Final Project

CS111: Structure: Mathematical and Computational Models

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December 2017

The HIV/AIDS Epidemic

HIV is a human immunodeficiency virus infection, which is predominantly spread through sexual relations with an infected individual. As the infection worsens it affects the immune system of the infected individual and can lead to acquired immune deficiency syndrome (AIDS).

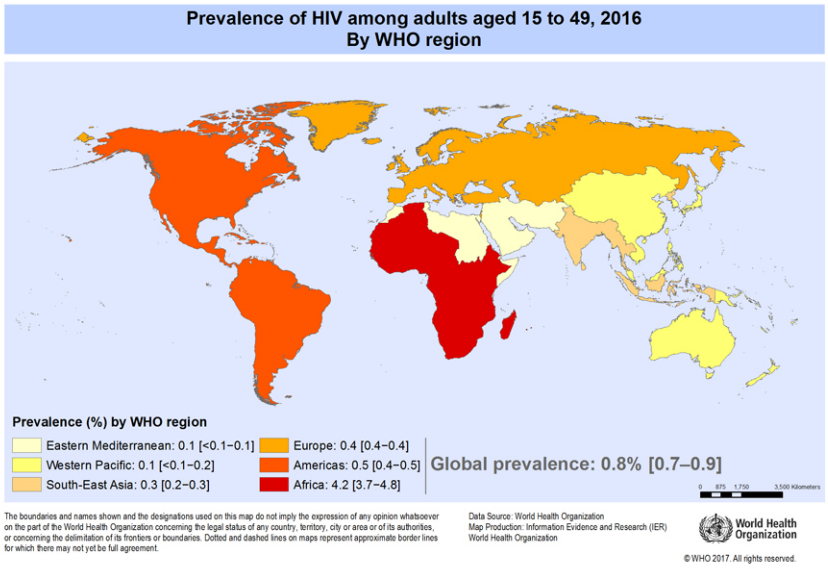


Figure 1. Choropleth world map, showing the prevalence of HIV in different world regions (WHO, 2016).

Beneficial reasons to model this system include, the ability to estimate

the funds which should be allocated to HIV prevention and medication in the future, as well as to analyse real world data using the model, and being able to notice trends in the disease spread or mitigation.

Mathematical Models

SIR is a common mathematical model used to model disease propagation. It is based on three types of the population at time, t:

- **S(t):** the number of *susceptible* persons to the disease
- **I(t):** the number of *infected* persons
- **R(t):** the number of *recovered* and deaths from the disease

As shown in Figure 2. on the next page, the relationship between the susceptible population and the infected population is βI which is the infection rate, and the relationship between the infected population and the recovered population is γ which is the recovery or death rate. These variables can also be thought of as probabilities, where βI is the probability of infection given contact with an infected person and γ is the probability of recovery or death given infection.

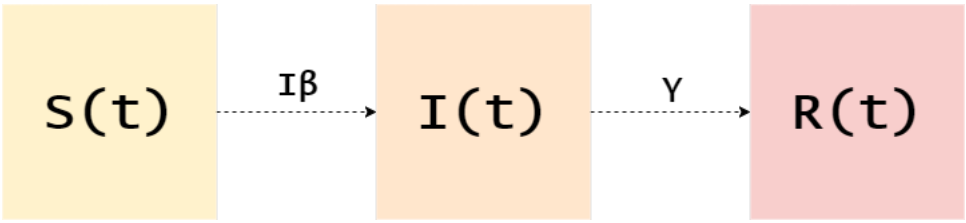


Figure 2. Visualisation of SIR model with relationship between populations.

SIR: Ordinary Differential Equations

If we assume, that the effect of the epidemic is faster than the effect of births and other deaths, then we can use the following ordinary differential equations to model the system in a deterministic way. This refers to there being no randomality within our model. If N is our population, then:

