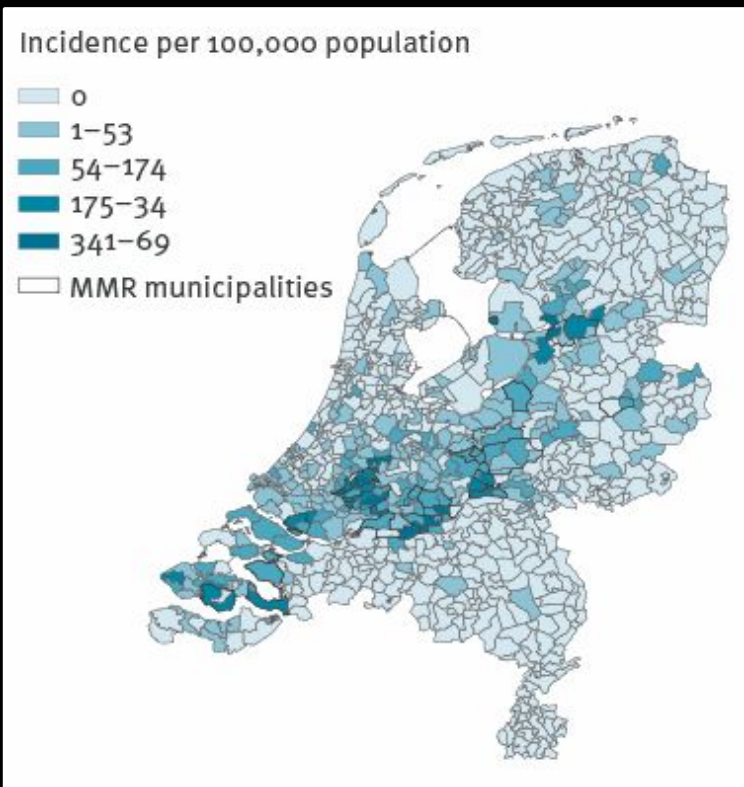


In the Netherlands, a Measles epidemic occurred from May 2013 until March 2014



- Highly contagious airborne disease caused by a virus
- Spreads through droplets generated by coughing or sneezing
- Causes lesions or papules to form on the skin
- Kills memory B-cells, leading to immune amnesia
- That is, loss of adaptive immunity
- MMR-1 vaccination is an effective preventive measure

Measles epidemic data from the Netherlands

Initial state: susceptibles, infectives, and removed (or recovered)

Variables and Parameters	Values
Dutch population in May 2013 (Total or N)	16.8 million people \Rightarrow N = 16,800,000 \Rightarrow 1 (as fraction of total population)
Total reported cases	2700
Removed or recovered cases (R)	1 (one infected child died due to complications) \Rightarrow R = 1 \Rightarrow 5.952381e-08
Total infected people (Infectives or I)	$2700 - 1 = 2699 \Rightarrow$ I = 2699 individuals \Rightarrow 16.06548e-05 fraction of total population
Susceptibles (S)	$S = N - I - R = 16.8 \text{ million} - 2699 - 1 = 16797300 \Rightarrow$ S = 16,797,300 individuals S = 16,797,300 individuals \Rightarrow 0.9998393 fraction of total population
Recovery rate (1/a) <i>Avg. number of days that a sick individuals takes to recover fully</i>	2 to 3 weeks = 14 to 21 days \Rightarrow 15 days \Rightarrow a = 1/15 recovery per day per individual
Reproductive rate (Ro) <i>Avg. number of secondary cases that can be caused by a single infected individual in a completely susceptible population, also called as basic reproduction rate</i>	12 to 18 people \Rightarrow 18 individuals \Rightarrow Ro = 18
Transmission rate (r) - new infections <i>Avg. number of new infections caused by a single infected individual per day, also called as effective reproduction rate</i>	$r = (Ro \times a) = (18 \times 1/15) = 1.201932 \Rightarrow$ r = 1.201932 new infections on avg. caused per day by an infective

