Raw Data

```
library(tidyverse)
Warning: package 'tidyr' was built under R version 4.4.2
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v dplyr 1.1.4 v readr
                                  2.1.5
v forcats 1.0.0 v stringr
v ggplot2 3.5.1 v tibble
                                 1.5.1
                                 3.2.1
v lubridate 1.9.3 v tidyr
                                  1.3.1
v purrr
           1.0.2
-- Conflicts ----- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()
               masks stats::lag()
i Use the conflicted package (<a href="http://conflicted.r-lib.org/">http://conflicted.r-lib.org/</a>) to force all conflicts to become
library(ggplot2)
library(dplyr)
library(janitor)
Attaching package: 'janitor'
The following objects are masked from 'package:stats':
    chisq.test, fisher.test
library(lubridate)
library(here)
```

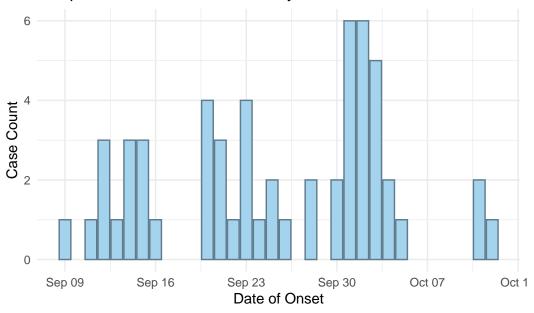
here() starts at C:/Users/maria/OneDrive/Documents/GitHub/EPI-569-Final-Project

```
rff_2024 <- readRDS("C:/Users/maria/OneDrive/Documents/GitHub/EPI-569-Final-Project/data/rf
roster_2024 <- readRDS("~/GitHub/EPI-569-Final-Project/data/roster_2024.rds")</pre>
transmission_pairs_2024 <- readRDS("~/GitHub/EPI-569-Final-Project/data/transmission_pairs_20
setwd("C:/Users/maria/OneDrive/Documents/GitHub/EPI-569-Final-Project/data")
tabyl(rff_2024$`Date_of_Onset`)
 rff_2024$Date_of_Onset n
                              percent valid_percent
             2024-09-09 1 0.01098901
                                         0.01785714
             2024-09-11 1 0.01098901
                                         0.01785714
             2024-09-12 3 0.03296703
                                         0.05357143
             2024-09-13 1 0.01098901
                                         0.01785714
             2024-09-14 3 0.03296703
                                         0.05357143
             2024-09-15 3 0.03296703
                                         0.05357143
             2024-09-16 1 0.01098901
                                         0.01785714
             2024-09-20 4 0.04395604
                                         0.07142857
             2024-09-21 3 0.03296703
                                         0.05357143
             2024-09-22 1 0.01098901
                                         0.01785714
             2024-09-23 4 0.04395604
                                         0.07142857
             2024-09-24 1 0.01098901
                                         0.01785714
             2024-09-25 2 0.02197802
                                         0.03571429
             2024-09-26 1 0.01098901
                                         0.01785714
             2024-09-28 2 0.02197802
                                         0.03571429
             2024-09-30 2 0.02197802
                                         0.03571429
             2024-10-01 6 0.06593407
                                         0.10714286
             2024-10-02 6 0.06593407
                                         0.10714286
             2024-10-03 5 0.05494505
                                         0.08928571
             2024-10-04 2 0.02197802
                                         0.03571429
             2024-10-05 1 0.01098901
                                         0.01785714
             2024-10-11 2 0.02197802
                                         0.03571429
             2024-10-12 1 0.01098901
                                         0.01785714
                   <NA> 35 0.38461538
                                                 NA
class(rff_2024$`Date_of_Onset`)
```

[1] "Date"

```
epicurveonset <-rff_2024 %>%
    filter(!is.na(`Date_of_Onset`)) %>% arrange(`Date_of_Onset`)
epicurveonset$Date_of_Onset <- as.Date(epicurveonset$Date_of_Onset)</pre>
epicurveonset <- epicurveonset[order(epicurveonset$Date_of_Onset), ]</pre>
epicurveonset$cumulative_case_count <- cumsum(!is.na(epicurveonset$Date_of_Onset))</pre>
head(epicurveonset)
# A tibble: 6 x 35
  caseID Infectedby Gender Course
                                        If you are in EPI 56~1 `Date of Exposure`
              <dbl> <chr> <chr>
   <dbl>
                                        <chr>
                                                               <date>
1
       1
                 NA Female EPI 569 (C~ Jessica Rothman
                                                               2024-09-09
2
                          EPI 569 (C~ Jessica Rothman
                                                               2024-09-10
3
                  2 Female EPI 569 (C~ Sara Kim
                                                               2024-09-12
                  5 Female EPI 569 (C~ Charlotte Doran
4
       6
                                                               2024-09-12
5
       7
                  5 Female EPI 569 (C~ Charlotte Doran
                                                               2024-09-12
                           EPI 569 (C~ Jessica Rothman
                  2 Male
                                                               2024-09-12
# i abbreviated name: 1: `If you are in EPI 569, which TA group are you in?`
# i 29 more variables: `Time of Exposure` <chr>, Date_of_Onset <date>,
    Date_Time_Onset <chr>, Date_Time_Exposure <chr>,
    `Did you have symptoms?` <chr>,
    `How many hours after exposure did you develop symptoms?` <dbl>,
    `How many hours after your symptom onset did you feel better?` <dbl>,
    Date_Time_Recovery <dttm>, Date_of_Recovery <date>, Severe <chr>, ...
ggplot(data = epicurveonset, aes(x = Date_of_Onset)) +
  geom_bar(fill = "lightskyblue2", color = "lightskyblue4") +
  labs(
    x = "Date of Onset",
    y = "Case Count",
    title = "Temporal Distribution of Cases by Date of Onset"
  ) +
  theme_minimal()
```

Temporal Distribution of Cases by Date of Onset



```
state_no <- data.frame(</pre>
 Date = sequeniald,
 Susceptible = numb_suceptible,
 Infectious = numb_infectious,
 Recovered = numb_recovered
)
state_no_long <- data.frame(</pre>
 Date = rep(sequeniald, times = 3),
 State = rep(c("Susceptible", "Infectious", "Recovered"), each = length(sequeniald)),
 Count = c(numb_suceptible, numb_infectious, numb_recovered)
)
library(ggplot2)
ggplot(state_no_long, aes(x = Date, y = Count, color = State, group = State)) +
  geom_line(size = 1) +
  labs(
   title = "Number of Susceptible, Infectious, and Recovered Individuals by Day",
   x = "Date", y = "Count of individuals "
  ) +
  scale_color_manual(
   values = c("Susceptible" = "chocolate3", "Infectious" = "darkslategray", "Recovered" = ";
  ) +
  scale_x_date(
   breaks = scales::date_breaks("2 days"),
   labels = scales::date_format("%b %d")
  ) +
  theme_minimal() +
 theme(
   legend.title = element_blank(),
   axis.text.x = element_text(angle = 45, hjust = 1)
```

Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0. i Please use `linewidth` instead.

Number of Susceptible, Infectious, and Recovered Individuals b

