Modeling an Epidemic

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1 Why model an epidemic?

Imagine that we are entrusted with a role to play in our government's fight against Covid-19. We have been given the responsibility to decide when and where to implement lockdowns in our country to slow the spread of the virus. This is a pivotal job because an inability to do it effectively would mean the loss of countless human lives.

So, how do we begin? Where should we implement lockdowns? The places with the highest number of cases today? That is a logical place to start, but note that for diseases like Covid-19 with a latency period of a few days, the disease would already have spread to a lot of other people and places. It's just that we don't know it yet because they haven't started showing symptoms. So if we impose a lockdown on a current hotspot, say location A, a few days later connected locations B, C, and D might become hotspots, and even if we lock them down, others will keep popping up. As a result, if we were simply reacting to live events, we would always be one step behind the virus.

The only solution to this problem is to come up with a way to predict where the virus is going to cause maximum damage next. We only looked at a particular kind of intervention here (lockdowns), but an ability to predict the evolution of the virus will boost the efficacy of whichever strategy we're trying to implement. This is the purpose that is served by epidemic models. The same disease will not spread at the same rate throughout the world because of various geographical, social, and cultural factors, which makes it is a difficult task to create a model that will exactly emulate the real-time evolution of a virus like Covid-19. However, as we'll see in this report, approximate models can provide important information that can help a government to prepare for an epidemic and minimize the loss of life. Consequently, it would not be an exaggeration to say that epidemic models are the most powerful tools in our epidemic-fighting arsenal.

2 The meta-population model

2.1 Overview

The models that we will consider here are called meta-population models. Meta-population models consider the existence of small, discrete geographical units within which people may intermingle freely, with multiple such units connected by some mode of transportation. When modeling a pandemic that is spreading throughout the world, we take cities with airports as our discrete sub-populations, among which people may travel via flights. With the availability of the International Air Transport Association (IATA) database, which has information on 3100 airports and 17182 connections

between them representing more than 99% of worldwide commercial traffic by plane [1] (this data is of 2008 when the paper [1] was published), we can create models that can cover a large percentage of the earth's urban population. These models also rely on census data to get population and population density information for various parts of the globe.

With the general structure now established, we can now write down a high-level equation for the rate of change of I_i which represents the number of infected people in a city i [1].

$$\frac{\partial I_i}{\partial t} = K_i(t) + \Omega_i(t) \tag{1}$$

where the first term on the RHS of the equation represents the variation of infected individuals due to the *infection dynamics inside the city*, and the second term corresponds to the net balance of infectious individuals *traveling in and out of the city*. This last term, which we call the transport operator Ω_i, depends on the probability p_{ij} that an infected individual will go from city i to city j, and may be written as

$$\Omega_i = \sum_{j \in V(i)} (p_{ji} I_j - p_{ij} I_I) \tag{2}$$

representing the number of infected people coming into the city minus those going out to all connected cities, and acting as a coupling term among the evolution of the epidemics in the various urban areas.

The model obtained by integrating all these data and the etiology of the disease within each city can be used to forecast the behavior of emerging diseases as well as to validate the approach. It allows for probabilistic predictions on the likelihood of local and global outbreaks, as well as quantitative predictions of their magnitude [1].

2.2 Disease evolution in a closed population

We now look into the function $K_i(t)$ in equation 1 which models the evolution of the epidemic within a city or a closed population. Unlike the transport operator for which we directly wrote down the expression, deriving an expression for $K_i(t)$ involves a few more steps, which we shall progressively explore in the next few subsections.

2.2.1 Compartmentalized models

To mathematically model the spread of a disease within a population, we use what are called compartmentalized models. Here the population is divided into compartments such as susceptible (S), infected (I), permanently recovered (R), diseased (D), etc. These compartments are mutually exclusive (a person can belong to only one compartment) and exhaustive (every person must belong to one of these compartments). A person can jump from one compartment to another with probabilities that depend on various parameters specific to the disease under consideration, such as the reproduction number R (the average number of secondary infections caused by an infected individual), the latency period (the time taken for a person who contracted the infection to show symptoms), the fatality and recovery rates, and so on. Provided we know these parameters, we can write down the equations that govern how the number of people belonging to each compartment change with time.