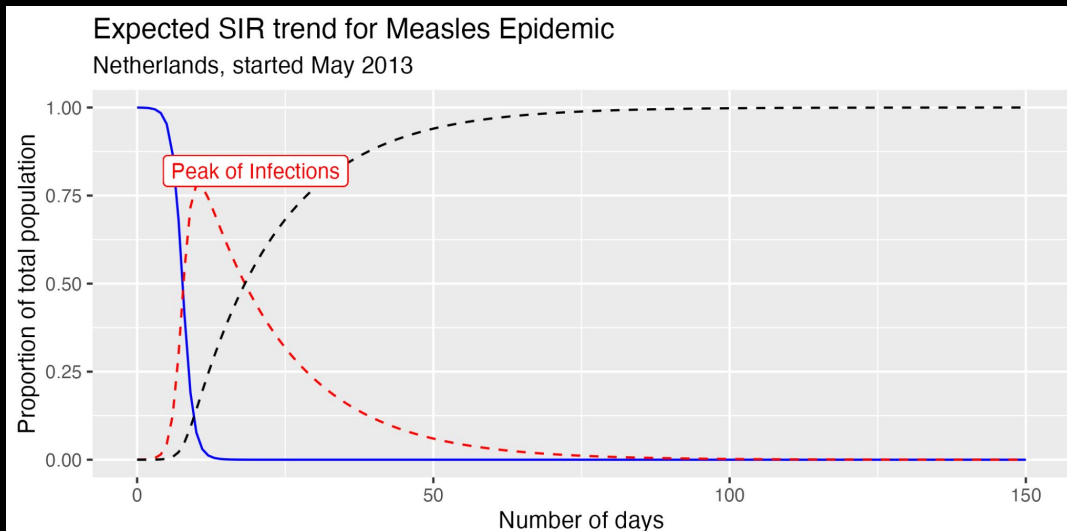
The SIR Model and its Parameters

Calculations

Values from previous slide	Rate of change in Susceptibles (dS/dt)	Rate of change in Infectives (dI/dt)	Rate of change in Removed (dR/dt)
$N = 1$	$dS/dt = -r \times S \times I$	$dI/dt = (r \times S \times I) - (a \times I)$	$dR/dt = a \times I$
$R = 5.952381e-08$	$-1.2 \times 0.9998393 \times 0.0001606548$ $= -0.0001927548$	$(1.2 \times 0.9998393 \times 0.0001606548) - (1/15 \times 0.0001606548) = 0.0001820445$	$1/15 \times 0.0001606548$ $= 0.00001071032$ $= 1.071032e-05$
$I = 16.06548e-05$			
$S = 0.9998393$	$S + R + I = 0.9998393 + 16.06548e-05 + 5.952381e-08 = 1 \Rightarrow N$		
$a = 1/15$ per day	$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \implies -0.0001927548 + 0.0001820445 + 0.00001071032 = 0$		
$r = 1.201932$			

The Results: Expected behaviour of the epidemic

Expected SIR trend, estimated reproductive rates, epidemic duration, and I_{\max}



time	S	I	R	R_o
0	0.9998393	0.0001607	0.0000001	17.997107
1	0.9994783	0.0005015	0.0000201	17.990610
2	0.9983602	0.0015575	0.0000823	17.970483
3	0.9949013	0.0048236	0.0002751	17.908223
4	0.9843110	0.0148194	0.0008697	17.717597
5	0.9528517	0.0444740	0.0026743	17.151331
6	0.8671157	0.1249715	0.0079128	15.608083
7	0.6793824	0.2991499	0.0214678	12.228883
8	0.4110083	0.5396040	0.0493877	7.398150
9	0.1911454	0.7169343	0.0919202	3.440618
10	0.0770811	0.7805449	0.1423739	1.387461

11 instances of $R_o \geq 1$
when epidemic definitely existed

- **Duration of epidemic = 140 days**

On Day 140, Infectives reached $\Rightarrow 2671.511$ and got below the initial value of 2699

- **Maximum number of infectives at any time during the epidemic: 13.11 million**

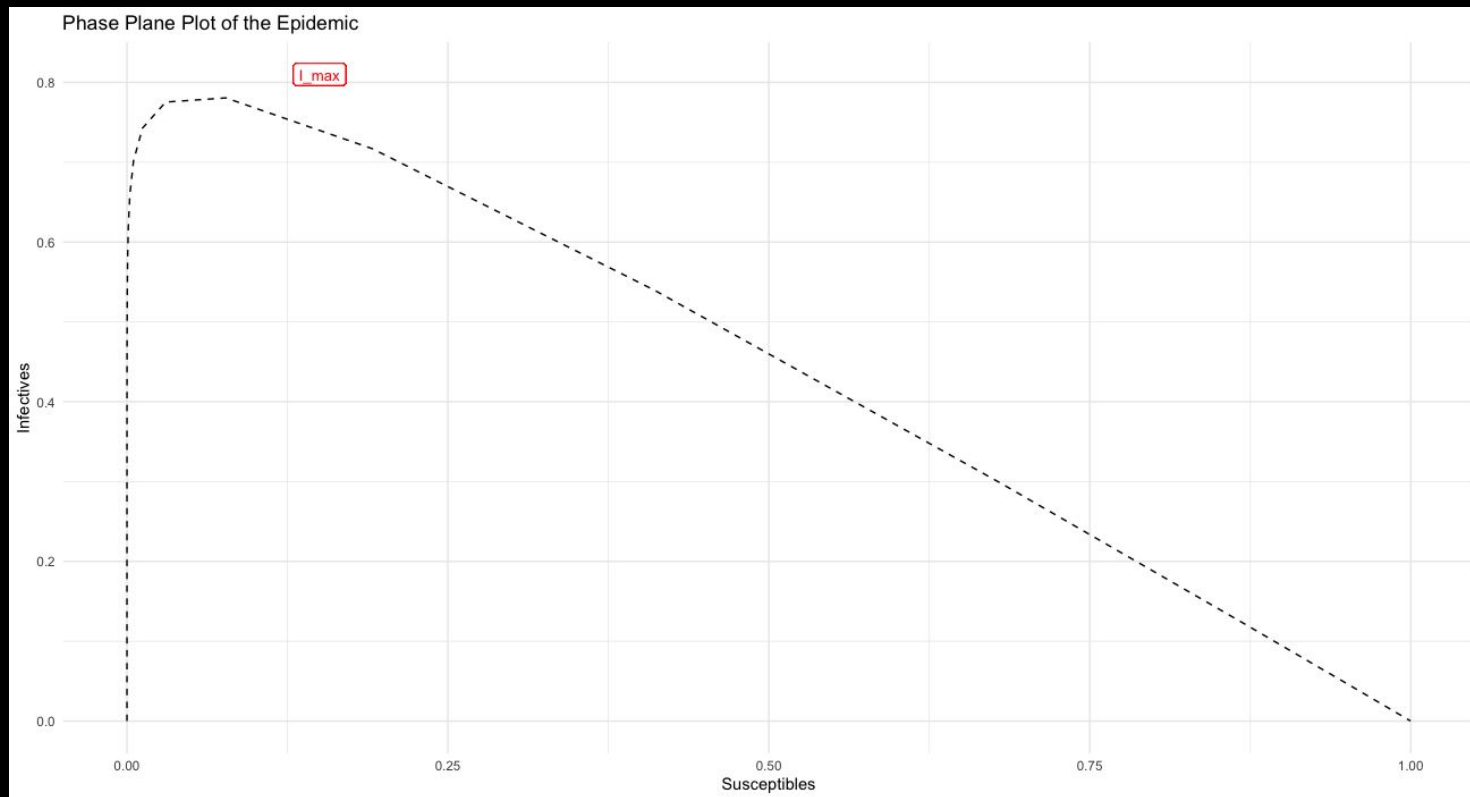
I_{\max} reached Day 11 $\Rightarrow 13,113,155 \Rightarrow$ which is 78% of the total population

