Projeto Final

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```
library(ggplot2)
library(outbreaks)
library(tidyverse)
```

```
## -- Attaching packages --------------------------- tidyverse 1.3.0 --
```

```
## v tibble  3.0.1     v dplyr   0.8.5
## v tidyr   1.0.2     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.5.0
## v purrr   0.3.4
```

```
## -- Conflicts ------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(ggraph)
library(tidygraph)
```

```
##
## Attaching package: 'tidygraph'
```

```
## The following object is masked from 'package:stats':
##
##     filter
```

```
data("measles_hagelloch_1861")
```

```
head(measles_hagelloch_1861)
```

```
##   case_ID infector date_of_prodrome date_of_rash date_of_death age gender
## 1       1       45               45   1861-11-21    1861-11-25          <NA>   7      f
## 2       2       45               45   1861-11-23    1861-11-27          <NA>   6      f
## 3       3      172              172   1861-11-28    1861-12-02          <NA>   4      f
## 4       4      180              180   1861-11-27    1861-11-28          <NA>  13      m
## 5       5       45               45   1861-11-22    1861-11-27          <NA>   8      f
## 6       6      180              180   1861-11-26    1861-11-29          <NA>  12      m
##   family_ID class complications x_loc y_loc
## 1        41     1           yes 142.5 100.0
## 2        41     1           yes 142.5 100.0
```

```
## 3          41      0           yes 142.5 100.0
## 4          61      2           yes 165.0 102.5
## 5          42      1           yes 145.0 120.0
## 6          42      2           yes 145.0 120.0
```

```r
#Quantidade de pessoas com erupção cutânea reportadas por dia
dates_rash <- table(measles_hagelloch_1861$date_of_rash)

dates_rash <- data.frame(Date = names(dates_rash),
                         Frequency = as.vector(dates_rash))

dates_rash$Date <- as.Date(dates_rash$Date, format = "%Y-%m-%d")

dates_rash
```

```
##           Date Frequency
## 1   1861-11-03         1
## 2   1861-11-06         1
## 3   1861-11-08         1
## 4   1861-11-11         2
## 5   1861-11-13         1
## 6   1861-11-15         2
## 7   1861-11-17         1
## 8   1861-11-18         1
## 9   1861-11-19         1
## 10  1861-11-21         3
## 11  1861-11-24         5
## 12  1861-11-25         9
## 13  1861-11-26        11
## 14  1861-11-27        12
## 15  1861-11-28         2
## 16  1861-11-29         7
## 17  1861-11-30         5
## 18  1861-12-02         5
## 19  1861-12-03         3
## 20  1861-12-04         8
## 21  1861-12-05        25
## 22  1861-12-06        17
## 23  1861-12-07        26
## 24  1861-12-08        12
## 25  1861-12-09         4
## 26  1861-12-10         4
## 27  1861-12-11         3
## 28  1861-12-12         1
## 29  1861-12-13         3
## 30  1861-12-15         4
## 31  1861-12-16         3
## 32  1861-12-17         2
## 33  1861-12-18         1
## 34  1861-12-19         1
## 35  1862-01-27         1
```

```
ggplot(dates_rash) +
  geom_line(aes(x = Date, y = Frequency)) +
  theme(axis.text.x = element_text(angle = 45, hjust = 1),
  plot.title = element_text(hjust = 0.5)) +
  scale_x_date(date_labels = "%d/%m/%Y", date_breaks = "5 day") +
  labs(x = "Datas", y = "Frequência",
  title = "Pessoas reportadas com erupção cutânea causada por sarampo")
```

Pessoas reportadas com erupção cutânea causada por sarampo


```
#Para quantas pessoas cada indivíduo infectado transmitiu a doença?
infector <- table(measles_hagelloch_1861$infector)
infector <- data.frame(Indivíduo = names(infector),
                  Infectados_por_ele = as.vector(infector))
infector
```

