

Review

Which approach to modeling? Predicting infectious disease dynamics in epidemics

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Received 28 August 2020 Accepted 11 November 2020

Disease outbreaks can be devastating to many nations. Interventions of all kinds are run alongside treatments or preventive measures. The effectiveness of the measures taken depends on the number of individuals who are susceptible, exposed, infectious or recovered. These in turn are a function of the nature of the disease: The mode of transmission, the risk of infection reproduction number and incubation period among others. Cases of epidemics are often difficult to contain owing to the fact that no one knows the dynamics of such diseases. In the absence of information the preparation and response to such disease is erratic and may entirely depend on predictions made. Epidemiologists and/or statisticians use the available data and parameterize the key indicators of a disease, do simulations so as to enable them make estimations. Wrong prediction or modeling may lead to huge variation in the predicted values and hence under-preparedness or over-preparedness. Both cases are costly. When properly done modeling can and has become extremely useful. This study reviews two approaches to modeling: The deterministic and the stochastic with merits and demerits of each discussed. The importance of modeling is also reviewed. It was found out that stochastic models are inevitably suitable when the population is small. For larger population the effect of randomness becomes negligible and hence deterministic approach which is relatively easier to model may be used. Stochastic model, as it was noticed, is also good in giving the range of the much desired numbers at every category of the disease.

Key words: Disease modeling, deterministic, stochastic, risk of infection, infectiousness, basic reproduction number.

INTRODUCTION

An organism is said to be infected when smaller organisms gain access into it. There are many invasive organisms in the environment with many being harmless

or even useful while others are just extremely lethal. The world is currently weighed down by an enormous burden of infectious diseases. Before the year 2020, many

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Table 1. A summary of this together with the common diseases caused.

Type of infection	Some examples of diseases/infections caused	Possibility of treatment
Viral	COVID-19, HIV /AIDS, Ebola, Rubella, Common colds, Measles, Polio Chicken pox, Norovirus, Herpes, Rabies, etc	As a preventive measure, vaccines (if already developed) can be administered. Mostly the treatment is that of relieving the patient from any symptoms so as to allow the immune system of the body to fight the infection. If the Immune system is overwhelmed it will be unfortunate
Bacterial	Syphilis, Gonorrhea, Tuberculosis (TB), Cholera, Tetanus, Bacterial Meningitis, Pneumonia, Whooping Cough, Bacterial Vaginosis etc.	The treatment is by use of the different antibiotics
Fungal	Ring worms, Athletes foot, Vaginal yeast, Histoplasmosis, etc	Usually treated with the respective antifungal medications.
Protozoa	Malaria	Antimalarial drugs .Use of bed nets etc

countries across the world did not anticipate major life-threatening cases. This was so because for about a century many nations had been in a position to contain or at least manage a number of diseases. This kind of management varies with the state of the economy of those affected countries. For instance according to WHO report of 1999 globally, 13.3 million deaths (an equivalent of 25% of all deaths), were as a result of infectious diseases. This statistics were besides respiratory, cancer and cardiovascular diseases (standing at 53% of all deaths) which may still be due to infections to a greater extent. In low-income countries (South East Asia and Africa) Infectious diseases caused up to 45% during the same period (World Health Organization, 1999).

In the past two decades the major infectious diseases that the world had been battling with included diarrhea, cholera, Malaria, Ebola , SARS, MERS, H1N1 and COVID-19 being the latest among others. It is important to note that many nations are often got unawares whenever outbreaks of such diseases occur. In fact in most cases the outbreaks are catastrophic and overwhelming when new strains of viral diseases such as those caused by corona virus are reported. There are various types of infections. These include but not limited to: Viral, bacterial, fungal , helminthes, protozoan among others. We give a summary of this together with the common diseases caused in Table 1.

