Network Analysis on Ebola Epidemic

EECE 506 - GROUP 5
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Outline

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- Math Problem
  - Assumptions
- Methodology
  - SIS, SIR, and SEIR Models
- Calculation
- Simulation
- Results
- Future Improvements

Background

- Ebola Virus – EBOV, *Zaire ebolavirus*
- Infectious disease with high case fatality
- Zoonotic pathogen
- Symptoms
  - Fever, Fatigue
  - Vomiting, Diarrhea
  - Hemorrhage

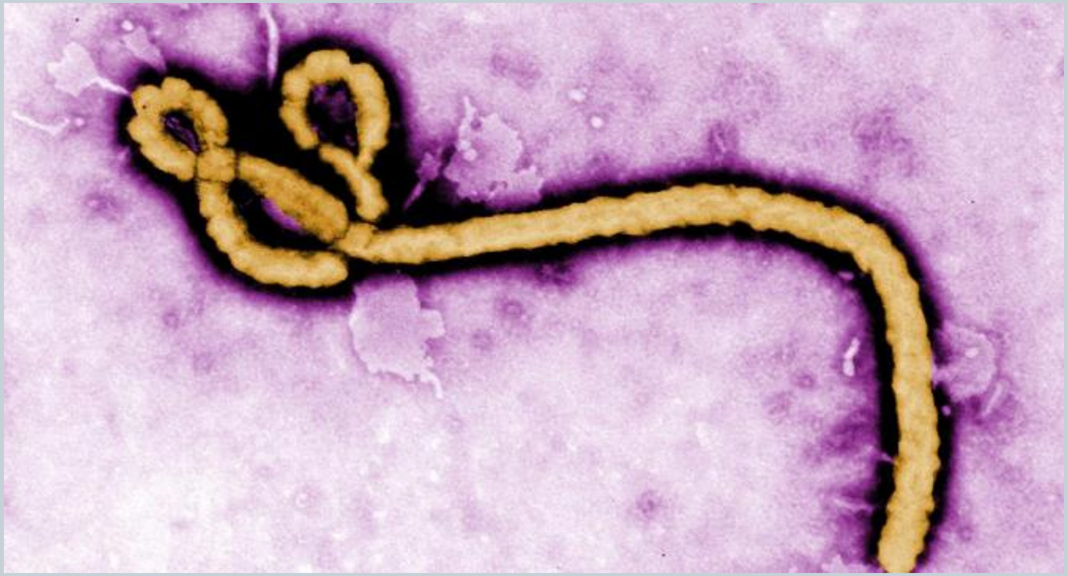


Figure 1: Ebola virus

Math Problem

- Virus growth rate in spreading within a population

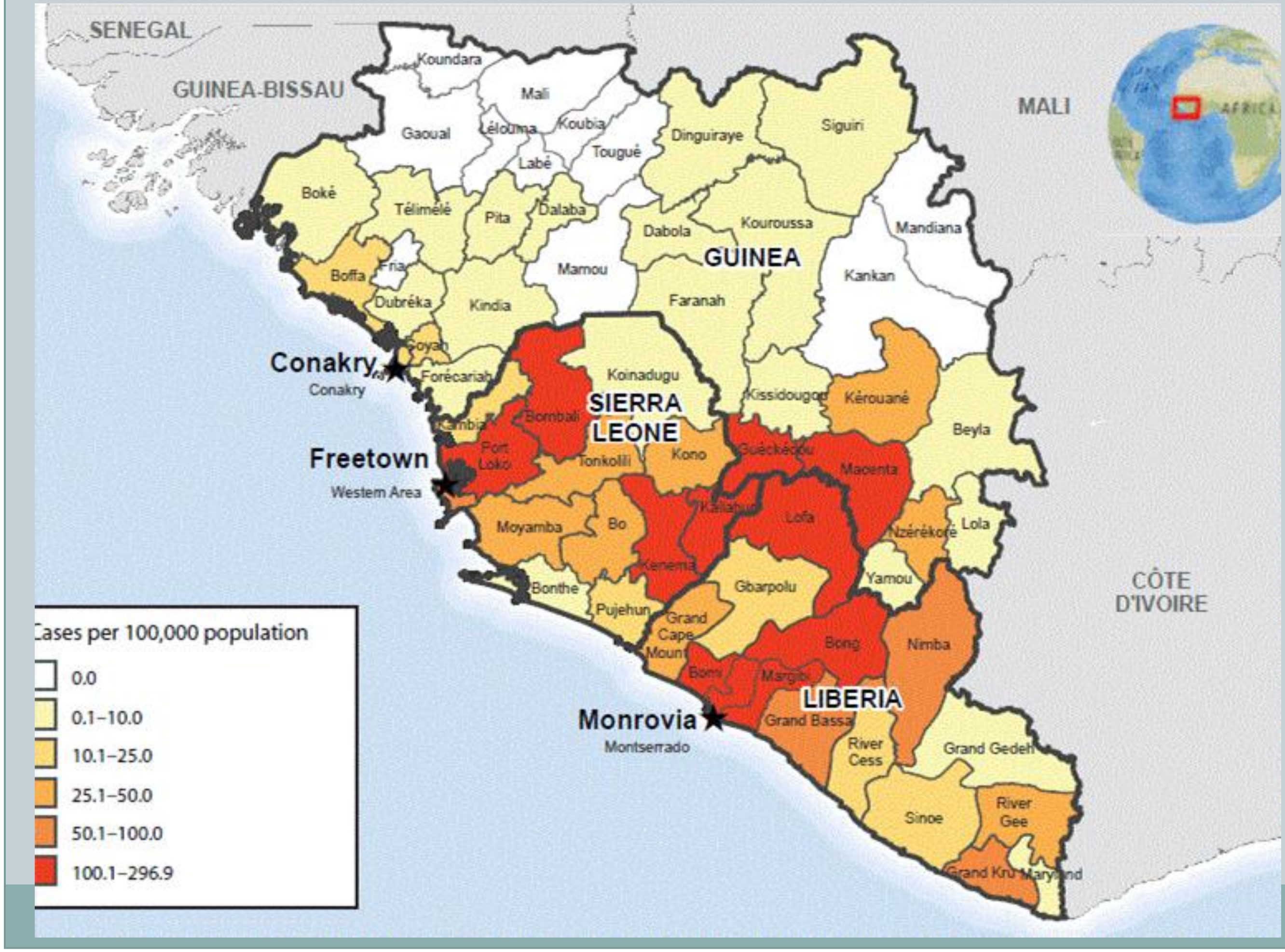


Figure 2: Reported cases in West Africa from October 2014

Math Problem

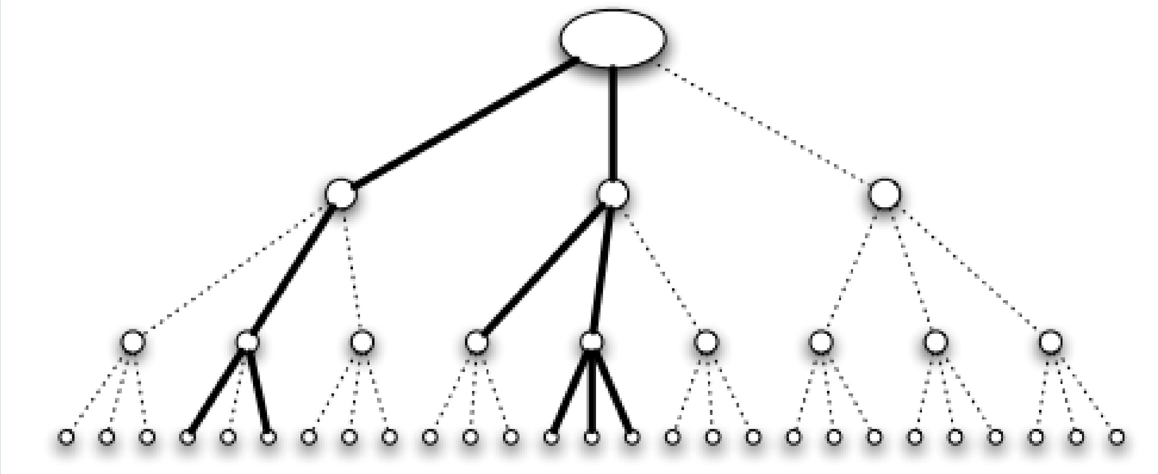


Figure 3: High contagion probability, virus spreads

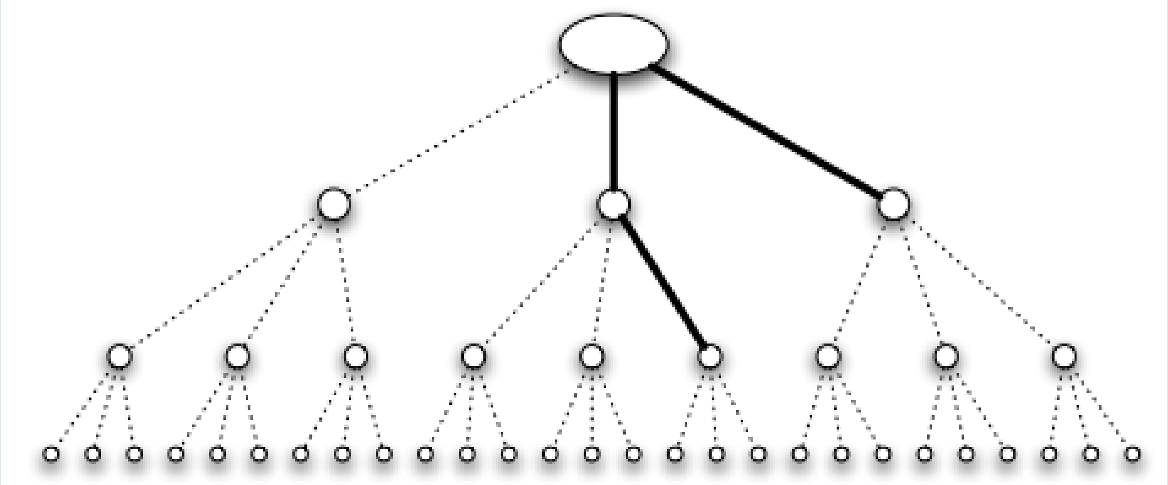


Figure 4: Low contagion probability, virus dies out

Assumptions

- Given data from Centers for Disease Control and Prevention (CDC) and the World Health Organization (WHO) is correct
- Incubation or latency period: 2 to 21 days
- Average time for death is 10 days after symptoms
- Has not evolved into airborne transmission
- There is no vaccine for this infectious disease
- For initial population, no individual diagnosed with symptoms