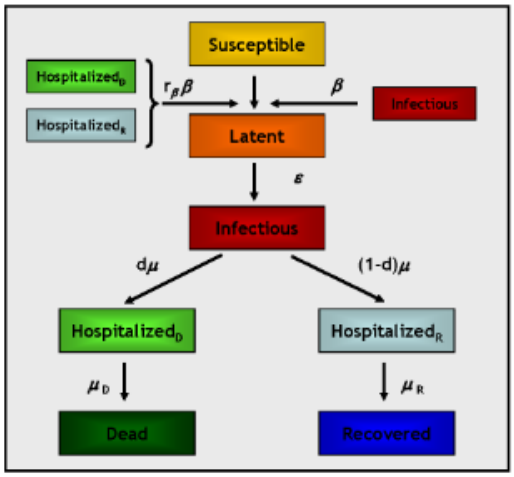

Figure 1: A possible compartmentalization of a population with various transition probabilities.

The notation we'll use is as follows. The total population of each city is N_j, and $X_j^{[m]}(t)$ is the number of individuals in the compartment $[m]$ in the city j at time t.

What are the various processes by which people change compartments? These transition processes are of two types. The first class of processes refers to the spontaneous transition of one individual from one compartment $[m]$ to another compartment $[h]$. In that case, the following equations hold.

$$X^{[m]} \to X^{[m]} - 1, X^{[h]} \to X^{[h]} + 1 \tag{3}$$

People recovering from the illness is an example of this kind of process. In this case the variation in the number of individuals $X^{[m]}$ is given by $\sum_h \nu_h^m a_h^m X^{[h]}$, where a_h^m is the transition rate from the class $[h]$ to the class $[m]$ and $\nu_h^m \in [-1, 0, 1]$ signifies whether people are added to or subtracted from $X^{[m]}$ due to this process [2].

The second class of processes refers to binary interaction among individuals such as when a susceptible person contracts the virus on interaction with an infectious one ($S + I = 2I$). In this case, the rate of variation of $X^{[m]}$ is given by $\sum_{h,g} \nu_{h,g}^m a_{h,g}^m X^{[h]} X^{[g]} N^{-1}$, where similar to the previous process, $a_{h,g}^m$ is the transition probability for the process and $\nu_{h,g}^m \in [-1, 0, 1]$. The factor N^{-1}, where N is the number of individuals, stems from the fact that the above expression considers what is known as the homogeneous approximation in which the probability for each individual of class $[h]$ to interact with an individual of class $[g]$ is simply proportional to the density $X^{[g]}/N$ of such individuals [2]. Combining both the processes, we can write the full deterministic equation as

$$\partial_t X_j^{[m]} = \sum_h \nu_h^m a_h^m X_j^{[h]} + \sum_{h,g} \nu_{h,g}^m a_{h,g}^m X_j^{[h]} X_j^{[g]} N^{-1} \tag{4}$$

2.2.2 Sources of stochasticity

In getting to the above equation, we made two major assumptions.

1. We know the transition rates exactly.
2. The transition rates are constants for the whole population.

For a real epidemic scenario, both of these assumptions are impractical, the second more so than the first. We can only calculate the transition rates from the data that we observe, and our knowledge of them evolves with the pandemic. Also, there are large variations in different people's calculations of these transition rates [3], and the best we can do is simply take the mean of various studies.

The more erroneous assumption is that the transition rates are constants for the whole population. As an illustrative example, let's consider the recovery rates of individuals. The strength of the immune system in people varies greatly with age, but it also is affected by other factors such as genetics and lifestyle choices. As a result, from a statistical point of view, the recovery rate of a particular individual in the population can only be described as random (within a given range), and this is not accounted for in the deterministic form of the equation we wrote earlier. In addition, decisions taken by the government or by the individuals themselves may also affect these values. For example, a person who chooses to go out less frequently during the

time of an epidemic will have a far less chance of contracting the virus than someone who chooses to do the opposite.

So we see that there are several factors that determine these transition rates, and it is only possible to incorporate them all at the expense of making the model exceptionally complicated. A far simpler alternative would be to simply treat this as a stochastic process, in which we acknowledge that these transition rates have characteristics of random variables. We can then incorporate this randomness into equation 4, which is what we'll do now.

2.2.3 The epidemic Langevin equation

To factor in the stochasticity inherent in the different processes, we rewrite equation 4 as a Langevin equation, by adding noise terms. Under the assumption of large populations, to each reaction term we associate a noise term with amplitude proportional to the square root of the reaction term [4]. The Langevin equation can then be written as [2]

$$\begin{aligned}\partial_t X_j^{[m]} = &\sum_h \nu_h^m a_h^m X_j^{[h]} + \sum_{h,g} \nu_{h,g}^m a_{h,g}^m X_j^{[h]} X_j^{[g]} N^{-1} \\ &+ \sum_h \nu_h^m \sqrt{a_h^m X_j^{[h]}} \cdot \eta_h + \sum_{h,g} \nu_{h,g}^m \sqrt{a_{h,g}^m X_j^{[h]} X_j^{[g]} N^{-1}} \cdot \eta_{h,g}\end{aligned} \tag{5}$$

where η_h and $\eta_{h,g}$ are statistically independent Gaussian noises.