Of these infections the most challenging ones are the viral type. They can be highly contagious and pose the greatest risk in containment of the transmission. The spread happens in what is normally called epidemiological triad, that is, the host, agent and the environment. The spread can be direct- if it happens through contact, touching, coughing or sneezing when another person is within the proximity of the carrier, kissing and sexual intercourse among others or indirect if someone touches

contaminated surfaces or objects. There are a number of environmental factors that influence the spread of communicable diseases that are prone to cause such epidemics; they include water supply sanitation, food and climatic conditions – thus waterborne and airborne diseases among others. Over 10% of all preventable ill-health today is due to poor environmental quality-conditions such as bad housing, overcrowding, indoor air pollution, poor sanitation and unsafe water (WHO, 1999).

LITERATURE REVIEW

Globally there are quite a number of diseases that have kept on emerging recently. These diseases have posed serious health challenges. Past experience shows that outbreak of these diseases could not only potentially cause large numbers of human deaths as they spread, but also have huge social and economic impact in today's interconnected world (World Health Organization, 2014). Among the emerging and/or Zoonotic viral diseases posing health security before 2019 included, Avian influenza, Chikungunya, Crimean-Congo haemorrhagic fever, Dengue, Ebola virus disease, Hantavirus, Hand, foot and mouth disease, Japanese encephalitis, Nipah virus, Novel human coronavirus, Rabies, Rift Valley fever, Viral hepatitis and West Nile Virus just to mention but a few (World Health Organization, 2005; Fauci et al., 2005). Some of the diseases such as avian influenza infection have been seen among wild birds such as bats, water fowl and poultry. Quite often, they are not expected to infect humans but contrary to this certain strains have been noted to cross the species barrier and infect humans. In most cases the immune system of humans may be low hence resulting in severe respiratory complication leading to fatalities. There were three such

pandemics in the twentieth century: in 1918, 1957, and 1968 all of which are associated with influenza of avian origin (World Health Organization, 2005).

The commonest emerging zoonotic bacterial diseases include: Anthrax, Botulism, Brucellosis, Leptospirosis, Listeriosis, Melioidosis, Plague, Salmonellosis, Scrub typhus, Tularaemia etc. Most of these diseases occur sporadically but when they occur they are deadly when left untreated. The modes of transmission in most epidemics have been known to be through contact which could be direct or indirect. This therefore informs on the measures that are supposed to be taken so as to control or prevent them. Obviously for those that are treatable then they can be treated but even though so, the problem is that usually the outbreaks are normally without warning and the spread is fast usually timed in weeks. This results in huge number of infections that end up outweighing the medical staff and facilities. The other problem is as a result of asymptomatic cases of the carriers. When the disease does not manifest itself within a short time from infection then it is possible for such a carrier to come in contact with so many other persons making the cases to rise exponentially. Among the measures that have been laid down by WHO to Control such diseases include: change of behaviour such as avoiding handshakes, use of vaccines, treatment- medication, modifying the environment improving drainage, for instance, infection control- use of Personal Protective Equipment (PPE), sanitization, sterilization, fumigation etc. (World Health Organization, 2007; Krämer et al., 2010; World Health Organization, 2018). Before 2019 probably among the most dreaded viral epidemic globally was perhaps Ebola Virus Disease (EVD) initially known as hemorrhagic fever caused by Ebola Virus. The Ebola virus causes an acute, serious illness which is often fatal if untreated. EVD first appeared in 1976 in 2 simultaneous outbreaks, one in what is now Nzara, South Sudan, and the other in Yambuku, DRC. The latter occurred in a village near the Ebola River, from which the disease takes its name (World Health Organization, 2020). The disease is known to be rare but its outbreaks have been characterized by fatalities that range from 25 to 90%. Another disease of viral origin is Severe Acute Respiratory Syndrome (SARS). SARS coronavirus normally abbreviated as (SARS-CoV) – virus was identified in 2003. SARS-CoV is thought to be an animal virus from an as-yet-uncertain animal reservoir, perhaps bats, that spread to other animals (civet cats) (CDC, 2017). It first infected humans in the Guangdong Province of southern China in 2002. Related to this disease is the Middle East Respiratory Syndrome (MERS). The first case was reported in 2012 in Saudi Arabia. Most people infected with MERS-CoV developed severe respiratory illness, including fever, cough, and shortness of breath (CDC, 2019). These are just a few examples; there are many other diseases that have emerged and have become a burden globally. All

these diseases have reported high fatalities as well as being highly contagious and with a unique speed of spreading fast.

