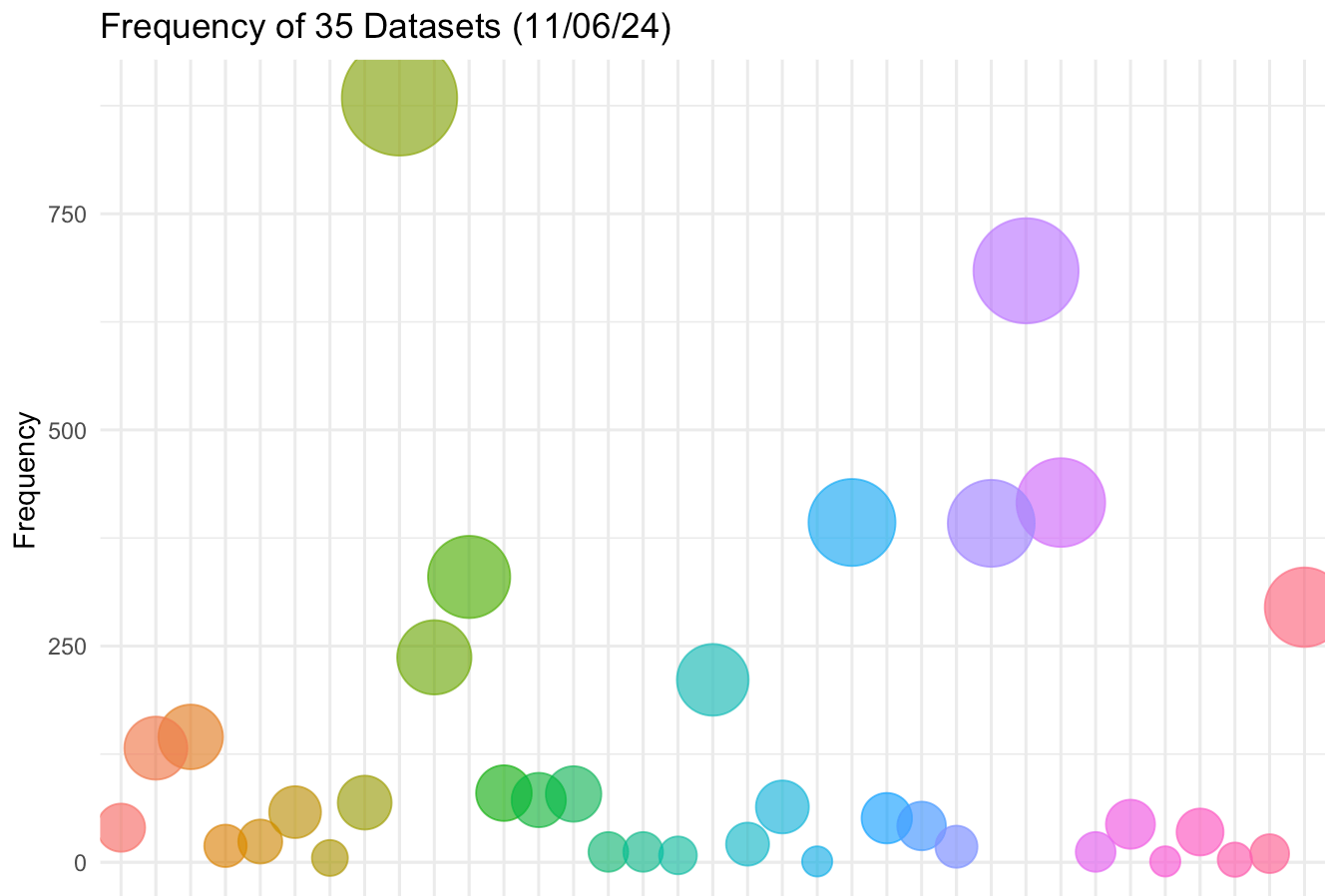
```
print(word_freqs)
```

```
## # 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, scale = 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 = ""
    )
```

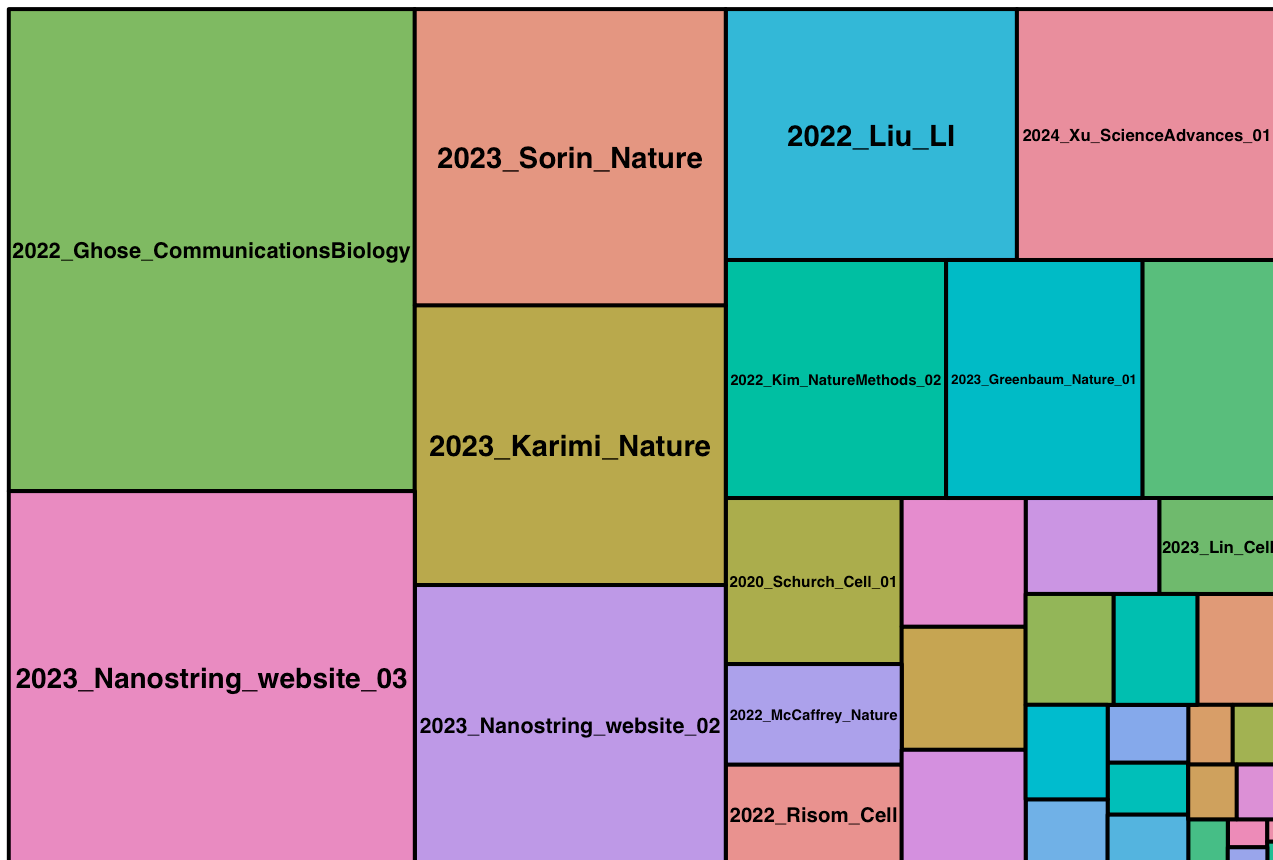


```
library(treemap)

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



## Frequency: 35 Unique Datasets



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

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