

ANALYSIS OF SIR EPIDEMIOLOGICAL MODEL OF INFLUENZA: INSIGHTS INTO THE FUTURE OF H1N1

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ABSTRACT

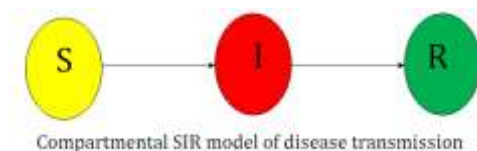
Review of the literature of influenza modeling studies and discussed how these models can provide insights into the future of the currently circulating novel strain of influenza A (H1N1), earlier known as swine flu. The fact how the feasibility of controlling an epidemic critically depends on the value of basic reproduction number, have been discussed. The R_0 for novel influenza A (H1N1) has recently been estimated to be between 1.4 and 1.6, which is below the values of R_0 estimated for the year 1918-19 pandemic strain (mean, range 1.4 to 2.8) and is comparable to values estimated for seasonal strain (mean, range 0.9 to 2.1). A recent modeling study has shown a global cooperative strategy is essential in order to control a pandemic. It is also been shown that by modeling cross-species transmission it may be possible to predict the emergency of pandemic strains of influenza.

INTRODUCTION

Mathematical models have been used to understand the spatial temporal transmission dynamics of influenza. These mathematical models have also been used as health policy tools to predict the effect of public health interventions on mitigating future epidemics or pandemics. A review of the literature of influenza modeling studied and discussed how results from these studies can provide insights into the future of the currently circulating strain of novel influenza A (H1N1). This strain was formerly known as swine flu [1].

BASIC EPIDEMIOLOGICAL MODEL FOR INFLUENZA

The first epidemiological model developed in the 20th century by Kermack and Mckendrick [2] can be used to describe an influenza epidemic. This model is known as susceptible-infected-recovered (SIR) model and is shown as a flow diagram in fig 1.



The population is partitioned into three classes: susceptible (S), Infected (I) and recovered (R). Individuals who become infected proceed from class S to class I at a rate which depends on the infectiousness of the virus and the prevalence of infection. Infectious individuals recover and move to class R at which point they are immune to the future infection. Each infected individual (I) transmits influenza with probability β to each susceptible individual S they encounter. The number of susceptible individuals decreases as the incidence increases. At a certain point the epidemic curve peaks and subsequently declines, because infected individuals recover and cease to transmit the virus. The severity of the epidemic and the initial rate of increase depend upon the value of the basic reproduction number R_0 . If $R_0 > 1$ an epidemic will occur and if $R_0 < 1$ the outbreak will die out. In SIR model the value of R_0 for influenza is equal to the transmissibility of the strain multiplied by the duration of the infectious period. Therefore once the value of R_0 has been obtained, the value of R_0 can be determined.

The simplest extension to the SIR model includes demographics: especially inflow and out flow of individuals into the population. Analysis of this demographic model shows that influenza epidemics can be expected to cycle with damped oscillations and reach a stable endemic level. By modifying the basic SIR model in various ways such as by including seasonality [3, 4], influenza epidemics can be shown to have sustained cycles. The SIR model has also been extended so that it can be used to represent or predict the spatial dynamics of an

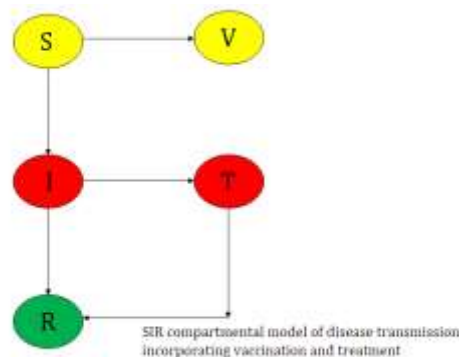
influenza epidemic. The first spatial-temporal model of influenza was developed in the late 1960's by Rvachev [5]. He connected a series of SIR models in order to construct a network model of linked epidemics.

PAST EPIDEMIOLOGICAL MODEL FOR INFLUENZA

Modeling studies have provided interesting insights into the severity of past influenza epidemics and pandemics [11-15]. Many modeling studies have investigated the three historical pandemics of the 20th century: Spanish flu 1918-1919 (H1N1), Asian flu 1957-1958 (H2N2) and Hong Kong flu 1968 (H3N2) [7,12,17]. Modeling has also been applied to assess the effect that interventions may have had in mitigating the 1918-1919 pandemic [12,17].

