

# Comparing Treatment and Social Distancing Strategies in two Connected Cities, the case of 2009 Flu Pandemic in Mexico

Paula González<sup>\*†</sup>  
Edgar Díaz<sup>‡</sup>

July 25, 2009

## Abstract

A discrete time *SIR* model to study the dynamics of influenza in a multi-city setting is introduced. Data from three cities in Mexico that include the rate of movement of individuals from city to city is used to explore the impact of “travel” on A/H1N1 outbreaks. The model is expanded in order to evaluate the potential impact of treatment and social distancing.

## 1 Introduction

Different continuous time models have been used to study the spread of influenza. (refs) To study the 2009 flu pandemic (A/H1N1) we formulate a discrete time *SIR* model, the motivation on using this type of model is because the confirmed infected cases are reported daily. Also, there are more than 500,000 Mexicans traveling everyday between the capital, Mexico City and their nearby towns.

1. What can be done about flu pandemics
2. what was done about this particular one

---

<sup>\*</sup>University of Texas -EL Paso

<sup>†</sup>Universidad Autónoma de Occidente

<sup>‡</sup>Arizona State University

3. how we incorporate the three features in our model: Treatment Social Distancing and movement.
4. Central research question; main difference from previous work
5. mapping out how our sections will answer our questions

The total population at time  $t$  is divided into susceptible  $S_t$ , infected (infectious)  $I_t$  and recovered  $R_t$ . The time of getting infected follows an exponential distribution with rate  $\beta \frac{I_t}{N_t}$ . We ignore the demographic change in the populations but take into account the disease induced deaths.

Social distancing is the public health practice of encouraging people to keep their physical distance from each other during disease outbreaks in order to slow the spread of infection. In our model we investigate the effectivity of social distancing by assuming that the contact rate  $\beta(t)$  is a function of time, i.e  $\beta$  is smaller during the time that social distancing policy is applied.

One of our aims is to compare two control strategies, treatment to infected individuals and social distancing, we want to study their efficacy in reducing the final size of the pandemic. In order to study treatment, we expand the model and include a class of treated infected individuals  $T_t$  assuming that they recover faster than not treated individuals.

Finally, we want to study the spread of the disease by looking at the movement of people between cities. There are two vacational periods per year where the number of travelers increases, e.g. spring break and christmas. We introduce a multi-city model where every city has its own dynamics and the movement parameter  $m_{ij}(t)$  from city  $i$  to city  $j$  depends on time, it is bigger during the vacational periods.

## 2 SIR Model

To begin we study the dynamic in one single city. For each city we consider a discrete SIR model, i.e. the total population is divided into susceptible ( $S$ ), infectious ( $I$ ) and recovered ( $R$ ) individuals. For discrete time models we think that events occurring only at discrete times. In this model we assume that recovery occurs at the beginning of the stage, after that some infected individuals die and some susceptible individuals that have contact with infectious individuals become to be infectious. Let  $G_t = e^{-\beta \frac{I_t}{N_t}}$  be the fraction of susceptible individuals at time  $t$  that remain susceptible at time  $t + 1$ ,  $\sigma_1$  the fraction of infectious individuals that get recovered and  $\delta$  the fraction of infected individuals that die due to the disease. We do not consider

birth and natural mortality. The model is given by the system of difference equation.

$$\begin{aligned} S_{t+1} &= S_t G_t \\ I_{t+1} &= S_t(1 - G_t) + (1 - \sigma_1)(1 - \delta) I_t \\ R_{t+1} &= R_t + \sigma_1 I_t \end{aligned} \quad (1)$$

As in the continuous model we want to verify that as  $t \rightarrow \infty$  there are susceptibles individuals that never get the infection and that the infection eventually dies out, in other words we want to proof that