Later in the year 2019, another new strain of corona virus was reported. The viral disease was first reported in Wuhan City in China. It has since then been referred to as Corona Virus Disease (COVID-19). Within only a period of six months (that is, May 2020) the COVID-19 pandemic had wreaked havoc across the world spreading in virtually all the countries of the world. By May, 16th 2020 it was reported that the disease had infected 4.7 million people worldwide resulting in over 300,000 deaths. On the positive side 1.7 million recoveries were reported at the same time. By this time, Kenya alone had confirmed 830 cases with 50 deaths and 301 recoveries. All these cases had hardly taken a period of three months since the first case was confirmed and in spite of the measures that the government had put in place (Government of Kenya, 2020).

The disease had challenged in equal measure both the developed and the not so developed nations ravaging its wrath not only on the poor communities or persons but also the rich. Frantic efforts have been put in place as a measure to prevent it since there is neither a known treatment nor a vaccine for the disease so far. Be that as it may real challenges brought by the measures which include curfews and even on the worst partial lockdowns, have been faced by many nations whose economies are at a near collapse. Many economies that had been closed temporarily have experienced untold negative impacts leading to laying off of some or all employees or complete overhaul of businesses and even shifting area of operation. Amidst these kinds of activities some countries are contemplating opening up their economies and even starting to offer services such as education that had earlier on been closed in an effort to contain the spread of the pandemic. This is happening even when there is no clear foresight as to when the disease would be fully controlled or at least within manageable levels. Yes the health workers are trying to put their best skills forward in terms of treating ailments brought by the disease as well as trying to put in place a direct acceptable treatment or a vaccine. Even with the best experience a medical staff can neither be relied on to predict when the pandemic can be brought to control nor to tell on the likely future trend of the disease so as to enable clear planning or preparation for any eventuality. Scientific research is still ongoing across the world. Whether or not full control or successful containment will ever be reached any time soon in the future remains a mystery. This is where the skills of a statistician and/or an epidemiologist with his/her knowledge in statistical modeling and epidemiology come in handy. These two are complementary.

Even with these specialists one would think things can move smoothly with accurate provision of the requisite

information on the infectious diseases but alas challenges never cease. A statistician will obviously require some sufficient data to enable him/her to model the trend as well as make reasonable estimates that can be relied on in planning. National Statistics- UK has outline key dimensions of quality as: relevance-which determines the coverage and content of the data, accuracy which is a function of the sampling approach, timeliness, accessibility and clarity of the analysis and the coherence (National Statistics, 2007). An epidemiologist similarly follows procedural steps on the other hand and will probably for example, require carrying out an observational cohort study from where they can monitor how the patients are responding to a given medication within certainly regulated environments. Just like in many investigations, Swiss Society for Public Health decided to propose what it termed as Essentials of Good Epidemiological Practice (EGEP) (Altpeter et al., 2005). Such procedures and policies lay down a firm foundation for determining the efficacy of the medication or measures taken to control or contain an epidemic. In both cases mitigation measures that have been put in place have to be considered as they are normally supposed to contribute towards making the situation better. A common challenge which is rare but has started emerging more frequently though of late is the fact that new disease simply has no data to with which these experts can work with. COVID-19 was discovered in December 2019 in Wuhan city of China a new disease caused by a new strain of corona virus (CDC, 2020; Alanagreh et al., 2020). So then what role does a statistician play and what are the available tools at his/her disposal? We look at these in the next section.