SIS Model

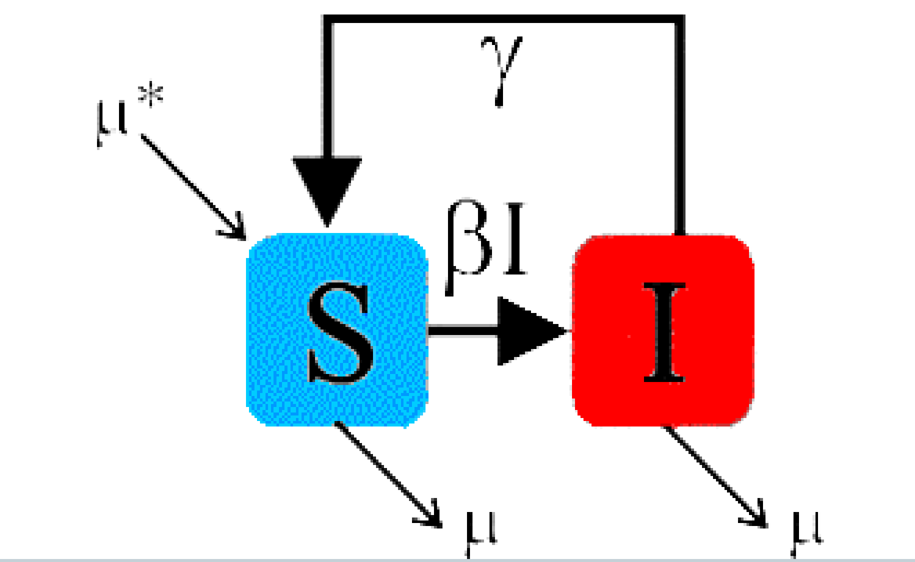


Figure 5: SIS Model

- Parameters:
  - S: Susceptible
  - I: Infectious
  - β: Contact rate
  - ϒ: Recovery rate
  - μ and μ*: Death/Birth rates
  - N: Total population

Equations Involved

- Total Population: $N=S(t)+I(t)$
- Rate of susceptible over time:
  - $dS/dt = -\beta SI/N + (\gamma + \mu)I$
- Rate of infectious over time:
  - $dI/dt = \beta SI/N - (\gamma + \mu)I$

Where, $\beta SI/N$ indicates how infected people transfer the disease to susceptible

- Reproductive number $R_0=\beta I$

  where,
  - $R_0 < 1$:infection will decrease and become null
  - $R_0 > 1$:disease is considered infectious

SIR Model

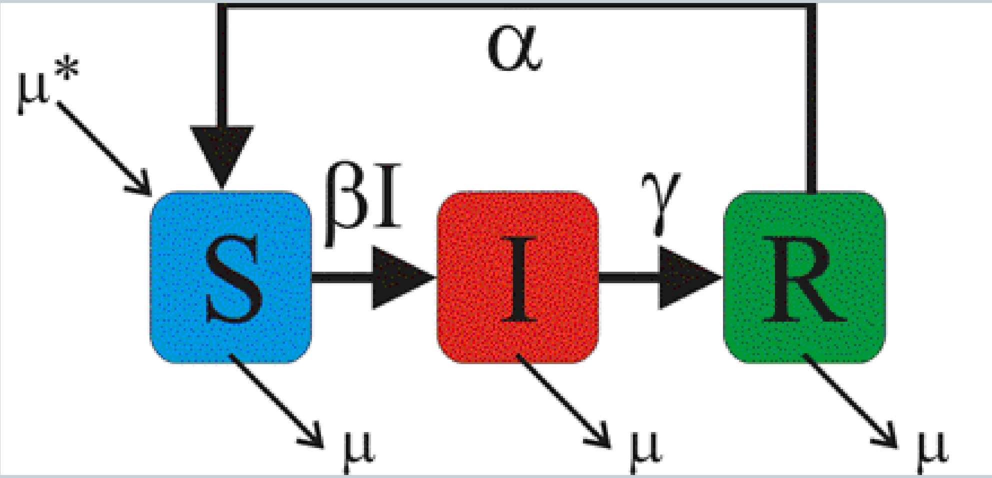


Figure 6: SIR Model

- Parameters:
  - Same variables used in SIS Model
  - R: Recovered with Immunity or removed due to death
  - α: Immunity loss rate

Equations Involved

- $N=S(t)+I(t)+R(t)$
- $dS/dt = -\beta SI/N + \mu(N - S) + \alpha R$
- $dI/dt =\beta SI/N - (\gamma + \mu)I$
- $dR/dt = \gamma I - \mu R - \alpha R$

Where, $\beta SI/N$ indicates how infected people transit the disease to susceptible

- Reproductive number is given by $Ro= \beta/\gamma+\mu$ where,
  - $Ro < 1$: infection will be cleared from the population.
  - $Ro > 1$: pathogen is able to invade the susceptible population.

