Predicting and Controlling Influenza Outbreaks

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ABSTRACT

The purpose of this paper is to present usable methods, and the efficacy of prevention systems, for influenza-type viruses. The most important variables regarding the prediction and control of viruses can be listed as the location(s) of an outbreak, the Type of outbreak, the Contagion rate of the virus, and the existence of existing protocols (if any) at the site of outbreak. The interactions between humans and the source of these viruses play a key role in where they emerge and how they spread as well as the level of precautions required to prevent widespread damage. These interactions can include contact with hosts, lack of prior medical treatment and economic and/or political status of the location. This type of virus has been known to originate in countries in South East Asia, China, and India. Within the countries mentioned, there are regions with low recorded vaccination rates and a lack of adequate awareness regarding local viruses.

Keywords: SARS, RNA, CoV, PSA SA

Subject: Medicine

INTRODUCTION

SARS-CoV-2 (better known as the Coronavirus) is an RNA virus and has been the major focus of attention for the past 3 years. It first emerged in 2019 in Wuhan, China. The SARS CoV-2 was a highly contagious and widespread disease that shared symptoms with diseases like the common cold and was frequently undiagnosed or misdiagnosed. This often led to an increase in serious symptoms and related deaths. The infection prevention methods disrupted supply lines and were inefficient in containing the spread of the virus. There are a variety of factors affecting the ability to predict outbreaks, in categories such as economic, behavioural, political and medical. There are models and observations for each category, and their respective efficacy is discussed below.

MATERIALS & METHODS

Justification
The method chosen was based on qualitative, with Fraser et al (2009) being the major source of this research paper, and using other papers such as Desai et al (2020)for accurate comparisons. The justification for these sources was 1. Factual data points with legitimate sources, 2. Relevancy; even if a topic does not directly relate to coronavirus, it has to relate to the concept of epidemics/pandemics and prevention methods and 3. Detail and diagrams. To be able to use the source for this paper, it is required to have sufficient detail on the topic, and include diagrams (especially in papers using models as an example).

The method used to collect information - Research online articles from Google scholar using the search terms "predicting pandemics"," effect of prior outbreaks", and" WHO Policies on pandemics". The majority of articles regarding coronavirus from 2015 and above were consulted to ensure accuracy and relevance to the current period (2022 and further).

Material for noting down sources and writing papers
Justification for choosing methods
Method - Secondary
Sources - Websites (PubMed, BMC medicine, EB medicine)
Research information - Research papers regarding coronavirus, H1N1, and Influenza strains.

The mode of secondary method is efficient as it allows for a professional mode of data collection, with backup from research, and basis in factual data throughout time periods, as to predict the future, examples in the past (with accurate descriptions) are needed.

DISCUSSION

Social and behavioural connections to viruses in the past

According to Fraser et al (2009) and Ferguson et al (2006), the biggest sources and causes of infection were trade, travel and immigration. This resulted in a worldwide lockdown on international travel and a near shutdown of most public transport. The methods implemented were border control, and quarantine of infected individuals. However, this proved more logistically challenging than predicted, especially with a lack of spaces in medical institutions like hospitals and clinics. The causes of pandemics have been the same for millennia - with the plagues travelling through trade routes in the Roman Empire, with over 100 million deaths as a result, as evaluated by Fraser et al (2009). Basic protocols such as armed guards along the routes, make sure none of the travellers contained the disease. This also proved inefficient as soon as the symptoms were delayed or not visible through basic scrutiny.

Even in the modern era, in most countries, testing and quarantining are conducted by humans, which is often inefficient.

Existing pandemic prevention methods

One way to map out and predict the rate and location of the disease is the *human mobility patterns*, which is data on where people travel from different locations, the dates and times of peak travel, and the number of people travelling such as the change in influenza rates in Canada in 1919 as recorded in Fraser et al (2009). These patterns are essential because they make systematic lockdowns, and screening far more efficient, and effective as sourced by Desai et al (2020). In the 1918-1919 influenza epidemic in the US, data was collected on mortality rates and location of maximum infections demonstrated with statistics in Ferguson et al (2006). Localised social distancing and quarantining measures reduced the mortality rate by 10-30% proven by Fraser et al (2009).

The interventions for reducing mortality and spread can be divided into 2 categories - (i) biological and (ii) behavioural prevention methods. The proven biologically based prevention methods for influenza and corona viruses are vaccines, practiced hygiene and recording of possible conditions that may make a person more susceptible to infection as categorized within Desai et al (2020). Behavioural methods include social distancing, quarantining which has been proven to reduce mortality rates by up to 30% during the 1919 Spanish flu, and the Hong Kong flu as record in Fraser et al (2009). Additionally, a recommended effective intervention method in containing the infections and spread of diseases is to shut down dense locations, such as malls, schools and pools considered as a standard measure by the WHO, for viruses with a similar R_0 value of coronavirus (1.4-2.8).

The function, purpose, application and variety of methods is already known, and their efficacy in a simulated environment. However, the situation in the real world has proven to be much different. Most countries in East Asia, where coronavirusis prevalent, have a high number of rural areas where pandemics originate and spread. This is supported by observations in Longini et al (1985) More recently, a paper by Giliberto Capano and Michael Howlett (2020) shows a similar pattern within rural and lesser developed areas. Epidemics with a high contagion rate require more extreme protocols and interventions, which become increasingly difficult as the pandemic progresses. It was identified in Longini et al (1985) that vaccination of 80% of children (under 19) is as effective as vaccinating 80% of the population. However,as researched in Longini et al(1985) to effectively prevent an epidemic, 80% of infected individuals have to be identified within 8 weeks for the administered antivirals to take enough effect to prevent an epidemic, the study also recommends higher priority in vaccination for demographics under 19 years old.