All individuals got infected at some point as per this model and its parameters.

Trend shown here is **without** taking into account certain factors like births, deaths due to other reasons, vaccination drives, and behaviour change (quarantine, social distancing, enhanced hygiene practices)

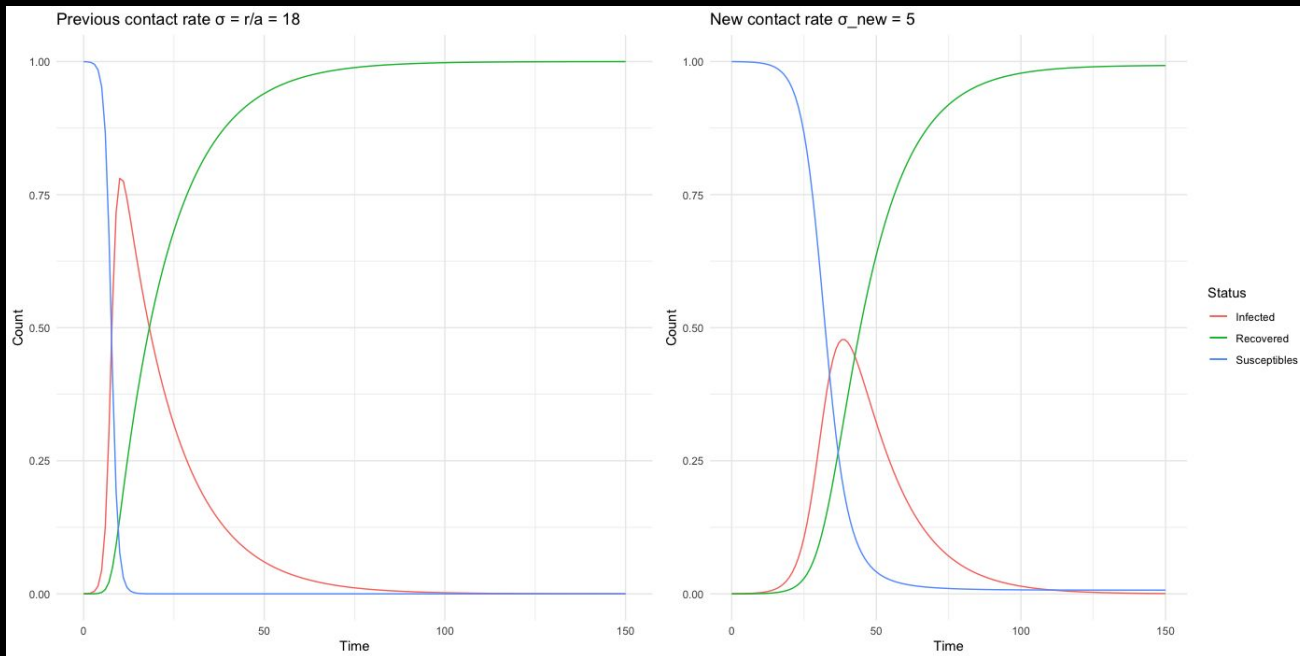
The Results: SIR Model

Phase plane plot: Infectives versus Susceptibles



The Results: SIR Model

Variation with change in contact rate, $\sigma = r/a$



Peak of infectives takes longer to arrive when social distancing and quarantine practices are followed.

R_0 , the basic reproduction number, or the contact rate, r/a suppose reduces due to effective self-quarantine measures.

Meaning sick people are not getting in contact with healthy people as much as possible
 $R_{0_new} = 5$

The number of infectives are fewer, a fraction of susceptibles did not get infected maybe due to lack of exposure to the virus.