SEIR Model

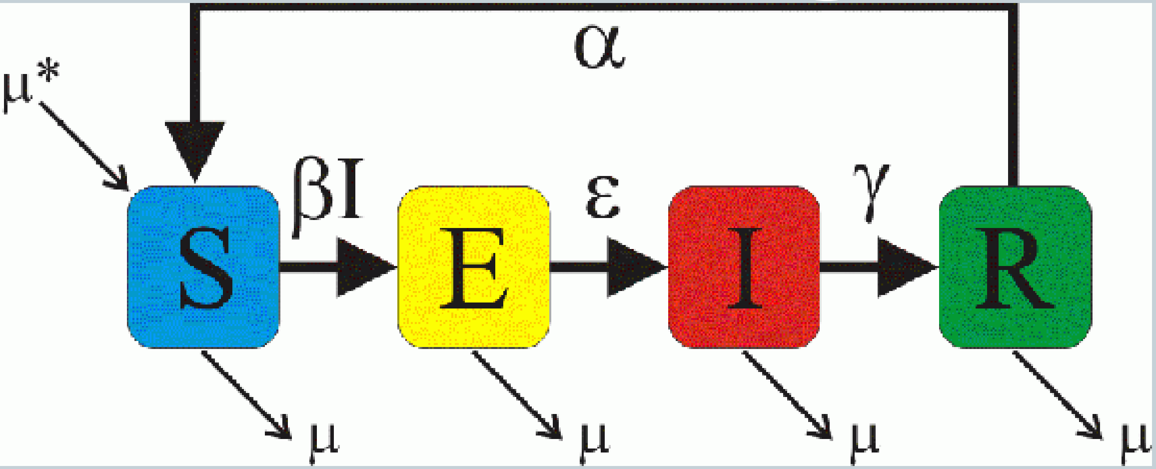


Figure 7:
SEIR Model

- Parameters:
  - Same variables used in SIR Model
  - E: Individuals exposed to virus that don’t show symptoms and are not contagious
  - ε: Constant that determines how likely to become infectious after exposure per individual

Equations Involved

Function of susceptible over time: $\frac{dS}{dt} = \frac{-\beta S(I + qE)}{N}$

Function of virus exposure over time: $\frac{dE}{dt} = \frac{\beta S(I + qE)}{N} - \delta E$

Function of infectious over time: $\frac{dI}{dt} = \delta E - \gamma I$

Function of recovery over time: $\frac{dR}{dt} = \gamma I$

Reproductive number: $R_0 = ({}^{\beta}/_{\gamma})(1 + {}^{q\gamma}/_{\delta})$

Reproductive number: $R_0 = \frac{\varepsilon\beta}{(\varepsilon + \mu)(\gamma + \mu)}$

Calculations

- Given:
  - Data I(t) and R(t) from CDC
- From assumption:
  - $\mu=0$
  - $\alpha=0$
  - $1/\varepsilon= 21$ days
  - $1/\gamma=10$ days
  - $R0=?$

- $R0=(\beta /\gamma)(1+q*\gamma/\varepsilon)$
- *q is an arbitrary number from 0 to 1

Finding β

- Daily infectious rate:
  - $dI/dt=\varepsilon E-(\gamma+\mu)I=0$ During Latency Period
- Cumulative latent data:
  - $E=\gamma*\varepsilon*I(t)$
- Daily latent data:
  - $dE/dt=\beta(I+q*E)-\varepsilon*E$
- Total infectious cases:
  - $I=\sigma*\gamma*E$
- $dE/dt=(\beta(\varepsilon*\gamma-\varepsilon))E$ <= Linear fit with Matrix
- Effective contact rate:
  - $\beta=$Linear fit slope$/(\varepsilon*\gamma-\varepsilon)$