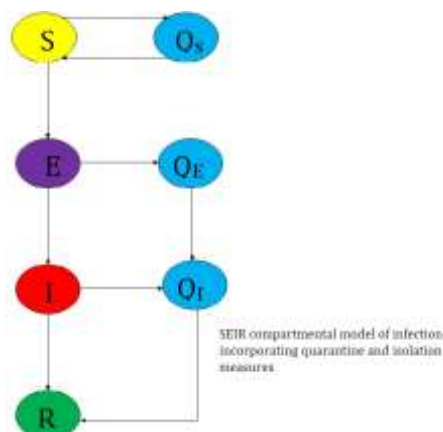
DESIGNING BIOMEDICAL PUBLIC HEALTH INTERVENTIONS

Biomedical interventions have been modeled using relatively simple extension of the SIR model or by implementing the SIR model within a framework of a detailed simulation model [10].



Susceptible individuals (S) who are vaccinated proceed to class V, at which point they are considered immune. Upon treatment, infectious individuals (I) proceed to class T, at which point their infectiousness is reduced. Once interventions have been included in the model the reproduction control number R_C can be determined. R_C is defined as the average number of new infections that case generates in an entirely susceptible population when an intervention is in place, during the time they are infectious. The value of R_C will depend on both the strength of the intervention and the severity of the epidemic in the absence of the intervention R_0 . R_C will always be less than R_0 , but if $R_C < 1$ the intervention will cause the epidemic to die out, whereas if $R_C > 1$ the intervention will only reduce the severity of the epidemic.

The effect of behavioral interventions such as closing schools, quarantining infected individuals or imposing travel restrictions have been modeled [17,18, 20-23]. It has been shown that behavioral interventions that increase social distancing, such as prolonged school closures could reduce the cumulative number of influenza cases by 13% to 17% [20].





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Studies have been useful for comparing interventions. For example, Ferguson et al. have determined that household quarantine could be more effective than closing schools [18]. The potential effectiveness of biomedical interventions have been modeled [19,24,25].

FEASIBILITY OF BIOMEDICAL AND BEHAVIORAL PUBLIC HEALTH INTERVENTIONS

Although many studies have identified potentially effective public health interventions they have not assessed their feasibility. For example studies evaluating mass vaccinations strategies have found a very high coverage is needed to prevent epidemics. However in the real world where vaccination is voluntary, high vaccination coverage is rarely achieved.

The feasibility of controlling an epidemic will critically depend on the value of R_0 . The results from all the modeling studies are in agreement, very high vaccination and treatment levels will be necessary to contain even a moderately severe pandemic. It will be difficult, but perhaps possible to achieve these goals for interventions in resource-rich countries. However clearly resource-constrained and resource-poor countries will be unable to achieve these goals unless they are given very large supplies of vaccines and antiviral by resource-rich countries.

MODELING INFLUENZA A (H1N1): EMERGENCE AND CONTROL

Influenza is a zoonotic disease that can infect a variety of host species. Strains can be transmitted between species and new strains can emerge through co-infection and genetic recombination in intermediate hosts. Wild ducks and wading birds are considered to be a reservoir for influenza because they can carry all subtypes and the virus is virulent to its avian hosts. Avian viruses are also found in other birds such as domestic ducks and poultry. New strains of avian influenza have recently emerged in South East Asia and have infected humans. These strains are not transmissible from human to human; however they are highly virulent in humans and have killed approximately 70% of infected individuals. The first modeling paper on influenza A (H1N1) has recently been published [19], by fitting an SIR model; to initial outbreak data from La Gloria in Mexico Fraser et al., estimated R_0 for this value in the lower end of previous values for the 1918-1919 strain (R_0 mean ≈ 2 : range 1.4 to 2.8) [18] and is comparable to R_0 values estimated for seasonal strains of influenza (R_0 mean ≈ 1.3 : range 0.9 to 2.1) [11].

So far there are only two published studies that have modeled interventions for influenza strains that arise due to cross-species transmission. Iwami et al. modeled epidemics that result as a consequence of cross-species transmission [26]. Their results show the potential effectiveness of quarantine as a control strategy and also the importance of simultaneously controlling influenza in the avian population [26].

CONCLUSION

As it is discussed in this review, mathematical models have been extremely useful in increasing our understanding of the spatial-temporal transmission dynamics of influenza. These mathematical models provided assistance in evaluating the potential effectiveness pandemics of varying severity, where the severity has been defined by the value of R_0 . It is also has stressed that although many theoretical interventions have been identified they may not be feasible. Furthermore pandemic control will only be attainable with a global cooperative strategy. This review has also shown that the current models may not be useful in identifying effective interventions for epidemics generated by strains such as influenza A (H1N1), that emerge due to recombination of species-specific strains and subsequent cross-species transmission. Therefore it is recommended that more biologically complex models need to be developed. Analysis of such models could assist in identifying interventions that would be effective in reducing the probability of cross-species transmission and in mitigating pandemics driven by multi-species transmission.

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