MODELING AND ITS CRUCIAL IMPORTANCE

Modeling enables researchers to draw many conclusions pertaining to epidemics. At the beginning of an epidemic growth rates can be determined to give an insight on how the disease is spreading or rather how new infections are occurring. With this knowledge it can help to develop quick interventions that can help to slow down or rid out infections. To evaluate such measures modeling will be necessary to indicate if the interventions are making any impact on the transmission (Emilia and Richard, 2010). It is also with the use of models that estimates of the number of those infected, recovering or dying can be obtained. These figures definitely will be of benefit to policy makers, government institutions and other interested organizations during planning and enforcement of interventions. In one of the Science articles, it is outlined that using models is advantageous in that the mathematical representation of biological processes enables transparency and accuracy regarding the epidemiological assumptions, thus enabling one to test

the understanding of the disease epidemiology by comparing model results and observed patterns (May, 2004).

Better models give better information and with such one obviously will draw better conclusions on the direction to take as a user. Epidemiological research entails investigating and determining the causes of a disease, describing the extent of a disease in terms of the kind of symptoms occurring and how frequently they occur, expressly outlining the natural history of a disease- the typical stages that a patient goes through, identifying the risk factors and protective factors (the factors that enhance or prevent the occurrence of a disease) and estimating disease burdens and health-care needs of a population. It also involves using statistical techniques to predict disease trends, in other words there is extrapolation of figures from observations made about time trends in risk factors and the future occurrence of the disease. Lastly but in no way least is the evaluation of the effectiveness of interventions and public health programs (Krämer et al., 2010). Clearly, for the precise predictions made within the model's virtual world to be relevant to reality, the model itself needs to correspond to or represent what is occurring in the real world -one cannot expect to obtain good predictions from false assumptions (Huppert and Katriel, 2013).

STATISTICAL MODELING AND EPIDEMIOLOGY

A model is as good as the assumptions made. The assumptions are a function of how far a modeler is able to imagine and visualize the variables at play whenever an epidemic occurs. There are quite a number of steps though that require to be put into consideration before setting up a model. Many researchers have given the details but in this paper we just highlight the main ones. Modeling starts with identification of the problem which is the infection or disease under consideration (Emilia and Richard, 2010). At this stage one would be interested in issues such as pre-infectious period, basic reproduction number, the time an individual remains infectious and whether or not all ages can be infected.

The next crucial stage is that of choosing a model. This is where natural history of infection is considered alongside the accuracy and time over which prediction is required. The simplest structural model is a case of S/I - (Susceptible \rightarrow Infectious) where once an individual is infected he/she remains both infected and infectious for life. Another model structure is the S/S - (Susceptible \rightarrow Infectious \rightarrow Susceptible) a case where an individual remains infectious after infection until he/she recovers following a treatment. This is usually used for curable sexually transmitted diseases such as syphilis. For the case where an individual acquires immunity after infection, the structural model is $SEIR$ - (Susceptible \rightarrow

Exposed (pre-Infectious) → Infectious → Recovered) or SIR- (Susceptible → Infectious → Recovered). Sometimes changes in immunity may still cause the last two cases to be susceptible hence the SEIRS and SIRS (Tibayrenc, 2007).

WHICH APPROACH TO MODELING: STOCHASTIC OR DETERMINISTIC?

There are two viewpoints to modeling- the deterministic approach and the stochastic approach. In the deterministic models, the input parameters like the rate of recovery or any other incidence, for example, are fixed so that prediction over time will be predetermined. On the other hand modeling can be done by allowing the number of individuals exiting or entering a given compartment to vary randomly. This is where the rate of recovery of infected or infectious individuals, for example, is thought of as happening randomly. This is a type of model referred to as stochastic model. Whereas deterministic model does not leave any room for uncertainty or randomness but it accounts for the mean trend of a process only, the stochastic model account for not only this mean trend but also for the variance structure around it (Tibayrenc, 2007). The stochasticity of the models is influenced by demographic and environmental events which are in most cases uncertain but are capable of being characterized by probability distributions instead of a constant value as it would be in the deterministic case. Because of the law of large numbers the two types of models are generally almost equally good for large populations while stochastic model is necessary for small populations since randomness cannot be neglected. This therefore takes us to the next section where we briefly look at how these models are set up.