Results

- β=Linear fit slope/(ε*γ-ε)=0.1941
- Ro=(β /γ)(1+qγ/ε)
- q= (0 ≤ q ≤ 1)

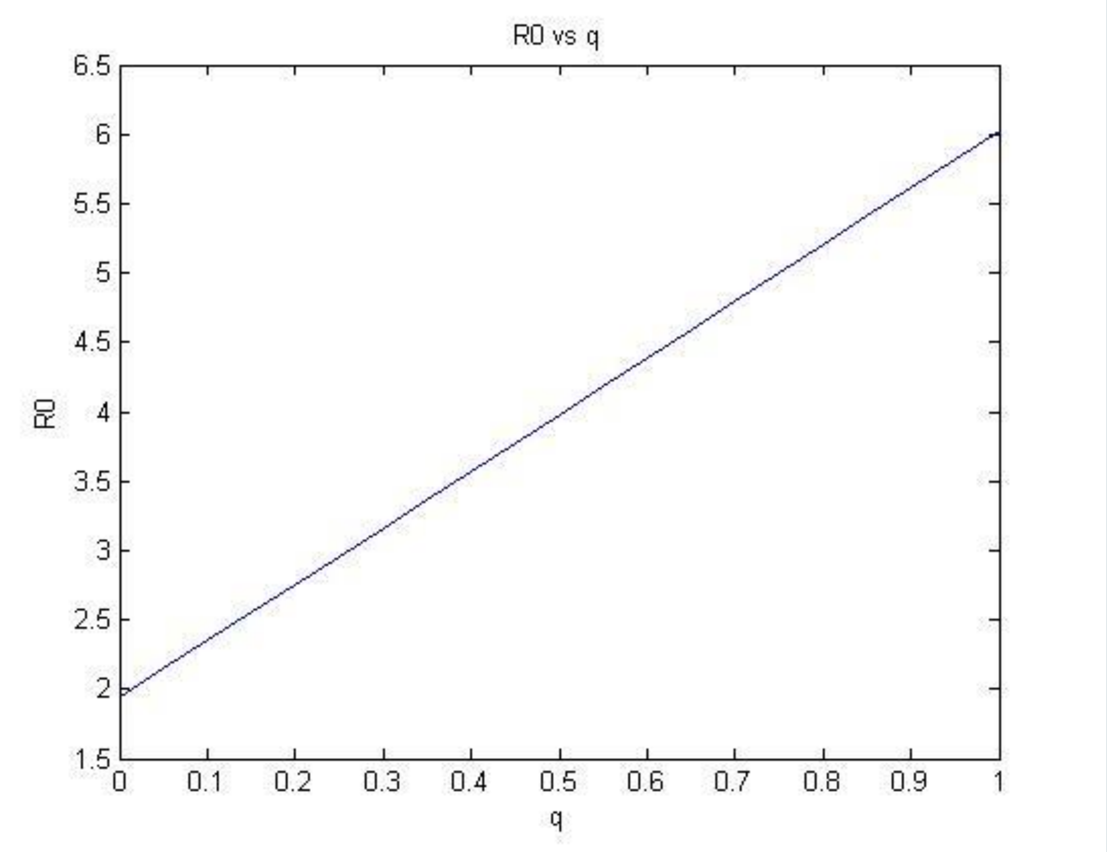
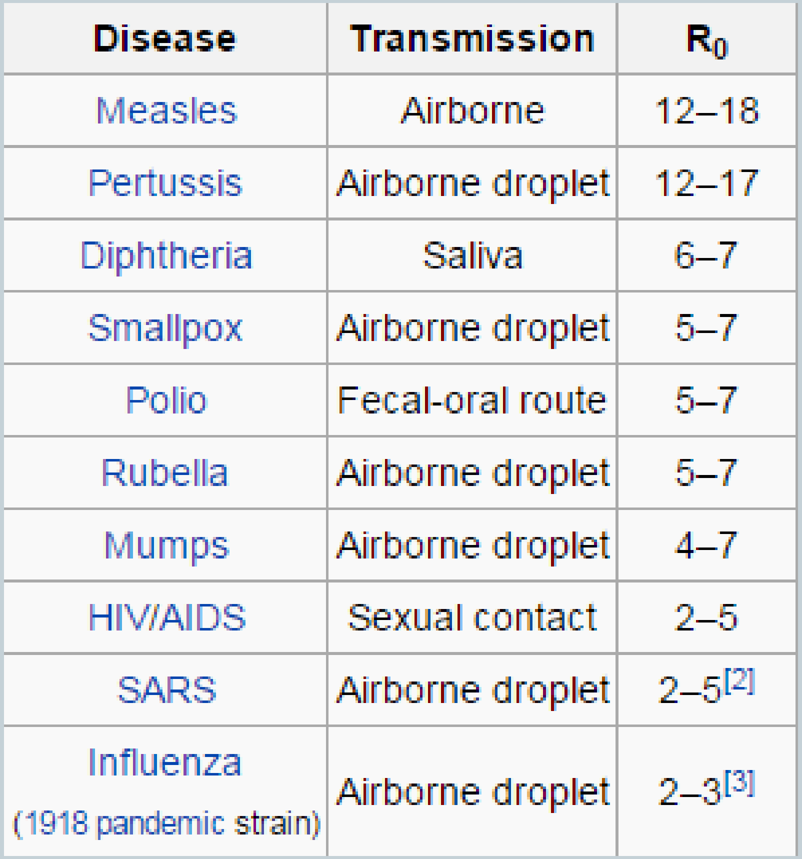