```
##     Indivíduo Infectados_por_ele
## 1         1                    1
## 2         4                    1
## 3         5                    1
## 4         6                    1
## 5         7                    7
## 6         8                    1
## 7        10                    4
## 8        11                    4
## 9        12                    4
## 10       14                    2
```
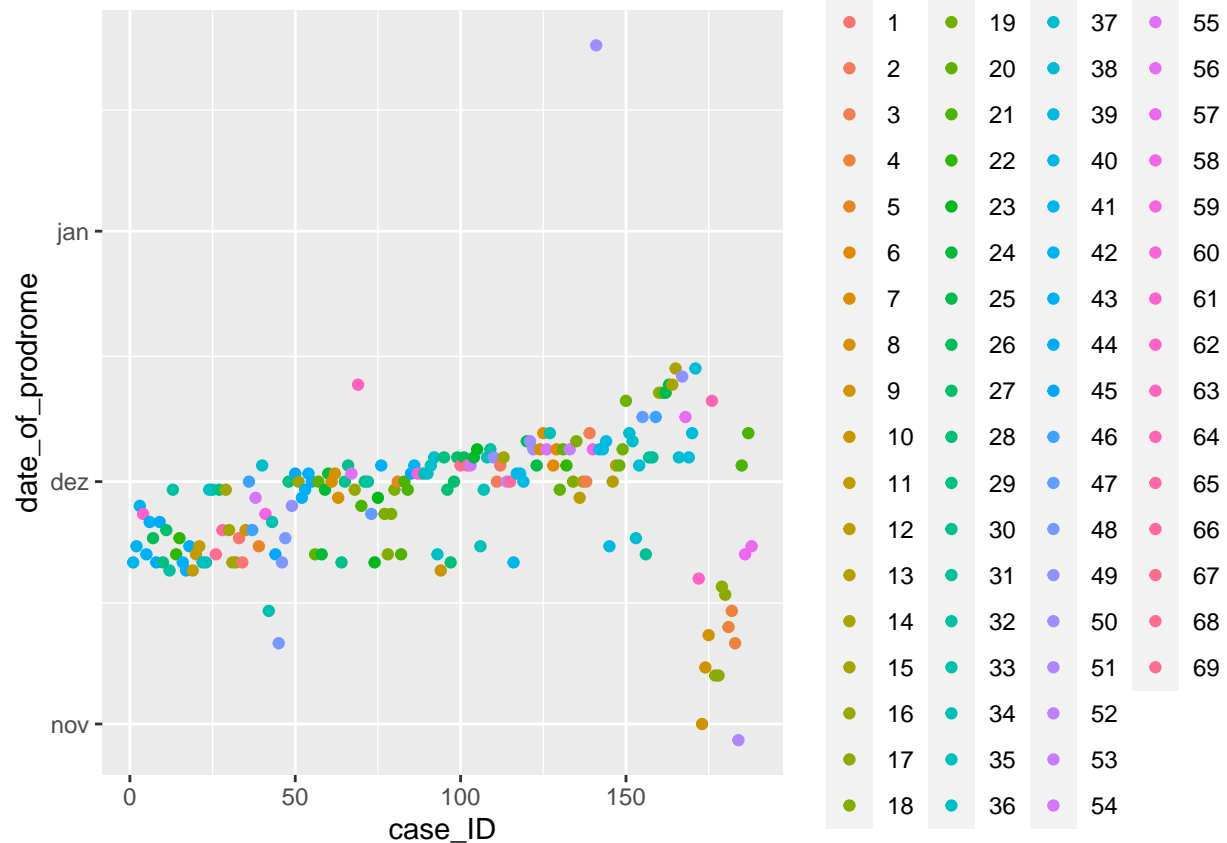
```
## 11         16                  2
## 12         17                  7
## 13         18                  3
## 14         19                  2
## 15         21                  2
## 16         22                  2
## 17         31                  3
## 18         34                  3
## 19         37                  3
## 20         39                  2
## 21         42                  3
## 22         44                  1
## 23         45                 30
## 24         47                  3
## 25         54                  1
## 26         56                  3
## 27         58                  3
## 28         64                  3
## 29         68                  1
## 30         73                  1
## 31         74                  2
## 32         78                  3
## 33         79                  1
## 34         82                  4
## 35         93                  4
## 36         97                  1
## 37         98                  1
## 38        102                  2
## 39        106                  2
## 40        110                  1
## 41        116                  3
## 42        123                  2
## 43        145                  3
## 44        146                  1
## 45        148                  2
## 46        153                  6
## 47        156                  2
## 48        169                  1
## 49        172                  2
## 50        173                  1
## 51        174                  1
## 52        175                  2
## 53        177                  2
## 54        178                  1
## 55        179                  2
## 56        180                  7
## 57        181                  8
## 58        182                  4
## 59        183                  1
## 60        184                  6
## 61        186                  1
## 62        188                  1
```