Mathematical Biology

Weekly Exercise 2: SIR Model

Swati Tak

2023-09-12

```
# WORK ENVIRONMENT
```

```
# Clear the work environment
```

```
rm(list = ls())
```

```
setwd("/Users/swati/Desktop/Mathematical Biology")
```

```
# Install required packages
```

```
# install.packages("deSolve")
```

```
# install.packages("ggplot2")
```

```
library(knitr)
```

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
```

```
## v dplyr      1.1.3      v readr      2.1.4
```

```
## v forcats    1.0.0      v stringr   1.5.0
```

```
## v ggplot2    3.4.3      v tibble    3.2.1
```

```
## v lubridate  1.9.2      v tidyr     1.3.0
```

```
## v purrr      1.0.1
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x dplyr::filter() masks stats::filter()
```

```
## x dplyr::lag()     masks stats::lag()
```

```
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(deSolve)
```

```
library(ggplot2)
```

```
library(gridExtra)
```

```
##
```

```
## Attaching package: 'gridExtra'
```

```
##
```

```
## The following object is masked from 'package:dplyr':
```

```
##
```

```
##      combine
```

```
library(cowplot)
```

```
##
```

```
## Attaching package: 'cowplot'
```

```
##
## The following object is masked from 'package:lubridate':
##
##      stamp

# DEFINITIONS

# S --> number of susceptible individuals
# I --> number of infected individuals
# R --> number of recovered, immune or dead individuals
# r --> rate of transmission
# a --> rate of recovery
# Ro --> initial reproduction rate
# R_o --> reproduction rates based on SIR model results

## -----
## -----

# SETTING UP THE CONDITIONS OF THE EPIDEMIC

# Measles epidemic in Netherlands during 2013-2014

# Total estimated population during 2013-2014 was approx. 17 million
Total = 16800000

# Reported number of cases of measles
# There could be more cases than this but not all were reported due to religious beliefs
Reported = 2700

# One child died (removed)
Removed = 1
R = Removed/Total # Fraction of removed cases

# Remaining infectives
Infected = Reported-Removed
I = Infected/Total # Fraction of infectives

# Cases that were not infected or removed, but susceptible to infection
Susceptibles = Total-Infected-Removed
S = Susceptibles/Total # Fraction of susceptibles

#print(S+I+R)

# Measles has a recovery rate of 2-3 weeks, going by that it is approx. 15 days spent in infectious sta
a = 1/15

# Average Basic Reproduction Number, Ro, for measles in 2013-2014 in the Netherlands was 12 to 18 peopl
Ro = 18 #average number of secondary cases that can be caused by a single infected individual in a comp

# Rate of transmission per day aka Effective Reproduction Number, r
r = Ro*a # average number of new infections caused by a single infected individual per day
```


APPLYING THE MODEL

Defining a function for the SIR model using the equations

```
sir_model <- function(time, state, params) {  
  with(as.list(c(state, params)), {  
    N <- S + I + R # Total population size  
    r <- r # Rate of transmission  
    a <- a # Rate of recovery  
  
    dS <- -r * S * I / N # Change in susceptible population  
    dI <- r * S * I / N - a * I # Change in infected population  
    dR <- a * I # Change in recovered population  
  
    return(list(c(dS, dI, dR)))  
  })  
}
```

Defining initial conditions and parameters

```
initial_state <- c(S=S, I=I, R=R)  
parameters <- c(r=r, a=a)
```

Defining the times