1.  $I_\infty = 0$
2.  $S_\infty > 0$

Let us notice that  $G_t \leq 1$ , then the sequence  $S_t$  is decreasing. Similarly if we add the equations for  $S$  and  $I$  from the model (1) we get

$$S_{t+1} + I_{t+1} = S_t + I_t(1 - \sigma_1)(1 - \delta),$$

where  $(1 - \sigma_1)(1 - \delta) \leq 1$ , therefore  $S_{t+1} + I_{t+1}$  is a decreasing sequence and has a limit  $S_\infty + I_\infty$  as  $t \rightarrow \infty$ . Now, if we take  $S_t \simeq N_t$  and  $I \simeq 0$  the equation for  $I$  from the model (1) has the following form

$$I_{t+1} = (1 - \sigma_1)(1 - \delta) I_t$$

or the equivalent expression  $I_{t+1} - I_t = -[1 - (1 - \sigma_1)(1 - \delta)]I_t$ , where it is clear that this sequence tends to zero and therefore  $I_\infty = 0$ .

## 2.1 Final Size

As we mentioned before the mortality due the epidemics  $\delta$  is consider to take into account the number of dead individuals. For the following calculations we consider  $\delta \simeq 0$ , in this case the population is almost constant and  $G_t = e^{-\beta \frac{I_t}{N}}$ . Let us observe first that

$$S_{t+1} = S_0 G_0 G_1 \cdots G_t,$$

now, taking logarithm in both sides and  $t \rightarrow \infty$ , the previous expression takes the following form

$$\ln \left( \frac{S_0}{S_\infty} \right) = \frac{\beta}{N} \sum_{i=0}^{\infty} I_i \quad (2)$$

By adding equation  $S$  and  $I$  in model (1) we obtain

$$S_{k+1} + I_{k+1} = S_k + (1 - \sigma_1)(1 - \delta) I_k$$

therefore

$$S_k - S_{k+1} = I_{k+1} - (1 - \sigma_1)(1 - \delta)I_k$$

and summing over  $k$  and taking  $t \rightarrow \infty$  we have

$$S_0 - S_\infty = (1 - (1 - \sigma_1)(1 - \delta)) \sum_{i=0}^{\infty} I_i - I_0$$

Then

$$N_0 - S_\infty = (1 - (1 - \sigma_1)(1 - \delta)) \sum_{i=0}^{\infty} I_i$$

From (2)  $\sum_{i=0}^{\infty} I_i = \frac{N}{\beta} \ln\left(\frac{S_0}{S_\infty}\right)$ , by replacing in the previous expression we obtain the final size relation

$$R_0 \left(1 - \frac{S_\infty}{N}\right) = \ln\left(\frac{S_0}{S_\infty}\right)$$

for

$$R_0 = \frac{\beta}{(1 - (1 - \sigma_1)(1 - \delta))} \quad (3)$$

Therefore the final reproductive number is given by (3).

### 3 Model with treatment

Now we assume that a fraction  $\tau$  of the infectious individuals get treatment at stage  $t + 1$ . Let  $p$  be the treatment effectivity and  $G_t = e^{-\beta \frac{I_t + pT_t}{N_t}}$  the fraction of susceptible individuals at time  $t$  that remain susceptible at time  $t + 1$ ,  $\sigma_2$  the fraction of treated individuals that get recovered. The model become to be

$$\begin{aligned} S_{t+1} &= S_t G_t \\ I_{t+1} &= S_t (1 - G_t) + (1 - \sigma_1)(1 - \tau)(1 - \delta) I_t \\ T_{t+1} &= (1 - \sigma_2) T_t + \tau(1 - \sigma_1) I_t \\ R_{t+1} &= R_t + \sigma_1 I_t + \sigma_2 T_t \end{aligned} \quad (4)$$