A published report by Ferguson et al (2006) stated that. that to contain an epidemic with an R_o of 1.6, (moderate) it would be required to use extreme social distancing protocols, and over 3 million doses of antivirals, in a location such as South East Asia.

The logistics of certain types of epidemic preventions pose a greater challenge in large countries, in the third world, or in locations with high population densities, with a proven and clear difference shown in the study 'Lessons from New Zealand's Covid19 success'(2020) by Parker which gives a direct comparison between the large and highly populated United States, and the lower populated, greater controlled New Zealand. Policies such as vaccination, monitoring and vigilance regarding an epidemic is highly dependent on these factors.

Political relations are also essential for preventing a pandemic. Countries with high stores of resources are expected to provide for the countries with high populations and high poverty, as cited in Capano et al (2020). Countries with better government control virtually eliminated the spread of the Coronavirus; it was recorded in Parker et al (2020) that New Zealand was able to successfully implement high efficacy measures, such as curbing travel and increasing vaccines and behavioural prevention methods. Each country has ranging amounts of government control, with higher developed countries advised to assist in the operations of lesser developed, such as the involvement of New Zealand, to work with the WHO and governments such as the United States, and Australia to create more effective prevention methods, they can be applied at both a national and local scale as found within Wilson et al (2020).

Global cooperation is required to achieve this feat at a much higher level than what was observed in the Coronavirus pandemic and past pandemics around the world, as identified in Fraser et al(2009) via modelling studies in China, the United States, and data collected from the European Union.

Models that can be used to predict pandemics

The models used to predict pandemics, epidemics and endemics are based on the use of medical interventions, or behavioural interventions classified in the Fraser et al (2009). One type of model used to predict outbreaks and disease spread is statistical models which operate on the current deaths and infections, per day, and scale based on government data such as the SIR model (Susceptible-Infected-Recovered) developed by Kermac and McKendrick in 1927, cited in Fraser et al (2009). This type of model is continually used to this day to be able to identify regions and capacity of infections.

Due to this, certain fixed models fail to account for 3rd party sources (foreign travel, delayed symptoms), and the interventions used, which are based on the statistical models (quarantine, vaccination doses). These assumptions that all interventions act the same in all locations, result in second and third waves recorded in Jewell et al (2020).

Understanding the properties of influenza are essential to creating efficient intervention. For example, the fact that they can be present in a variety of host species such as swine, avian or other subspecies, with an example in *Figure 1* mapped in Fraser et al (2009). Certain species such as wild ducks are known to carry nearly all subtypes of influenza as observed by Fraser et al (2009). A newly identified strain of influenza has emerged in Southeast Asia, identified by the WHO as 'Avian Influenza type A'and while it is not transmissible from human to human, it has been recorded to have a lethality rate of 70% among susceptible individuals within UN records.

The current models can predict the cross strains between swine, avian and human influenza types, which has been recorded via applying an SIR model, recorded by Fraser et al (2009). There is also the observation of a 'super strain' as quoted by Fraser et al (2009), which is created by a pig being used as a sort of 'mixing vessel' where different strains co infect the same creature, which then infect humans, causing epidemics such as H1N1, or swine flu.The effects and data are represented in Figure 1.

By observing the interaction between humans and pigs, it could be used to predict the emergence of outbreaks of the 'super strain' in countries within which it commonly happens, such as China, India, or other South-East Asian nations. The observations recorded in experiments with H1N1 type strains, by Cobrun Fraser in Fraser et al (2009) show that strains with an infectivity value between 2.3 - 3.8 have the highest infection rates, and greatest potential for an outbreak, due to high transmissibility modes, through multiple species and vessels. According to a paper by Coburn Fraser et al (2009), the infection depends on the degree of interaction between humans and the vessel of contagion. These are currently the most up-to-date models on cross species transmission.

CONCLUSIONS

There are advanced models and proof methods that have the potential to prevent large-scale epidemics and influenza outbreaks. These are well studied to ascertain that the sources of these epidemics and efficient prevention methods are known. While it is not possible to have a 100% accurate prediction for outbreaks, it is possible to observe the way humans interact with the known sources of outbreaks, such as mosquitos, pigs and other animals. With the information on these interactions, it's possible to identify locations and the emergence of outbreaks and place containment measures which can predict and control outbreaks before they become an epidemic.

Images & Graphs
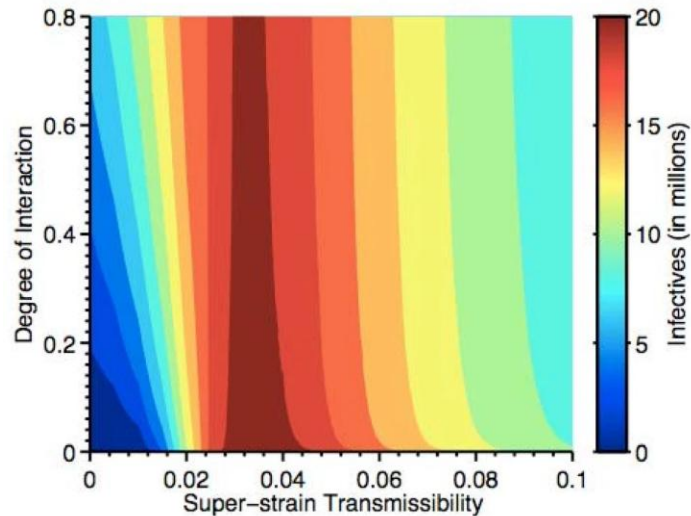
Figure 1: Transmissibility of a super strain, categorized by infectives, and the degree of interaction with the strain. Source: Fraser et al. (2009)

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