```
times <- seq(0, 150)
```

Applying the ode function to solve the equations

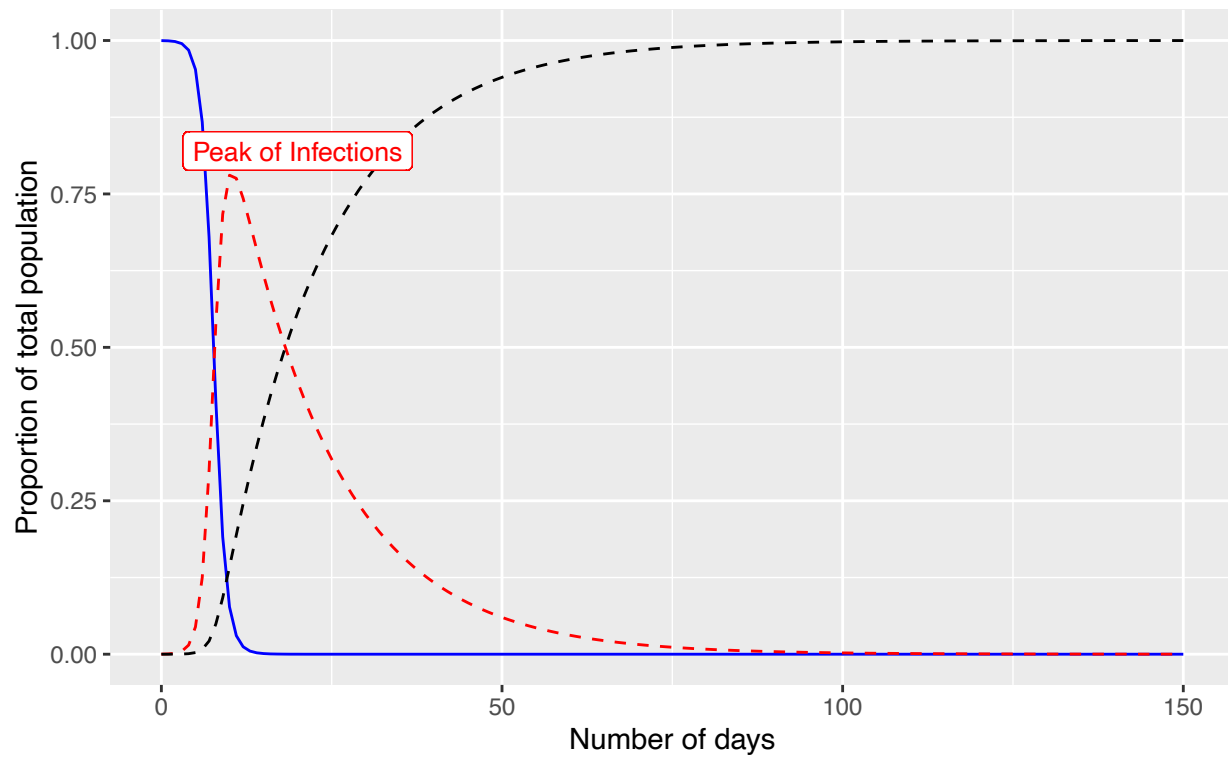
```
sir_sim <- as.data.frame(ode(y = initial_state, times = times, func = sir_model, parms = parameters))
```

PLOTTING THE RESULTS

Making a fancy plot with colors for sir_sim

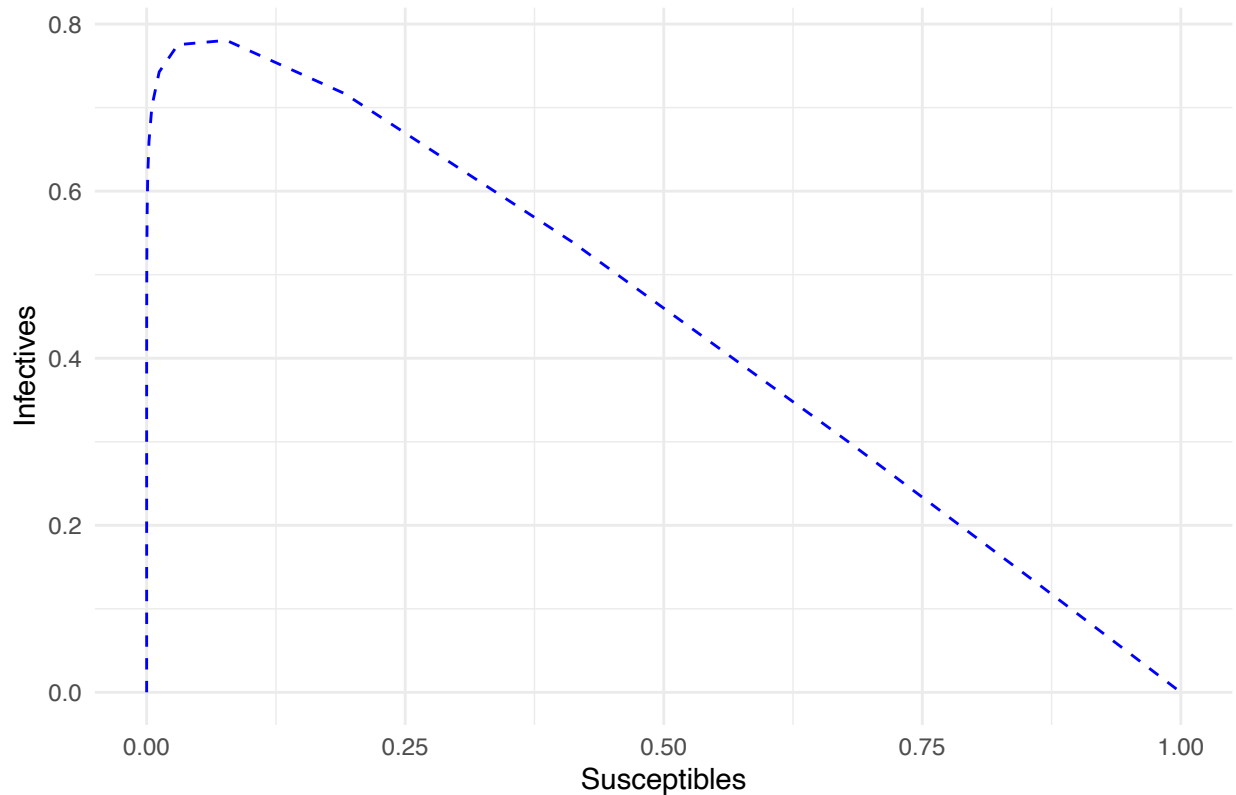
```
ggplot(sir_sim) +  
  geom_line(aes(x=time, y=S), linetype=1, linewidth=0.5, color="blue") +  
  geom_line(aes(x=time, y=I), linetype=2, linewidth=0.5, color="red") +  
  geom_line(aes(x=time, y=R), linetype=2, linewidth=0.5, color="black") +  
  labs(title="Expected SIR trend for Measles Epidemic", subtitle="Netherlands, started May 2013", x="Num")  
  geom_label(aes(x = 20, y = 0.82, label = "Peak of Infections"),  
    color = "red", size = 3.5)
```

Expected SIR trend for Measles Epidemic Netherlands, started May 2013



```
# Plotting the relation between Infected and Susceptible individuals
ggplot(sir_sim, aes(x=S, y=I)) +
  geom_line(color="blue", linetype="dashed", linewidth=0.5) +
  labs(title="Susceptibles Vs Infectives", x="Susceptibles", y="Infectives") +
  theme_minimal()
```

Susceptibles Vs Infectives



EXERCISE QUESTIONS

```

sir_sim <- sir_sim %>%
  mutate(Susceptibles=S*Total,
         Infectives=I*Total,
         Removed=R*Total)

head(sir_sim)

```

##	time	S	I	R	Susceptibles	Infectives	Removed
## 1	0	0.9998393	0.0001606548	5.952381e-08	16797300	2699.000	1.000
## 2	1	0.9994783	0.0005015374	2.011881e-05	16791236	8425.829	337.996
## 3	2	0.9983602	0.0015575096	8.230673e-05	16772451	26166.161	1382.753
## 4	3	0.9949013	0.0048235768	2.751198e-04	16714342	81036.090	4622.013
## 5	4	0.9843110	0.0148193597	8.696717e-04	16536424	248965.243	14610.485
## 6	5	0.9528517	0.0444740001	2.674306e-03	16007908	747163.202	44928.333