```r
#Fazer o espaçamento do eixo y maior
ggplot(infector) +
  geom_point(aes(x = Indivíduo, y = Infectados_por_ele)) +
  coord_flip()
```
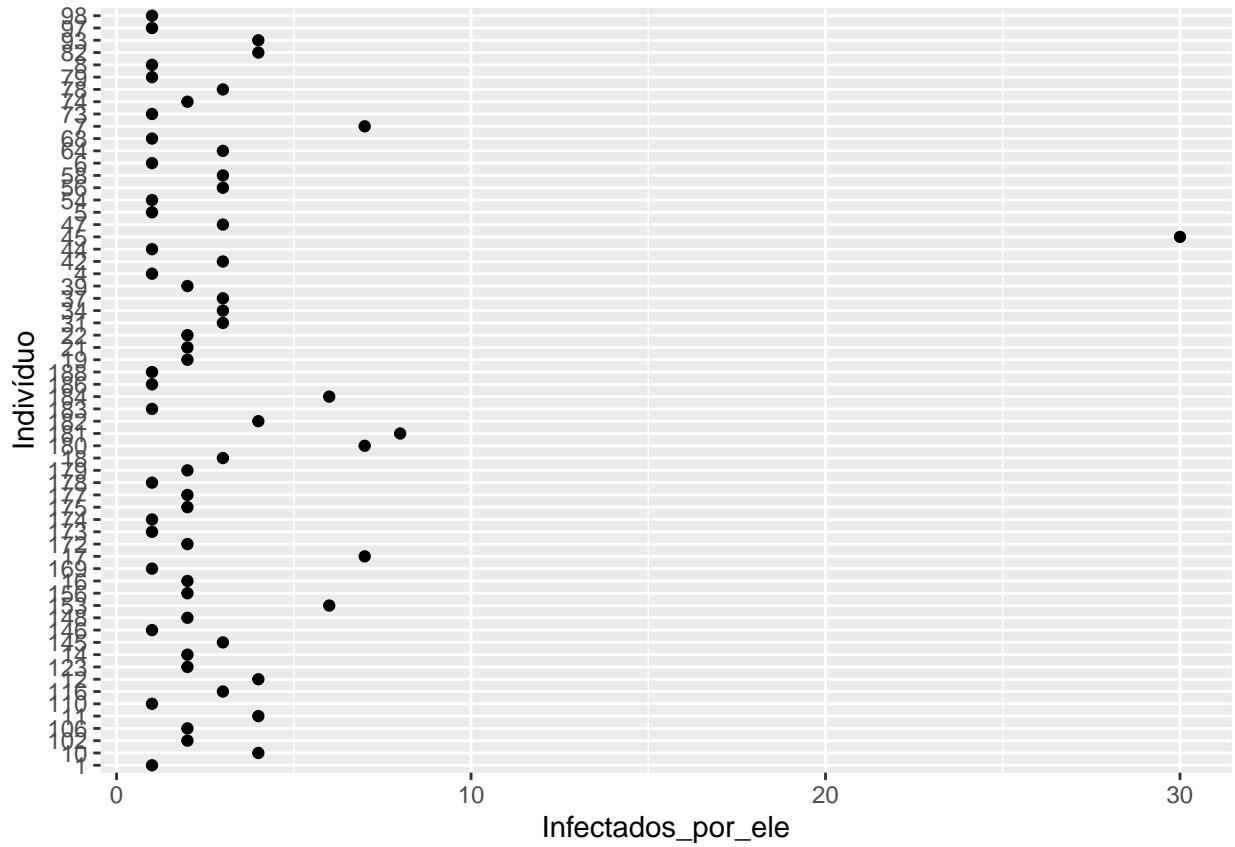


```r
#Quantas famílias foram afetadas?
ggplot(measles_hagelloch_1861) +
  geom_point(aes(x = case_ID, y = date_of_prodrome, color = factor(family_ID)))
```

ggplot plot with x-axis "case_ID" and y-axis "date_of_prodrome", y labels jan, dez, nov; x labels 0, 50, 100, 150. Legend values 1–69.