Similar to the previous model we have that  $I_\infty = 0$ . In order to obtain an expression for the final size; we assume that  $N$  is constant therefore  $G_t = e^{-\beta \frac{I_t + pT_t}{N}}$ . Besides

$$S_{t+1} = S_0 G_0 G_1 \cdots G_t,$$

and taking logarithm in both sides and  $t \rightarrow \infty$ , the previous expression takes the following form

$$\ln \left( \frac{S_0}{S_\infty} \right) = \frac{\beta}{N} \sum_{i=0}^{\infty} (I_i + pT_i) \quad (5)$$

therefore

$$\frac{N}{\beta} \ln \left( \frac{S_0}{S_\infty} \right) = \sum_{i=0}^{\infty} I_i + \sum_{i=0}^{\infty} pT_i \quad (6)$$

By the other hand adding equations for  $S_{t+1}$  and  $I_{t+1}$  in (4) we obtain

$$S_{k+1} + I_{k+1} = S_k + (1 - \sigma_1)(1 - \tau)(1 - \delta) I_k$$

therefore

$$S_k - S_{k+1} = I_{k+1} - (1 - \sigma_1)(1 - \tau)(1 - \delta) I_k$$

and summing over  $k$  and taking  $t \rightarrow \infty$  we have

$$S_0 - S_\infty = (1 - (1 - \sigma_1)(1 - \tau)(1 - \delta)) \sum_{i=0}^{\infty} I_i - I_0$$

Then

$$N_0 - S_\infty = (1 - (1 - \sigma_1)(1 - \tau)(1 - \delta)) \sum_{i=0}^{\infty} I_i \quad (7)$$

From equation for  $T_{t+1}$  in (4) we have

$$T_{t+1} - (1 - \sigma_2) T_t = \tau(1 - \sigma_1) I_t$$

and summing over  $k$  and taking  $t \rightarrow \infty$  we have

$$(1 - (1 - \sigma_2)) \sum_{i=0}^{\infty} T_i - T_0 = \tau(1 - \sigma_1) \sum_{i=0}^{\infty} I_i$$

Notice that  $T_0 = 0$ , then

$$\sum_{i=0}^{\infty} T_i = \frac{\tau(1 - \sigma_1)}{\sigma_2} \sum_{i=0}^{\infty} I_i$$

combining the previous equation with (6) we get

$$\frac{N}{\beta} \ln \left( \frac{S_0}{S_\infty} \right) = \sum_{i=0}^{\infty} I_i + \frac{\tau(1 - \sigma_1)p}{\sigma_2} \sum_{i=0}^{\infty} I_i = \left( 1 + \frac{p\tau(1 - \sigma_1)}{\sigma_2} \right) \sum_{i=0}^{\infty} I_i$$

therefore

$$\sum_{i=0}^{\infty} I_i = \frac{\sigma_2}{\sigma_2 + p\tau(1 - \sigma_1)} \frac{N}{\beta} \ln \left( \frac{S_0}{S_{\infty}} \right) \quad (8)$$

substituting (8) in (7)

$$N_0 - S_{\infty} = (1 - (1 - \sigma_1)(1 - \tau)(1 - \delta)) \left( \frac{\sigma_2}{\sigma_2 + p\tau(1 - \sigma_1)} \frac{N}{\beta} \ln \left( \frac{S_0}{S_{\infty}} \right) \right)$$

Therefore

$$\ln \left( \frac{S_0}{S_{\infty}} \right) = R_C \left( 1 - \frac{S_{\infty}}{N} \right)$$

for

$$R_C = \frac{\beta}{1 - (1 - \sigma_1)(1 - \tau)(1 - \delta)} \frac{\sigma_2 + p\tau(1 - \sigma_1)}{\sigma_2} \quad (9)$$

Notice that for  $\tau = 0$ , i.e. when we do not get treatment the expression (9) is equal to (3).