```

# What are the reproductive rate R0 (not the initial value of R)?
R_o = (r*sir_sim$S)/a # Reproduction rates of infection as per the model results
sir_sim$R_o <- (r*sir_sim$S)/a

```

```

# Instances where basic reproduction rate was higher or equal to 1
R_o_epidemic <- sir_sim %>% filter(R_o > 1)
count(R_o_epidemic)

```

```
##      n
```

```
## 1 11
```

```
kable(R_o_epidemic)
```

time	S	I	R	Susceptibles	Infectives	Removed	R_o
0	0.9998393	0.0001607	0.0000001	16797300	2699.000	1.000	17.997107
1	0.9994783	0.0005015	0.0000201	16791236	8425.829	337.996	17.990610
2	0.9983602	0.0015575	0.0000823	16772451	26166.161	1382.753	17.970483
3	0.9949013	0.0048236	0.0002751	16714342	81036.090	4622.013	17.908223
4	0.9843110	0.0148194	0.0008697	16536424	248965.243	14610.485	17.717597
5	0.9528517	0.0444740	0.0026743	16007908	747163.202	44928.333	17.151331
6	0.8671157	0.1249715	0.0079128	14567544	2099521.692	132934.490	15.608083
7	0.6793824	0.2991499	0.0214678	11413624	5025717.982	360658.276	12.228883
8	0.4110083	0.5396040	0.0493877	6904940	9065346.738	829713.669	7.398150
9	0.1911454	0.7169343	0.0919202	3211243	12044497.060	1544259.739	3.440618
10	0.0770811	0.7805449	0.1423739	1294963	13113155.155	2391881.577	1.387461

```
# sir_sim <- sir_sim %>% select(Susceptibles, Infectives, Removed, R_o)
head(sir_sim)
```

```
##   time      S      I      R Susceptibles Infectives   Removed
## 1    0 0.9998393 0.0001606548 5.952381e-08   16797300   2699.000     1.000
## 2    1 0.9994783 0.0005015374 2.011881e-05   16791236   8425.829     337.996
## 3    2 0.9983602 0.0015575096 8.230673e-05   16772451  26166.161    1382.753
## 4    3 0.9949013 0.0048235768 2.751198e-04   16714342  81036.090    4622.013
## 5    4 0.9843110 0.0148193597 8.696717e-04   16536424 248965.243   14610.485
## 6    5 0.9528517 0.0444740001 2.674306e-03   16007908 747163.202   44928.333
##      R_o
## 1 17.99711
## 2 17.99061
## 3 17.97048
## 4 17.90822
## 5 17.71760
## 6 17.15133
```

```
# What is the duration of the epidemic?
```

```
# Determine when number of infectives reaches below its initial number of infectives, 2699
sir_sim$Infectives <- as.numeric(sir_sim$Infectives)
end_of_epidemic_index <- which(sir_sim$Infectives < 2699)
print(paste("Duration of the epidemic (in days):", end_of_epidemic_index[1]))
```

```
## [1] "Duration of the epidemic (in days): 140"
```

```
# What is the maximum number of infected at any time during the epidemic?
```

```
max_infected <- max(sir_sim$Infectives)
print(paste("Maximum number of infected at any time during the epidemic:", round(max_infected)))
```

```
## [1] "Maximum number of infected at any time during the epidemic: 13113155"
```

```
# How does the epidemic change when the contact rate changes?
```

```
a = 1/15 # previous recovery rate
```

```
a_new = 1/15 # new recovery rate keeping it the same
```

```
# Ro = 18 basic reproduction number, or the contact rate, r/a suppose reduces due to effective self-quarantine
```

```
# Meaning sick people are not getting in contact with healthy people as much as possible
```

```
Ro_new = 5
```

```
r_new = Ro_new*a_new/S
```

```
r
```

```
## [1] 1.2
```

```
# Defining new conditions and parameters
```

```
parameters_new <- c(r=r_new, a=a_new)
```

```
# Defining new times
```

```
times <- seq(0, 150)
```

```
# Applying the ode function to solve the equations
```

```
sir_sim_new <- as.data.frame(ode(y = initial_state, times = times, func = sir_model, parms = parameters_new))
```

```
# Applying the ode function to solve the equations
```

```
sir_sim_new <- as.data.frame(ode(y = initial_state, times = times, func = sir_model, parms = parameters_new))
```

```
# Adding R_o_new to the new model results
```

```
sir_sim_new$R_o_new <- (r_new*sir_sim_new$S)/a_new
```

```
head(sir_sim)
```

```
##      time      S      I      R Susceptibles Infectives   Removed
## 1      0 0.9998393 0.0001606548 5.952381e-08      16797300      2699.000        1.000
## 2      1 0.9994783 0.0005015374 2.011881e-05      16791236      8425.829       337.996
## 3      2 0.9983602 0.0015575096 8.230673e-05      16772451     26166.161      1382.753
## 4      3 0.9949013 0.0048235768 2.751198e-04      16714342     81036.090     4622.013
## 5      4 0.9843110 0.0148193597 8.696717e-04      16536424    248965.243    14610.485
## 6      5 0.9528517 0.0444740001 2.674306e-03      16007908    747163.202    44928.333
##      R_o
## 1 17.99711
## 2 17.99061
## 3 17.97048
## 4 17.90822
## 5 17.71760
## 6 17.15133
```