The full equation that models the epidemic will include the transport operator (resolved in terms of the various compartments) added to the above equation. To get a feeling for the complexity involved in trying to solve this set of equations, note that the total number of equations in the model is equal to the number of urban areas (3100 in the IATA dataset) times the number of compartments needed to describe the infection dynamics. Analytically solving this set of equations would be a mammoth challenge, but computational advances have made numerical approaches feasible. Since this is a first-order equation, a simple Euler method would suffice to get a solution.

3 Predictability

3.1 Quantifying model predictability

Now that we have a model, all that is left to do is to come up with a method to find its reliability, or how well it predicts the evolution of an epidemic. To do this, first observe that in equation 5, we are free to set whatever value for the noise functions. As a consequence, it is not possible to put particular values for the noise functions and claim that the model would be $x\%$ accurate while the epidemic is still evolving.

What we do instead is create multiple realizations of the epidemic, and check the level of similarity between various pairs. A realization is an evolution of the epidemic from the same set of initial conditions but different noise values. The logic is that if a large number of realizations are fairly similar, then the model should have decent accuracy because we're tried out a lot of different possible values for noise.

We need to quantify and make concrete what we mean by similarity by giving it a mathematical structure. Consider the vector $\vec{\pi}(t)$ whose components are $\pi_j(t) = I_j(t)/\sum I_l$ which is the normalized probability that an infected individual is in city j. Let the similarity between two outbreak realizations A and B be quantitatively measured by the statistical similarity of the vectors $\vec{\pi}^A(t)$ and $\vec{\pi}^B(t)$. Such a measure of similarity $sim(\vec{\pi}^A(t), \vec{\pi}^B(t))$ is given by a function called the Hellinger affinity, which is given by [2]

$$sim(\vec{\pi}^A(t), \vec{\pi}^B(t)) = \sum_j \sqrt{\pi_j^A \pi_j^B} \tag{6}$$

Along with this, we need to consider the possible differences in the total percentage of infected people worldwide given by $i = \sum_j I_j/P$ where P is the total global population. This is done using the similarity function $sim(\vec{i}^A(t), (\vec{i}^B(t))$ where $\vec{i}(t) = (i, 1-i)$. So the total overlap function measuring the similarity between two different outbreak realizations is defined by [2]

$$\Theta(t) = sim(\vec{i}^A, \vec{i}^B) \cdot sim(\vec{\pi}^A, \vec{\pi}^B) \tag{7}$$

The overlap is maximal when the very same cities have the very same number of infectious individuals in both realizations, and $\Theta(t) = 0$ if the two realizations do not have any common infected cities at time t. A large overlap corresponds to a predictable evolution, providing a direct measure of the reliability of the epidemic forecast. An example of this sort of analysis is given in figure 3.1.

In figure 3.1, look at the WAN plot (worldwide air-transportation network). At time 0, the overlap function is 100%, because all realizations start from the same initial