DETERMINISTIC APPROACH TO MODELING

This is done by first stratifying the population into subgroups commonly referred to as compartments. These compartments refer to the different subgroups that are susceptible, pre-infectious, infectious immune or recovered and/or removed. In each of the category the transmission of infection is described in the model with key reference to the total number of individuals. Suppose we assume a closed population where we do not allow entry or exit of new individuals within the boundaries. This is a population which is constant with no births, immigration, emigration or deaths occurring. Then the difference equation for the number of susceptible group of individuals under SEIR model, for instance, shall be as follows:

$$S_{t+1} = S_t - \lambda_t S_t \tag{1}$$

Where, S_t = is the number of individuals susceptible in the population at time t . λ_t = is the risk of a susceptible individual becoming infected between time t and time $t + 1$ (it is also known as force of infection) such that $\lambda_t S_t$ = is the number of the newly infected individuals between time t and time $t + 1$; S_{t+1} = is the number of individuals susceptible at time $t + 1$; t = is the time which could be in days, months, etc.

The difference equation for the number of individuals of the pre-infectious (exposed) category under the same model is:

$$E_{t+1} = E_t + \lambda_t S_t - fE_t \tag{2}$$

Where, E_t = is the number of pre-infectious individuals at time t who are at the subgroup; E_{t+1} = is the number of pre-infectious individuals at time $t+1$ who are at the subgroup; f = is the risk of an individual at the pre-infectious category becoming infectious between time t and time $t+1$ such that fE_t = is the number of individuals who become infectious between time t and time $t+1$; $\lambda_t S_t$ = is as defined in Equation 1.

Similarly the number of infectious individuals at time $t + 1$ is given by:

$$I_{t+1} = I_t + fE_t - rI_t \tag{3}$$

Where, I_{t+1} = is the number of infectious individuals at time $t + 1$; I_t = is the number of infectious individuals at time t ; fE_t = is the number of individuals who become infectious between time t and time $t+1$; r = is the chance of an infectious individual recovering or getting immunized such that rI_t = is the number of infectious individuals who have ceased being infectious between time t and time $t+1$

Lastly we have the following equation for the number of recoveries at time $t + 1$:

$$R_{t+1} = R_t + rI_t \tag{4}$$

Where, R_{t+1} = is the number of individuals who have since become immune at time $t + 1$; R_t = is the number of immune or recovered individuals at time t ; rI_t = is as defined in Equation 3. Thus the summary of difference equations for the SEIR model is given by:

$$\begin{aligned}
S_{t+1} &= S_t - \lambda_t S_t \\
E_{t+1} &= E_t + \lambda_t S_t - fE_t \\
I_{t+1} &= I_t + fE_t - rI_t \\
R_{t+1} &= R_t + rI_t
\end{aligned} \tag{5}$$

The difference equations may be used to make predictions given the number of individuals in say susceptible category and if the values of λ_t , (the product of risk of susceptible individual being pre-infectious), f and r , then the rest of the number of individuals in each category can be derived. If however, these values are not given, then the model will require that it is first fitted on the reliable data. For some new epidemics such as COVID-19 getting reliable data can be a challenge, hence the attempt to work with easier ways. One way is by taking advantage of the constant of proportionality, β , - the proportion of risk to the number of infectious individuals. The relation is given by:

$$\lambda_t = \beta I_t \tag{6}$$

The parameter, β , gives the risk of infection relative to the number of the infectious individuals per unit time. It is actually the rate at which two individuals come into effective contact per unit time. The effective contact happens depending on a number of factors such as the method of transmission (for example, sexual, respiratory or vector-borne etc.), age, behavior change (social distancing and avoidance of handshakes among others), environmental set up (rural and urban set ups) and time (it affects the numbers of individuals e.g reduction of crowding may be due to improved facilities of accommodation).