Figure 8: Reproductive number vs. weight factor

Results

- Reproduction Number: $Ro = 2 \leq R0 \leq 6$



Disease	Transmission	R_0
Measles	Airborne	12–18
Pertussis	Airborne droplet	12–17
Diphtheria	Saliva	6–7
Smallpox	Airborne droplet	5–7
Polio	Fecal-oral route	5–7
Rubella	Airborne droplet	5–7
Mumps	Airborne droplet	4–7
HIV/AIDS	Sexual contact	2–5
SARS	Airborne droplet	2–5[2]
Influenza (1918 pandemic strain)	Airborne droplet	2–3[3]

Figure 9: Reproductive number values of infectious diseases

Results

- SIS Model doesn’t include recovery case
- SIR model is missing the consideration of a latency period
- On comparing the three models, SEIR model calculations were the most accurate
  - Incubation period
- Graph results

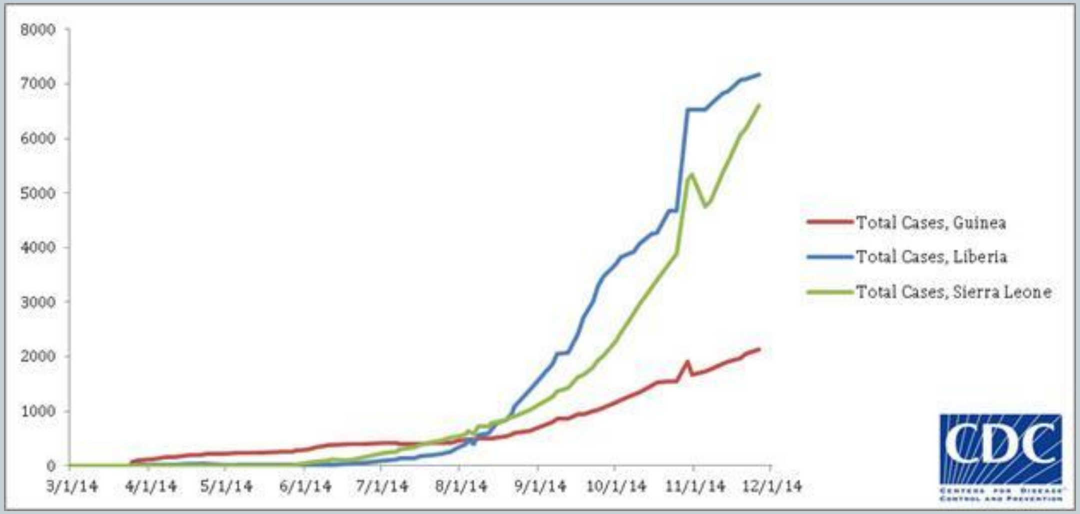


Figure 10: Cumulative reported cases in West Africa

Future Improvements

- SEIR model limitation - Population size
- Using a continuous model
  - By integrating continuous variables over a time span in the above equations, we can obtain more realistic and feasible results.
- Use new parameters
  - Ebola virus evolves into different transmissions
  - There is a cure or vaccine discovered
- Environment conditions
  - Quarantine

Current News

- Current death toll is about 7,000
- Setting up more Ebola Treatment Units in West Africa
- Vaccine currently in trial stage

Figure 11: Participant receiving dose of vaccine

Programming Code

```
% EECE 506
% Project (Ebola Outbreak)
clear all
close all
clc
%% Given
sigma=1/21; % 21 days for 90% of the individual who was latent becomes infectious
gamma=1/10; % Average of 10 days for death after the individual become infectious
N=22400000; %West Africa(Liberia, Guinea, Sierra Leone) Total Population