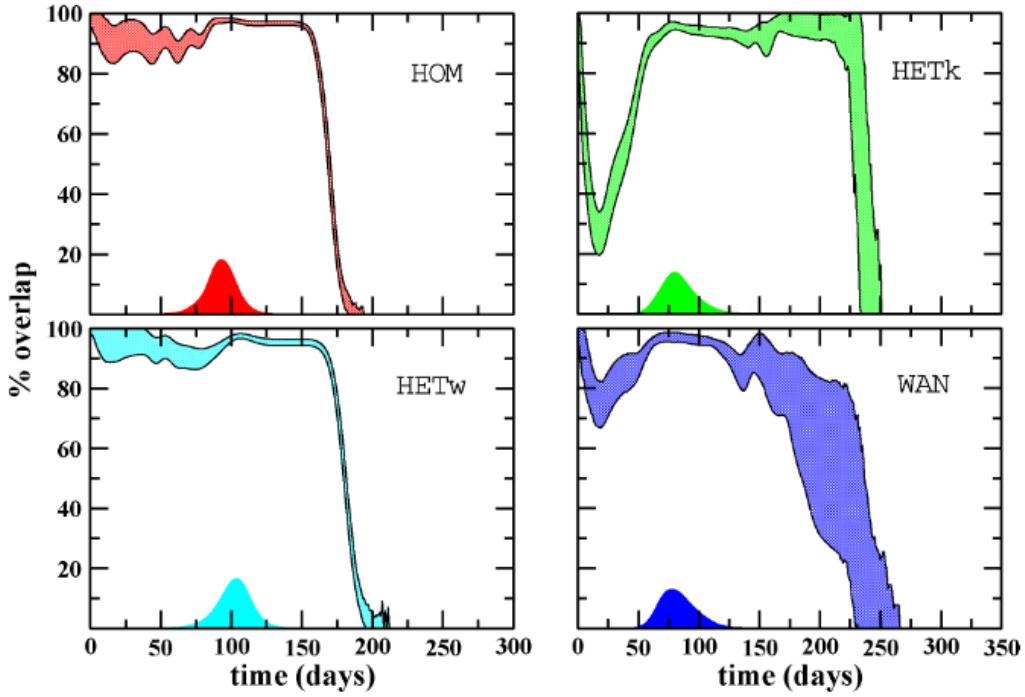

Figure 2: Overlap functions plotted for 5000 pairs of realizations of an epidemic [1]. The four plots are for four different air-trasportation datasets of which WAN (bottom-right) is the complete one. The shaded areas denote standard deviations. The small bumps at the bottom of each of the four graphs are prevalence profiles of the epidemic (with different units on the y-axis).

conditions. This is followed by a sharp dip, which shows that the early days of the epidemic are very prone to stochastic fluctuations. The overlap function subsequently rises to above 90% at around the same location as the peak of the prevalence function (the small bump on the x-axis). This means that when the epidemic is at its most widespread, the models have great predictability. This is the key takeaway here. Then the overlap function quickly dips to zero as the epidemic dies down.

Why are different realizations similar when they have very different noise values? This has got to do with the heterogeneity in the airline transportation network. For example, Dubai airport has a much larger number of daily flights and passengers than Bhubaneswar airport. As a result, the chances of Dubai having a much higher incidence of cases (relative to its population) compared to Bhubaneswar during a pandemic is significantly higher, whatever the value of noise. Models are very good at identifying places (and routes with a large number of daily travelers) like this that are especially vulnerable to large-scale infections, and that is what makes them very accurate, particularly during times when the epidemic/pandemic is at its height.

3.2 Verfiying the model against SARS outbreak

In reference [1], the authors applied this model to the SARS pandemic of 2002-03, and the model's predictive power was tested against available empirical data from the World Health Organization (WHO). It was found that the overlap function takes values larger than 0.7 for a large portion of the time window investigated, which points to relatively strong computational reproducibility. This implies that the simulated disease followed a very similar evolution at each realization of the process. The origin of such reproducibility was attributed to the emergence of epidemic pathways, ie, preferential channels along which the epidemic will more likely spread [1] (which we discussed in the previous section).

4 Conclusions and applications

From our previous analysis of the model, the following application is the most evident, and perhaps the most impactful. The epidemic pathways that a model can resolve identifies for each country the possible origins of infection and provides a quantitative estimation of the probability of receiving the infection from each identified origin. It is therefore of crucial importance for the development and assessment of preparation plans of single countries. Travel advisories or limitations and medical screenings at the ports of entry will strongly benefit from the analysis and identification of such epidemic pathways [1].

It is also worth noting here that the models have the greatest predictive power when the epidemic is at its worst, which may also be the time when we need the most help. This is the time when hospitalsrun out of ICU beds and ventilators, and doctors have to make choices of saving one person at the expense of another. Being able to foresee and avoid such situations is an incredible power indeed, and if used to its fullest potential, may save thousands of lives.

References

[1] Vittoria Colizza, Alain Barrat, Marc Barthélemy, and Alessandro Vespignani. Epidemic predictions and predictability in complex environments. In *Biophysical Reviews and Letters*, volume 3, pages 217–226, 2008.

[2] Vittoria Colizza, Alain Barrat, Marc Barthélemy, and Alessandro Vespignani. The modeling of global epidemics: Stochastic dynamics and predictability. *Bulletin of Mathematical Biology*, 68(8):1893–1921, 2006.

[3] Matthew Biggerstaff, Benjamin J. Cowling, Zulma M. Cucunubá, and et al. Early insights from statistical and mathematical modeling of key epidemiologic parameters of covid-19. *Emerging Infectious Diseases*, 26(11), November 2020.

[4] Daniel T. Gillespie. Chemical Langevin equation. *Journal of Chemical Physics*, 113(1):297–306, 2000.