```
#Encontrando quem é a família do infector
infecções_fora_da_familia <- cbind(Family_infector= measles_hagelloch_1861$family_ID[measles_hagelloch_
     Family_person = measles_hagelloch_1861$family_ID)

head(infecções_fora_da_familia)
```
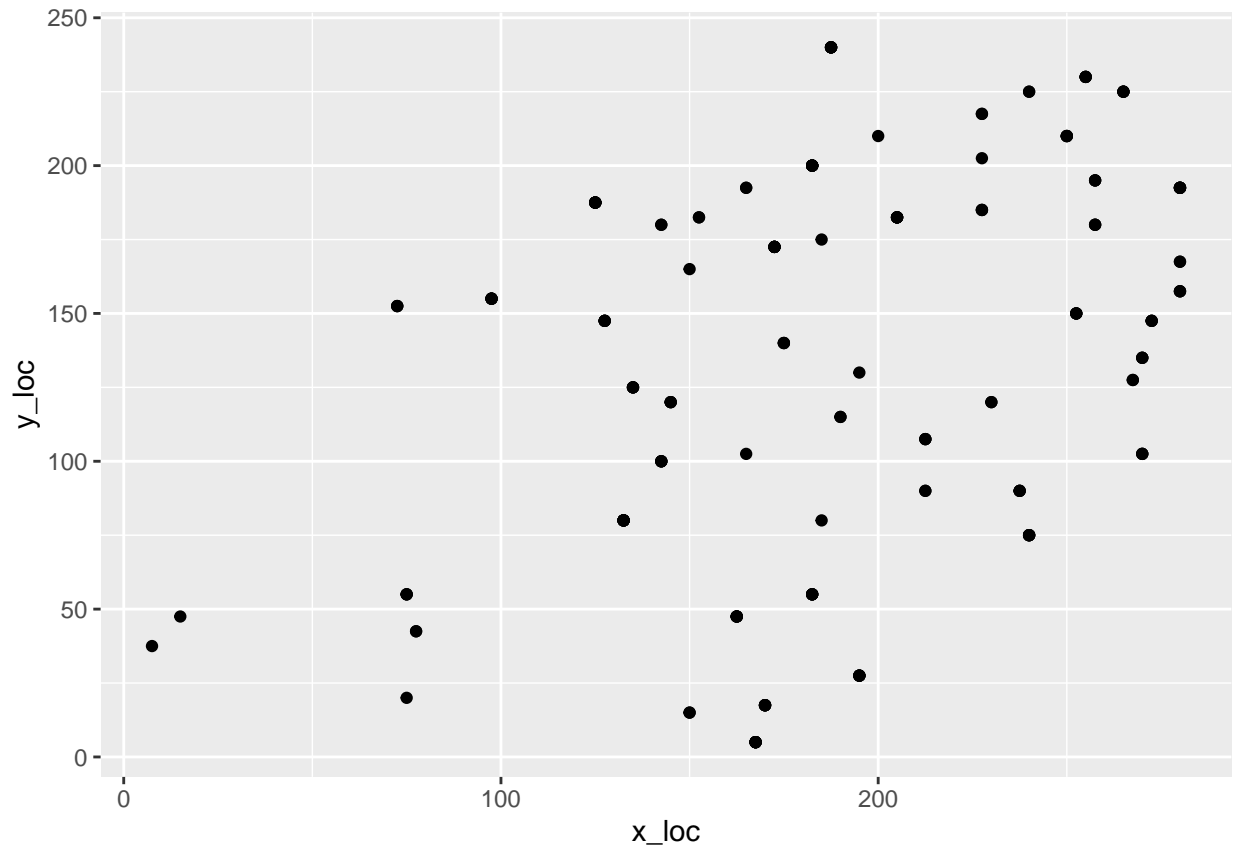
```
##      Family_infector Family_person
## [1,]             48            41
## [2,]             48            41
## [3,]             62            41
## [4,]             17            61
## [5,]             48            42
## [6,]             17            42
```

```
#Os indivíduos que estão na mesma familia tem a mesma localização
#Há algo que posso acrescentar na visualização das posições?
ggplot(measles_hagelloch_1861) +
  geom_point(aes(x = x_loc, y = y_loc))
```

```r
infector_edge <- measles_hagelloch_1861 %>%
  select(infector, case_ID) %>%
  rename(from = infector) %>%
  rename(to = case_ID) %>%
  na.omit()

head(infector_edge)
```

```
##    from to
## 1    45  1
## 2    45  2
## 3   172  3
## 4   180  4
## 5    45  5
## 6   180  6
```

```r
#Quem foi infectado por quem?
infector_tidy <- tbl_graph(edges = infector_edge, directed = TRUE)
infector1 <- ggraph(infector_tidy, layout = 'linear') +
  geom_edge_arc()

infector1
```