$$\frac{dS}{dt} = -\frac{\beta IS}{N} \tag{1}$$

$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I \tag{2}$$

$$\frac{dR}{dt} = \gamma I \tag{3}$$

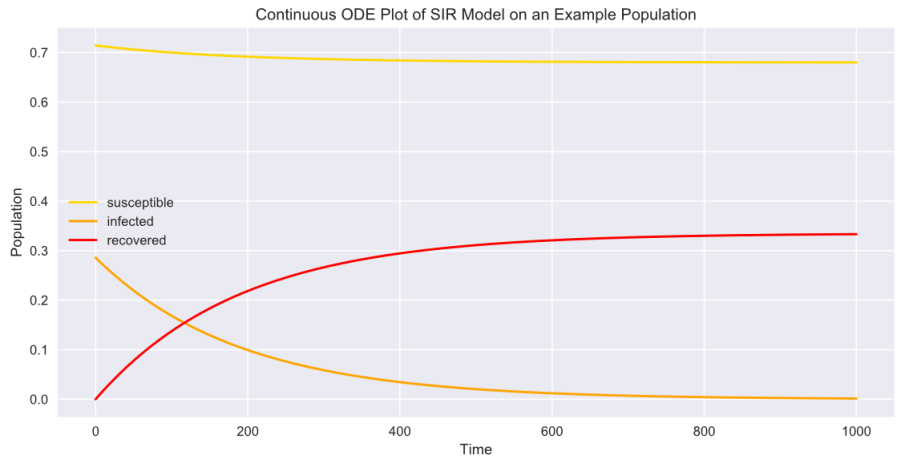
Equation 1. is the rate of change of our susceptible population, which is therefore decreasing proportionally to our rate of infection multiplied by our current susceptible population and our infected population (as you can only contract the disease through contact with an infected person).

Equation 2. is the rate of change of our infected population. In this case, it is proportional to our rate of infection multiplied by our current susceptible population and our infected population, which we subtract from it the amount of persons recovered (i.e. our recovery rate multiplied by our current infected population size).

Finally, Equation 3. is the rate of change of our recovered population

which is equal to our recovery rate multiplied by our infected population.

Graph 2. below shows an example of how SIR works within a fake population.




```
Final susceptible: 0.68011910709
Final infected: 0.00144529745812
Final recovered: 0.333280882783
```

Graph 2. Plot showing the population characteristics at time = 1000, when the starting N = 700, S = 500, I = 200 and R = 0, with $\beta = \frac{1}{11}$ and $\gamma = \frac{6.8}{11}$. Graph created in Python. Code can be found in Appendix.

SIR: Markov Chains

Modelling with Markov Chains is a stochastic modelling method since it takes into account the random possibilities with infection and recovery.

A Markov Chain works by defining a system in specific states. In the SIR model for disease propagation, these states would be *susceptible*, *infected* and *recovered*. For a person at a certain time, they will have a probability of being in any of the states, given their current state, in the next time period. This probability is known as the transition probability. Since each state will have a transition probability, we can create a transition matrix to show the probability of being in any one of the different states, given the current state.

$$T = \begin{array}{c|ccc} & S & I & R \\ \hline S & P_{SS} & P_{IS} & P_{RS} \\ I & P_{SI} & P_{II} & P_{RI} \\ R & P_{SR} & P_{IR} & P_{RR} \end{array} \tag{4}$$

In Equation 4. the P_{ij} values are the transition probabilities from state i to state j.

The states S, I and R are known as the state space while the vector of probabilities at time = 0 is the distribution of the Markov Chain system.

To calculate the probability that a system is in a state after n steps, we can use the following equation, where u is the starting distribution and T is the transition matrix:

$$u_n = uT^n \tag{5}$$

Since the assumption is that a person reaching the recovered state stays in the recovered state, the Markov Chain in the SIR model is absorbing. This is also true since every other state can reach the absorbing state, even if not in one step.

Additionally, a person in the susceptible state cannot transition into the recovered state, and a person in the infected state cannot transition into the susceptible state.

Therefore, our transition matrix for the SIR model will have the following characteristics:

$$T = \begin{array}{c|ccc} & S & I & R \\ S & P_{SS} & P_{IS} & 0 \\ I & 0 & P_{II} & P_{RI} \\ R & 0 & 0 & 1 \end{array} \tag{6}$$

Application in HIV Modelling

Ordinary Differential Equations

In Baryarama et al.'s paper (2006), the authors attempt to model the HIV epidemic using Ordinary Differential Equations. Here, the SIR model is adapted to an SIA model, where the third population type is now individuals who have acquired AIDS.