%% R(t)
R=[59
60
77
```

```
dI=diff(I);
figure(2)
plot(I)
title('I(t)')
xlabel('days(Recorded)')
ylabel('Cumulative Infected Cases')
%dI(t)/dt should be plotted for positive values since we don't considered
%death on I(t). Also It is exactly same number as the Real Data.
figure(3)
bar(dI)
title('dI/dt')
xlabel('days(Recorded)')
ylabel('Infected Cases')
xlim([0 65])
ylim([0 4000])
```

```
%% Find S(t)
S=N-E-I-R;
figure(6)
plot(S)
title('S(t)')
xlabel('Days(Recorded)')
ylabel('Susceptibles')
%% Find Beta the contact rate
B=A/(sigma/gamma-sigma)
%% Find R0
q=0:0.05:1; %arbitrary weight
R0=(B/gamma).*(1+q*gamma/sigma) %Equaled to 2<R0<6
figure(7)
plot(q,R0)
title('R0 vs q')
xlabel('q')
ylabel('R0')
```

```
%% Finding E(t)
t=1:1:21;
E=gamma*I/sigma;
dE=diff(E);
[r,m,b] = regression(t',dE)
A=inv(E(t)'*E(t))*(E(t)'*dE(t))
Y_hat=A*E(t);
%Linear Fit Line
figure(4)
plot(E)
title('E(t)')
xlabel('Days(Recorded)')
ylabel('Cumulative Latent data')
figure(5)
hold on
bar(dE(t))
plot(Y_hat)
title('dE/dt)')
xlabel('Days(Recorded)')
ylabel('Latent data')
```

References

- [1] - http://media1.s-nbcnews.com/i/newscms/2014_40/586866/140727-ebola-jms-2109_1ed47d529151d5ad829c219cb5173ced.jpg
- [2] – http://www.cdc.gov/mmwr/preview/mmwrhtml/mm6343a3.htm?s_cid=mm6343a3_w
- [3, 4] – http://www.cs.cornell.edu/home/kleinber/networks-book/networks-book-ch21.pdf
- [5, 6, 7] – https://wiki.eclipse.org/Introduction_to_Compartment_Models
- [8] - Programming Code (MATLAB)
- [9] - http://en.wikipedia.org/wiki/Basic_reproduction_number#cite_note-4
- [10] – http://www.cdc.gov/vhf/ebola/outbreaks/2014-west-africa/cumulative-cases-graphs.html
- [11] - http://www.nih.gov/news/health/nov2014/niaid-28.htm

Questions?