Modelling for the Identification of Mechanisms Driving Cholera Outbreaks in Endemic Regions

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EXTENDED ABSTRACT

Introduction

Cholera is an infectious diarrheal disease that continues to affect 47 countries across the globe today. Every year around 2-3 million people develop the disease, of which around 100,000 die [1]. Cholera deaths generally occur due to severe dehydration, meaning that the largest portion of victims are children under the age of five. The disease is transmitted via the faecal-oral route and therefore outbreaks are strongly linked to water, sanitation and hygiene (WASH) facilities. However, despite consistent improvement in such facilities worldwide, there has been no significant corresponding reduction in cholera incidence [2]. This is due to other factors such as increased population density, increased travel, and climate change counteracting the positive infrastructure improvements made by governments and NGOs.

Many current approaches to cholera modelling focus on forecasting outbreaks. This is generally achieved by applying statistical methods to long-range weather forecasts to produce relative probabilities of cholera outbreaks occurring in a particular region at a particular time [3][4]. This has the benefit of providing public health officials with an early warning of around three to four weeks, allowing them to direct limited resources such as vaccines and treatments where they are needed the most. However, many issues are associated with this type of approach to modelling. Firstly, huge uncertainties in the output results are inevitable due to the intrinsic uncertainties embedded within weather forecast inputs and little consideration to non-weather factors. This can lead to errors in the deployment of valuable resources, and consequently distrust in the models and scientific community. Secondly, the modelling approach often targets short-term solutions suitable for epidemic situations, such as those that have arisen recently in Haiti and Yemen, where the main goal is generally to limit the damage caused by the epidemic until it eventually dies out. However, in endemic regions such as Bangladesh where cholera has remained a problem for decades, short-term modelling is not appropriate. A long-term approach to cholera prevention in endemic regions requires a comprehensive understanding of the mechanisms which drive cholera and the complex way in which they interact. The traditional statistically-based model is only capable of concluding correlations between variables, and not their causative relationships. In other words, it is essentially addressing the symptoms of the cholera problem, rather than the cause.

This study aims to develop a long-term strategy for strengthening the resilience of a society against future outbreaks in endemic regions via tackling two key challenges. First, a holistic understanding of the mechanisms driving cholera spread will be delivered. This is currently little understood due to limited data sources in developing regions where cholera is endemic, and the complex non-linear interplay between factors. Second, insight into the most significant factors affecting cholera incidence in the future. With a changing community and climate, the biggest risk factors today will not necessarily be the same in 20-30 years' time. Resilient strategies and infrastructure to mitigate such health threats require a comprehensive understanding of both present and future scenarios for long-term adaptation planning and implementation.

Methods and Materials

To address the above-mentioned challenges, we will establish a mathematical model using data analytic and machine learning methodology, and apply the model to Bangladesh as a case study. We adopt the framework of a Susceptible-Infected-Recovered (SIR) model [5] to categorise the human population into three compartments, and include an additional 'Bacterial Concentration' compartment. These four compartments are shown in Figure 1, and briefly described as below:

1.   *Susceptible – Individuals assumed to have no immunity to cholera and are at risk of developing the disease*

2.   *Infected – Individuals with symptomatic cholera, who are capable of spreading the disease*

3.   *Recovered – Individuals considered immune to cholera due to previous infection of vaccination*

4.   *Bacterial Concentration – Concentration of cholera bacteria in the local aquatic environment*
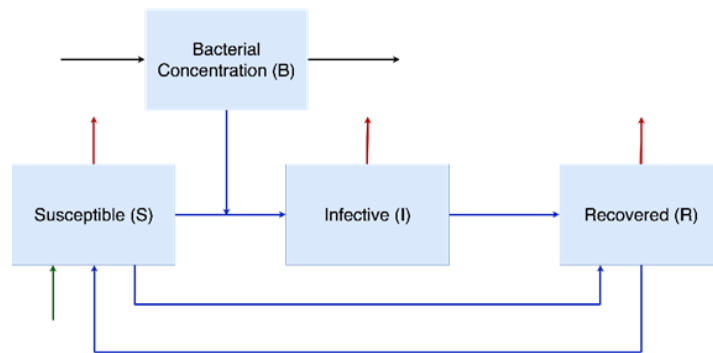
Figure 1. Flow diagram of the proposed model. Green arrows represent individuals entering the system (through birth/migration); red arrows represent individuals leaving the system (through death/migration); blue arrows represent transfer of individuals between compartments; black arrows represent changes to concentration of cholera bacteria in the local aquatic environment

The rate at which individuals move in, out, and between compartments is described by a set of coupled differential equations that are given as functions of environmental and socio-economic variables. These variables will act as input to the model and include (1) Flood extent / drought; (2) Air temperature; (3) Sea surface temperature; (4) Hygiene and safe drinking water availability; and (5) Sanitation (access to safe toilets, sewerage).

Further model parameters (e.g. rate of immunity loss, disease recovery rate, etc.) will be taken from literature where available, or calibrated using historical cholera case data. The output to the model can be considered as the total number of individuals becoming infected in a given timeframe.

Conclusions

The main benefit intended from this model is the provision of a validated understanding of the mechanisms that contribute to cholera outbreaks – something currently lacking in the research community. The next stage of the project will aim to utilise this benefit in the following ways. Firstly, to simulate the relative effectiveness of different intervention options. This can be achieved by altering the input factors to reflect the changes made by the intervention (e.g. reducing the 'flood extent' factor to simulate flood mitigation practices), and then assessing any corresponding change in infected individuals over time. The flexibility of inputs into the model would allow fast, cheap and ethical comparisons between options. This could ultimately be integrated into a Decision Support Tool used by local policy makers. Secondly, it could be used to quantify the effects of climate change in the modelled region. By using climate forecasts as environmental inputs and assessing effect on the simulated number of infected individuals, valuable insights could be gained into the future challenges faced in the fight against cholera.

Acknowledgement

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