The system of equations used by Baryarama et al. can be seen in Equations 7., 8. and 9.:

$$\frac{dS}{dt} = \Lambda(t) - \eta(A)\frac{SI}{N} - \mu S \tag{7}$$

Here, $\Lambda(t)$ is the population size at time t which becomes susceptible by reaching a sexually active age. $\eta(A)$ is similar to the previously defined β as it relates to the infection rate, but this model allows the infection rate to change over time. Finally, μ is the constant for the amounts of natural deaths which occur.

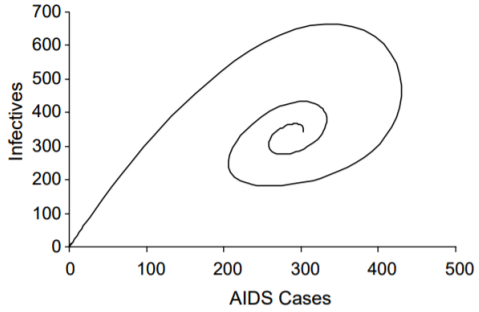
$$\frac{dI}{dt} = \eta(A)\frac{SI}{N} - (v + \mu)I \tag{8}$$

In Equation 8. v is the recovery rate, and therefore the population removed from the infected is based on both recovery rate and the natural deaths, μ, of the population.

$$\frac{dA}{dt} = vI - (\sigma + \mu)A \tag{9}$$

Finally, in Equation 9. $\sigma + \mu$ is the accelerated death rate due to AIDS.

These systems of equations led to the following example phase portrait showing the equilibrium of the infected population versus the AIDS cases.



Graph 3. Phase portrait for $\eta(A) = 0.433 - 0.001A$, $v = 0.125$ and $\mu = 0.02$ (Baryarama et al., 2006).

Markov Chains

In a paper by Lee et al., the HIV/AIDS epidemic is modelled using Markov Chains, for African Americans and Caucasians. In this model, the sample states consists of 4 different states:

- S: susceptible state
- I: HIV infected state
- A: AIDS infected state
- D: death from HIV/AIDS state

Using data collected over the course of 4 years (2006 - 2010), the following transition matrix was calculated for the model for African Americans:

$$T = \begin{array}{c|cccc} & S & I & A & D \\ \hline S & 0.99893 & 0.00066 & 0.00041 & 0 \\ I & 0 & 0.97033 & 0.00005 & 0.02962 \\ A & 0 & 0 & 0.95776 & 0.04224 \\ D & 0 & 0 & 0 & 0 \end{array} \tag{10}$$

Using the above transition matrix, Graph 4. was created to predict the HIV/AIDS infection and deaths.

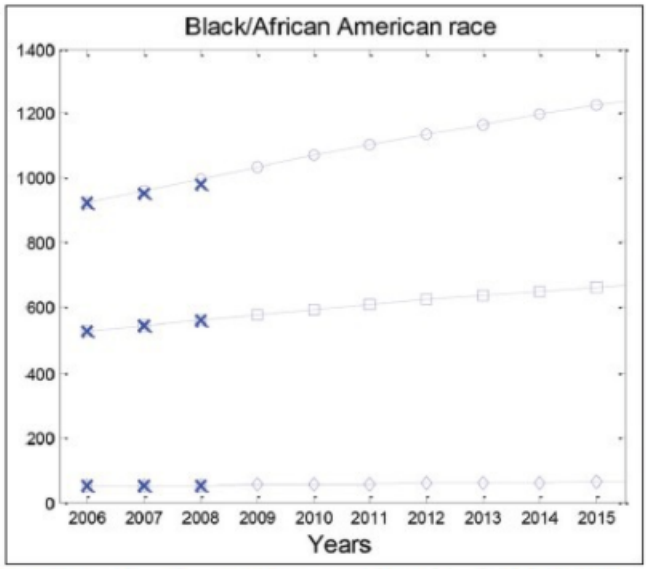
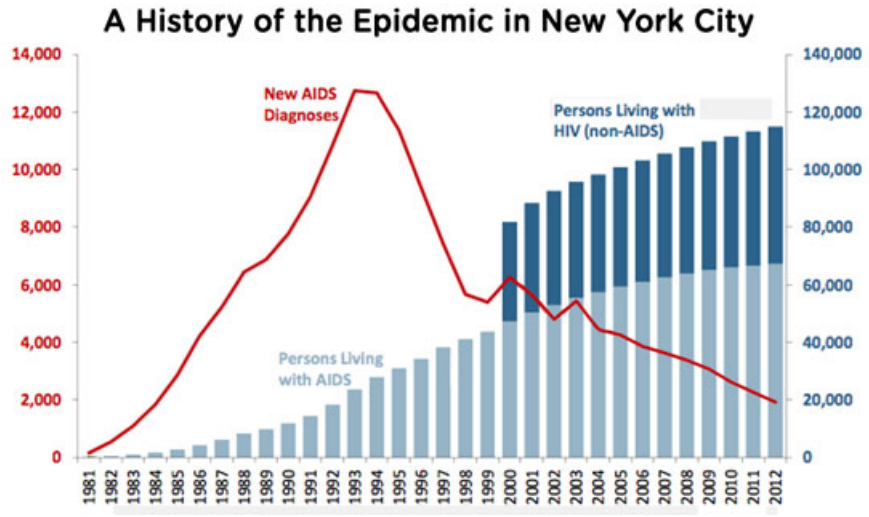