In modeling identifying effective contacts can be a nightmare to trace except for the sexually transmitted infection probably and the vector transmission. The case of COVID-19 was particularly difficult because of infectious individuals who may be asymptomatic as well as getting infection even from contaminated surfaces. This has led to the use of the following estimation in Equation 7.

$$\beta = \frac{R_0}{ND} \tag{7}$$

Where, R_0 = is the basic reproduction number, that is, the average number of secondary infectious individuals in the susceptible population. N = is the total population

size; D = is the duration of infectiousness; The average contacts, C_e , per unit time (assuming all factors are kept constant) at the end of duration D , can be given by:

$$C_e = \frac{R_0}{D} \tag{8}$$

Equation 9 follows directly from Equation 7 and 8 on substitution. That is:

$$\beta = \frac{C_e}{N} \tag{9}$$

To avoid the problem of step time brought by use of difference equations in model (5) the applied mathematicians use the differential equations with time steps made so small so that any further reduction beyond such a time does not produce a difference in the resulting predictions. In other words convergence shall have been attained. In differential equations the rates of change of the number of individuals over time for each category are looked at- thus we have rate of change for the number of susceptible, pre-infectious (exposed), infectious and recovered (immunized), etc over time. This leads to the following summarized equations given in Equation 10 for transmission dynamics for an immunizing infection in a closed up population.

$$\left. \begin{aligned}
\frac{dS(t)}{dt} &= -\lambda(t)S(t) \\
\frac{dE(t)}{dt} &= \lambda(t)S(t) - fE(t) \\
\frac{dI(t)}{dt} &= fE(t) - rI(t) \\
\frac{dR(t)}{dt} &= rI(t)
\end{aligned} \right\} \tag{10}$$

A critical look at the equations given in Equation 10 shows that at every category the rate of change of the number of individuals can be obtained by adding those joining the category less those exiting per unit time. For instance the number of susceptible per unit time is less those who become pre-infectious per unit time, that is, $-\lambda(t)S(t)$. Equation 10 are limited to the simple case of how rates of individuals change with respect to time only. Other complex situations may have an interest of how changes may happen with respect to certain age groups, gender, vaccines and environment among others. A more realistic situation is also a model that incorporates births

and deaths as at every category of individuals in the population. There are packages already in place with vast literature on how to manipulate the difference as well as differential equations so as to make predictions. This was not the goal of this paper and the reader is at liberty to do some exploration on this. In the next section we explore the nature and how stochastic models can be set up.

STOCHASTIC APPROACH MODELING

These models allow contact between individuals to be determined by randomness. Perhaps the weakness with the above deterministic model can be seen when the size of the population susceptible is small. The model becomes unreliable (Tibayrenc, 2007). The predictions and interpretations of results from this model are unrealistic and meaningless for small populations. It can occur for this type of model that one susceptible individual may contact more than one infectious person when in reality infection would only occur with one infectious person. This may not be accounted for by the deterministic model (Emilia and Richard, 2010). It should be noted, however, that deterministic models are good when the population is sufficiently large as to effectively subdue the effect of chance and make it negligible.

Stochastic models incorporate effect of randomness (chance) on the possible outcome. They are of various types and include those that are individual-based, discrete-time compartmental and continuous time compartmental also referred to as time to next event models. For the first case a chance is allowed to determine whether or not an individual becomes infected, recover etc. at every time step. In the second case the whole category is treated as a single entity and allows chance to determine those transiting to the next category at a given span of time. In the third case chance allowed determines when the next event of infection or recovery, for example, will occur. The risk of infection for example, in the first method, would be obtained using the equation given by:

$$\lambda_t = 1 - (1 - p)^{I_t} \tag{11}$$

Where $p = \frac{R_0}{N}$ is the probability of effective contact between two specific individuals in a given place or community at a given time interval. I_t is the number of individuals who are infectious at time t ; $(1-p)$ is the probability of avoiding infection with all the infectious individuals