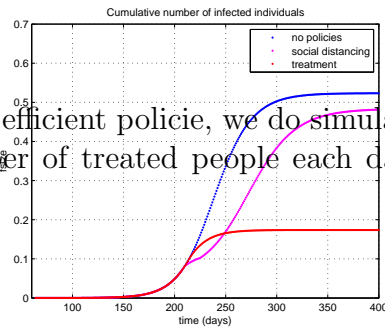
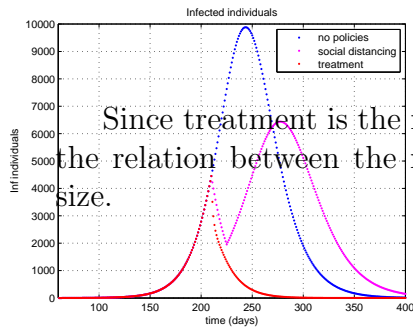
### 3.1 Control Policies

With the detection of the first outbreak of a new strain of influenza A virus subtype H1N1, Mexico city was shut down within a few days, many businesses were closed for a five-day break on a government order to slow the spread of the disease, there were no school classes for almost three weeks. In our model we investigate the effectivity of these policies by reducing the contact rate. In our simulations we study the different scenarios of when to apply these control policies, at the beginning or at the peak of the epidemic.

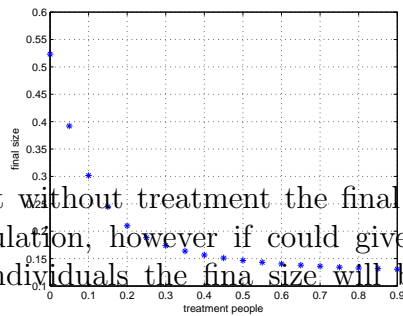
In order to study the impact of social distancing we reduce the contact rate during two weeks it looks like

we also assume that treatment is applied at the same time, i.e.  $\tau$  is given by

the figure shows how the number of infected individuals change when we apply these policies. Notice that treatment has a stronger impact in order to reduce the final size. Also we verify that policies have more impact when they are applied at the beginning of the epidemic.



Since treatment is the most efficient policie, we do simulations that show the relation between the number of treated people each day and the final size.



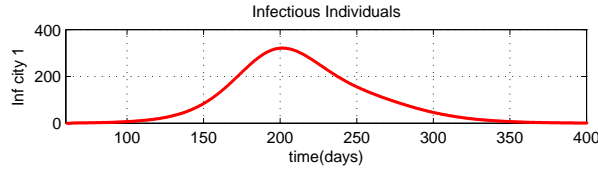
Notice that without treatment the final size will be more than 50% of the total population, however if could give treatment at least at 50% of the infected individuals the final size will be least than 15% of the total population.

## 4 Multi City Model

Now consider a nodal connection between cities and assume that every city has its own dynamic. Let  $S_t^i$ ,  $I_t^i$ ,  $T_t^i$  and  $R_t^i$  the number of susceptible, infectious, treated and recovered in the city  $i$  at stage  $t$ . Assume  $m_{ij}$  is the number of individuals that travel from city  $i$  to city  $j$  every day. The model is given by

$$\begin{aligned}
S_{t+1}^i &= S_t^i G_t^i \left( 1 - \sum_{i \neq j} \frac{m_{ij}}{N_i} \right) + \sum_{i \neq j} \frac{m_{ji}}{N_i} S_t^j G_t^j \\
I_{t+1}^i &= (S_t^i (1 - G_t^i) + (1 - \sigma_1) (1 - \tau) (1 - \delta) I_t^i) \left( 1 - \sum_{i \neq j} \frac{m_{ij}}{N_i} \right) \\
&\quad + \sum_{i \neq j} \frac{m_{ji}}{N_i} (S_t^j (1 - G_t^j) + (1 - \sigma_1) (1 - \tau) (1 - \delta) I_t^j) \\
T_{t+1}^i &= ((1 - \sigma_2) T_t^i + \tau (1 - \sigma_1) I_t^i) \left( 1 - \sum_{i \neq j} \frac{m_{ij}}{N_i} \right) + \sum_{i \neq j} \frac{m_{ji}}{N_i} ((1 - \sigma_2) T_t^j + \tau (1 - \sigma_1) I_t^j) \\
R_{t+1}^i &= (R_t^i + \sigma_1 I_t^i + \sigma_2 T_t^i) \left( 1 - \sum_{i \neq j} \frac{m_{ij}}{N_i} \right) + \sum_{i \neq j} \frac{m_{ji}}{N_i} ((1 - \sigma_2) T_t^j + \tau (1 - \sigma_1) I_t^j)
\end{aligned}$$