```
tail(sir_sim_new)
```

```
##      time      S      I      R   R_o_new
## 146   145 0.006999119 0.0007973996 0.9922035 0.03500122
## 147   146 0.006997317 0.0007477153 0.9922550 0.03499221
## 148   147 0.006995628 0.0007011264 0.9923032 0.03498376
## 149   148 0.006994045 0.0006574400 0.9923485 0.03497584
```

```
## 150 149 0.006992560 0.0006164753 0.9923910 0.03496842
## 151 150 0.006991168 0.0005780628 0.9924308 0.03496146
```

```
sir_sim_new <- sir_sim_new %>%
  mutate(Susceptibles=S*Total,
         Infectives=I*Total,
         Removed=R*Total) %>%
  select(Susceptibles, Infectives, Removed, R_o_new)

# Determine when the epidemic ends (I reaches close to 0)
# Determine when number of infectives reaches below its initial number of infectives
sir_sim_new$Infectives <- as.numeric(sir_sim_new$Infectives)
end_of_epidemic_index2 <- which(sir_sim_new$Infectives < 2699)
print(paste("Duration of the epidemic (in days):", end_of_epidemic_index2[1]))
```

```
## [1] "Duration of the epidemic (in days): NA"
```

```
# Defining new times
times <- seq(0, 150)

# Applying the ode function to solve the equations
sir_sim_new <- as.data.frame(ode(y = initial_state, times = times, func = sir_model, parms = parameters))

# Create a function to plot the epidemic dynamics
plot_epidemic_dynamics <- function(data, title, custom_text = NULL) {
  # Create the title by combining the base title and custom text
  full_title <- paste(title, ifelse(!is.null(custom_text), custom_text, ""), sep = " ")

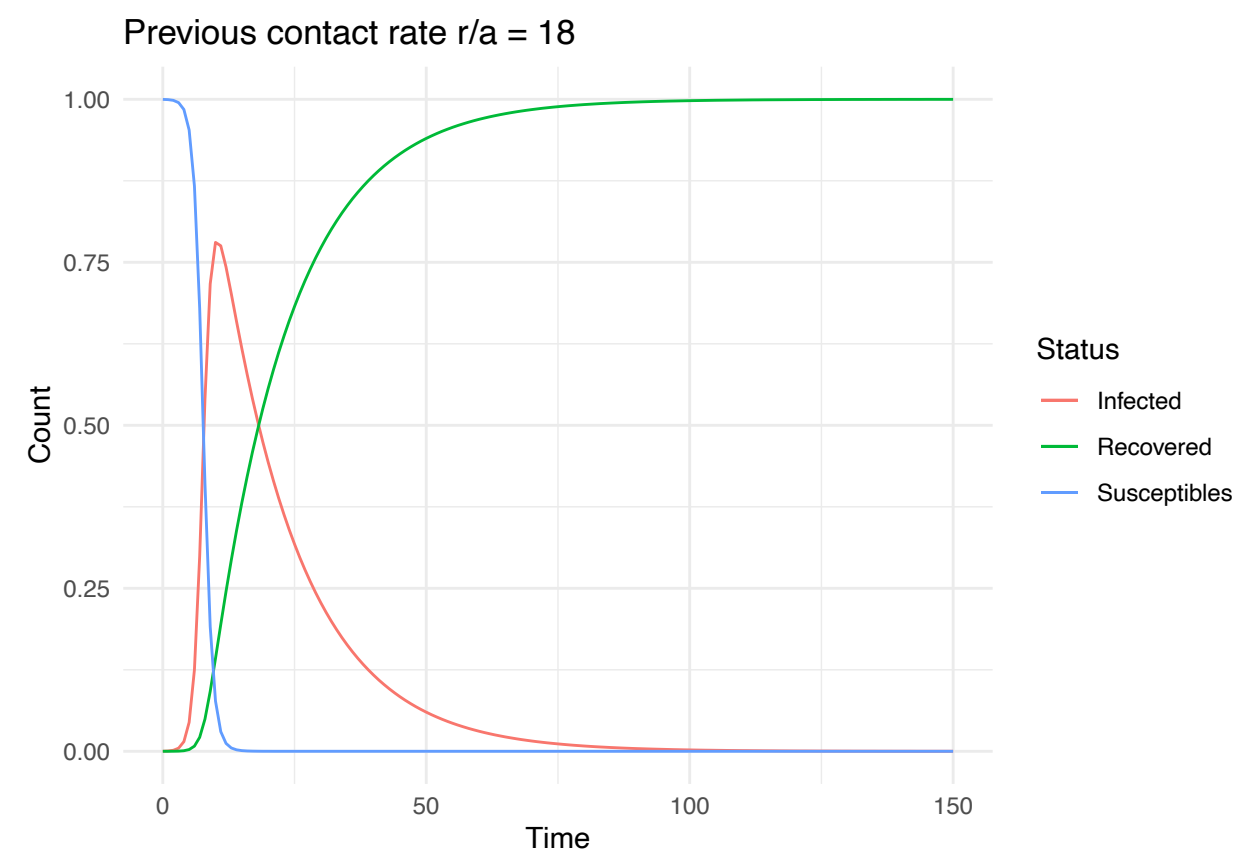
  ggplot(data, aes(x = time)) +
    geom_line(aes(y = I, color = "Infected")) +
    geom_line(aes(y = R, color = "Recovered")) +
    geom_line(aes(y = S, color = "Susceptibles")) +
    labs(x = "Time", y = "Count", color = "Status") +
    ggtitle(full_title) +
    theme_minimal()
}