An individual becomes infectious if a random number in the draw representing that person is less than the risk of infection, λ_t at that time $t = 1$ for iteration 1. If greater the

individual remains susceptible. In the second iteration the individual who was infectious is assumed to have become immunized at time $t = 2$. The number of iterations depends on the random numbers drawn at every step. If all are now immunized and no number is less than, λ_t , implying the population has remained susceptible without further infection then iteration may be stopped. The second method follows a binomial distribution. If we have, S_t , susceptible individuals of which x_i are likely to get infected with a risk of λ_t , then its probability is given by:

$$P(X = x_i) = \binom{S_t}{x_i} \lambda_t^{x_i} (1 - \lambda_t)^{S_t - x_i} \tag{12}$$

Equation 12 can be used similarly to also compute probabilities for the individuals in the exposed, infectious or recovered categories. At a small time interval, $t + \delta t$, the number of individuals infected, for example, can be obtained as follows:

$$I_{t+\delta t} = I_t + x_i - x_r \tag{13}$$

Where: x_i is those joining the infectious category from the susceptible group at time $t + \delta t$; x_r is the number recovering at time $t + \delta t$; The third method makes the use of the so called hazard rate (H_t). This is given by:

$$H_t = \lambda_t I_t + r I_t \tag{14}$$

And for a number $0 < n < 1$ drawn at random, the time to the next transition occurrence is given by:

$$T = -\ln(n) / H_t \tag{15}$$

Thus the probability of an event occurring by time T is given by the following cumulative density function:

$$F = 1 - e^{-M_t T} \tag{16}$$

The probability, P_s , that one susceptible individual becomes infected and infectious in the next step time, in an **SIR** model for example, would be given by:

$$P_s = \lambda_t S(t) / H_t \tag{17}$$

These computations provide mechanism of determining the total number individual cases at every category in a given model of interest. Readers may wish to refer to

detailed illustration in Emilia and Richard (2010). Another very good reference worth reading is that of Tom and Etienne (2019). Accurate information on infectious diseases helps in making quick and appropriate decisions. When epidemics strike, whether known, emerging or re-emerging, many nations, states and even communities affected may be having all facilities and resources but may not know when and how to respond or take a given intervention with a view to counteracting the disease. Governments may not really know how to manage the public, let alone handling the sick in various treatment facilities. In the wake of novel viral diseases such as COVID-19 many nations across the globe were severely affected not only by the pandemic itself but also by even the measures they took. Many services and businesses were closed leading to economic recession and therefore loss of jobs to many. It is at this juncture where the knowledge of epidemiologists and high ranking statisticians is essential. The predictions made by these modeling experts will be important as it will show time when an outbreak would probably be at its peak, how many individuals will be at every category, the likely time the epidemic will take for it to be eliminated or contained and what interventions, personnel and resources would be required to mitigate the burden.

DISCUSSION

This study has shown that while deterministic models give on average the number of individuals at every category as fixed values, the stochastic models on the other hand incorporate the idea of randomness to give the range of the likely outcome. It was seen that the latter is probably inevitable especially for small populations that cannot escape the influence of chances. For large populations however, it became clear that deterministic models would be good because at such numbers the effect of chance is negligible. Modelers would require clearly figuring out the epidemic and incorporating all the possible scenarios. For instance this paper only looked at the cases of closed population. It would be different obviously, when births, deaths immigration and emigration are factored in. In general however once the model is in place simulation can be done to mimic the trends of the actual disease from where inference can be made.

The precision of the predictions are usually influenced by a number of factors which include but not limited to the availability of data, history of the disease and its transmission, the size of the population as well as the model and the parameters factored. It is also worth noting that some methods in modeling are computationally laborious. Hence this can determine the choice of modeling approach to be taken. The purpose of the information required is also a determinant.

CONFLICT OF INTERESTS

The author has not declared any conflict of interests.

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