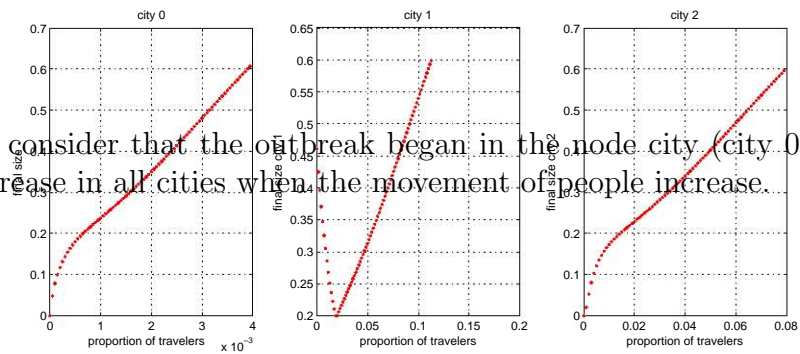
By the complexity of the model we do not have analytical results. We do simulations in order to study the impact of mobility in the spread of the disease. In the simulations let  $N_0^0 = 200000$  be the total population in the big city (node city),  $N_0^2 = 10000$  the population in city 2; assume all of them are susceptible and let  $S_0^1 = 7000$ ,  $I_0^1 = 1$  and  $R_0^1 = 0$  the initial conditions in city 1. and let  $m_{10} = m_{01} = 44$  and  $m_{20} = m_{02} = 50$  the number of travelers between city  $i$  and city  $j$  for  $i, j = 0, 1, 2$ .



In the previous figure we observed a natural delay when an infected individual is introduced in the small city. The disease “arrive” to the node city and after to city 2. We want to study how the mobility affect the final size in each city. Notice that if the disease began in city 1 (small one), a little movement of people make the final size decreasing in this city but when the movement is more than 2% the final size increase. In the node city and city 2 the final size increase when the movement of people increase.

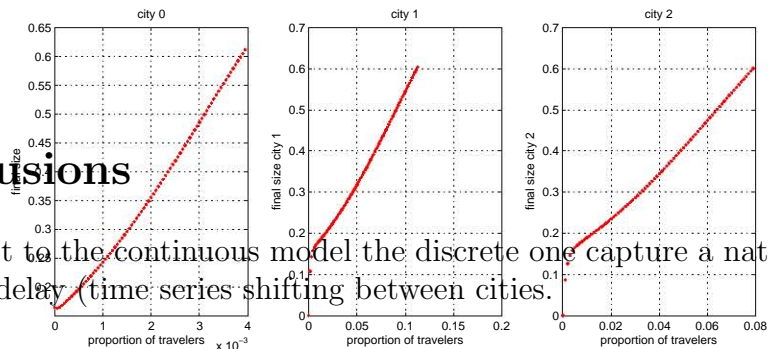


Finally if we consider that the outbreak began in the node city (city 0) the final size increase in all cities when the movement of people increase.



## 5 Conclusions

- In contrast to the continuous model the discrete one capture a natural epidemic delay (time series shifting between cities).
- The policies are more efficient if they are implemented at the beginning of the epidemic.
- Treatment has a stronger impact in reducing the final size.
- At least 60% of the infected individuals should get treatment every day.
- Movement of people make increase the final size of the epidemic in every single city.



## **6 References**

## **7 Acknowledgments**

This project has been partially supported by grants from the National Science Foundation (NSF - Grant DMPS-0838704), the National Security Agency (NSA-Grant H98230-09-1-0104), the Alfred P. Sloan Foundation and the office of the Provost of Arizona State University.