# Define the contact rate for plot titles
sigma=round(r/a)
sigma_new = round(r_new/a_new)

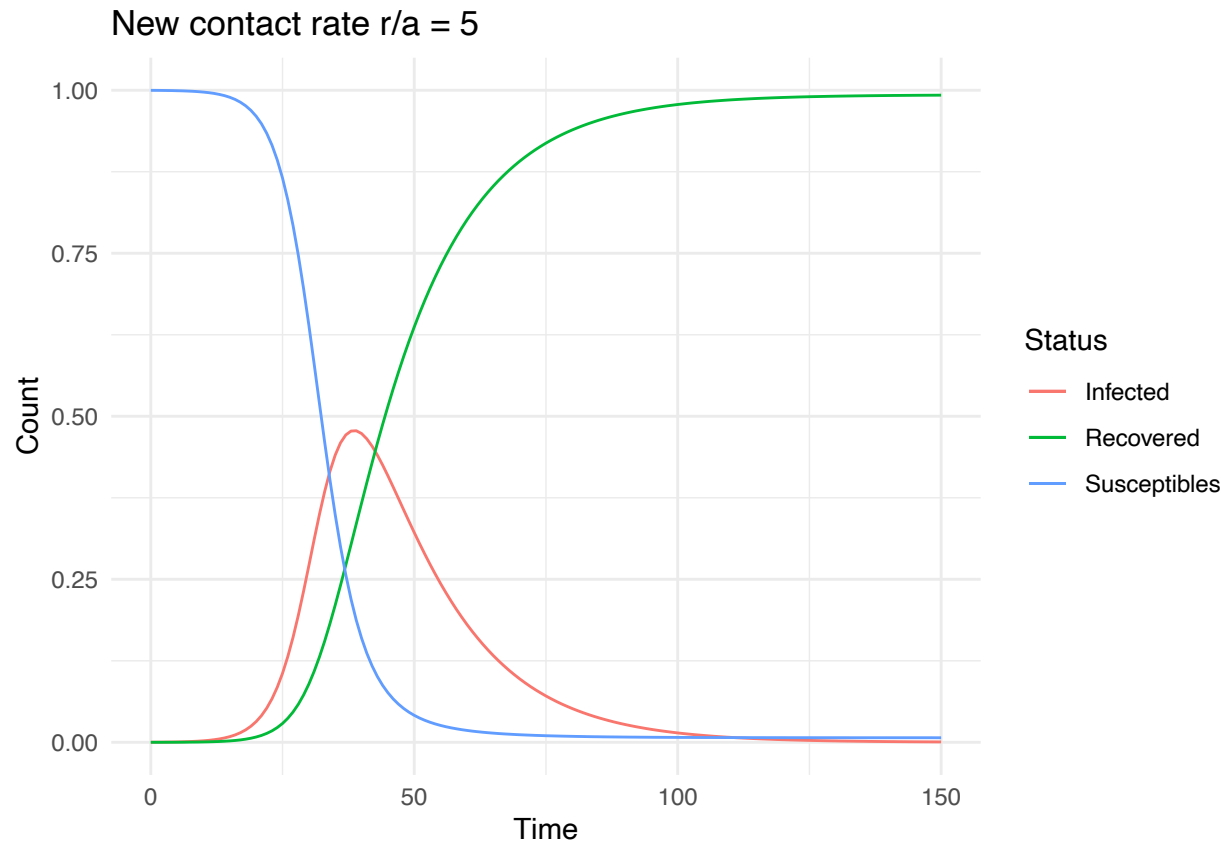
# Define plot titles
custom_text1 <- paste("r/a =", sigma)
custom_text2 <- paste("r/a =", sigma_new)

# Draw the plots
plot_prev <- plot_epidemic_dynamics(sir_sim, "Previous contact rate", custom_text1)
plot_new <- plot_epidemic_dynamics(sir_sim_new, "New contact rate", custom_text2)

plot_prev
```



plot_new



```
# # Combine the plots for comparison
# combined_plot <- plot_grid(plot_prev, plot_new, ncol = 2, align = "v", axis = "tb")
# combined_plot
```

```
max_infected_new <- max(sir_sim_new$I)
```

```
print(paste("Maximum number of infected at any time during the epidemic for a/r=18 is => ", round(max_in
```

```
## [1] "Maximum number of infected at any time during the epidemic for a/r=18 is => 13113155"
```

```
print(paste("Maximum number of infected at any time during the epidemic for a/r=5 is =>", round(max_in
```

```
## [1] "Maximum number of infected at any time during the epidemic for a/r=5 is => 8026458"
```

```
# How does the phase plane plot of the epidemic look like?
```

```
ggplot(sir_sim, aes(x = S, y = I)) +
  geom_line(color = "black", linetype = "dashed", linewidth = 0.5) +
  labs(title = "Phase Plane Plot of the Epidemic", x = "Susceptibles", y = "Infectives") +
  theme_minimal() +
  geom_label(aes(x = 0.15, y = 0.81, label = "I_max"),
    color = "red", size = 3.5)
```


Phase Plane Plot of the Epidemic