Fig. 2: Predicted number of living and deaths with AIDS diagnosis/ HIV infection for African Americans.
Monotonic increases in the rates of living with AIDS diagnosis and HIV infection are projected and our study is forecasting the rate of 662.2 of living with AIDS diagnosis and the rate of 1225.3 of HIV infection by the year of 2015. In contrast, deaths of persons with either AIDS diagnosis or HIV infection are forecasted to be quite stable and constant over the years. —◇— Living with HIV infection, —□— Living with AIDS diagnosis, —◇— Death with HIV or AIDS dianosis, × Reported numbers.

Graph 4. Markov Chain model predictions for HIV/AIDS infection and deaths for African Americans, made using MATLAB (Lee et al., 2014).

Optimisation: Finding the Peak in Real Data

We can use optimisation to find the peak of a disease during an epidemic. Graph 5. below shows the amount of AIDS diagnoses over time in New York City.



Graph 5. Line and bar chart showing the history of HIV/AIDS in New York City from 1981 to 2012 (Futterman & Jackson, 2015).

We could fit a curve to this data, and then use Newton's Method to find the peak. There is one global maxima and two local maxima in this curve which Newton's method could arrive at, depending on our starting point. Finding all three of these maximas, however, is still beneficial since we can analyse what occurred during these years which led to the peak, and the subsequent descent.

Analysis

The advantage of the stochastic model is that it is able to make predictions based on the individual probability of acquiring the disease, rather than on a whole population, which is less accurate. This is because in reality,

disease propagation is discrete, but for simplification of the model, ODE uses a continuous population. However, as seen in the example above, the ODE approach is able to add further variables that affect the system, such as rate of population becoming susceptible, natural deaths occurring, and an infection rate which changes over time. The stochastic model becomes very complex once all these factors are accounted for, and the probabilities would have to be calculated by analysing the data of the population over many years.

Appendix

```
import matplotlib.pyplot as plt
%matplotlib inline
%config InlineBackend.figure_format = 'svg'

N = 700
S = 500./N
I = 200./N
R = 0
beta = 1./11
gamma = 6.8/11
time_step = 0.01
final_time = 1000
time = range(1001)

## ds = -betaIS/N
## di = betaIS/N - gammaI
## dr = gammaI

ds = [S]
di = [I]
dr = [R]

for i in range(final_time):
    prev_s = S
    if I > 0:
```

```
        prev_i = I
    else:
        prev_i = 0
    prev_r = R
    S += time_step*(-beta*prev_i*prev_s)
    ds.append(S)
    if prev_i != 0:
        I += time_step*((beta*prev_i)- (gamma*prev_i
   ))
    else:
        I = 0
    di.append(I)
    R += time_step*(gamma*prev_i)
    dr.append(R)

plt.style.use('seaborn')
plt.figure(figsize=(10,5))
plt.title("Continuous ODE Plot of SIR Model on an
   Example Population")
plt.xlabel("Time")
plt.ylabel("Population")
plt.plot(time, ds, label = "susceptible", color = "
   gold")
plt.plot(time, di, label = "infected", color = "
   orange")
plt.plot(time, dr, label = "recovered", color = "red
   ")
```

```
48 plt.legend()
49 plt.show()
50 print "Final susceptible:", ds[-1]
51 print "Final infected:", di[-1]
52 print "Final recovered:", dr[-1]
```

Listing 1: Code used to generate Graph 2.

References

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