

Estimation of ML Algorithms for Epidemics of Infectious Diseases

¹Mohita Sharma, ²Dr. R.S. Parihar

¹Ph.D. Scholar, ¹Professor
Sunrise University, Alwar

Abstract: The study is based on an extension of the well-known machine learning algorithms and models. It is shown how social measures such as distancing, regional lockdowns, quarantine and global public health vigilance, influence the model parameters, which can eventually change the mortality rates and active contaminated cases over time, in the real world. As with all mathematical models, the predictive ability of the model is limited by the accuracy of the available data and to the so-called level of abstraction used for modeling the problem. In order to provide the broader audience of researchers a better understanding of spreading patterns of epidemic diseases, a short introduction on biological systems modeling is also presented and the python source codes for the simulations are provided online.

Keywords: Machine Learning Algorithms (ML Algorithm), Infectious Diseases, Epidemics

I. Introduction

Emerging and re-emerging epidemics of infectious diseases are on the increase with catastrophic health, social and economic effects, especially in developed countries. One of the lessons learnt from the Ebola virus fever epidemic in Nigeria is that it is important to handle efficiently the quick mobilization of public health and political capital to control the epidemic in a timely manner. Lassa fever, a viral hemorrhagic disease, was first identified in Nigeria in 1969, and since then, epidemic proportions have occurred annually in different parts of the world. The impetus was the need for healthcare staff to be mindful of an evolving disease management system that has been useful elsewhere for useful preparedness and reaction to epidemics in general and outbreaks of Lassa fever in particular. Here, using the Emergency Operations Center (EOC) model, this address the concepts of disease control, study the epidemiology of Lassa fever in Nigeria, and include advice on what to anticipate to be accomplished to plan for epidemics in health facilities. The comprehensive disease monitoring and response plan is utilized at the educational, municipal government, and state levels.

How Diseases Emerge

An illustration of an emerging illness triggered by environmental and human causes is influenza (or influenza). The influenza virus is considered to change your genetic material because of its capacity. Significant improvements may trigger epidemics in the influenza virus since the human immune system is not prepared to recognize the latest strain and protect it. When humans coexist near farm animals such as chickens, ducks, and pigs, the risk of major genetic changes arising and their spread to humans rises. These animals are normal hosts for the influenza virus and may serve as mixing containers to make fresh, previously non-existent, copies of influenza. Avian influenza (or avian influenza) H5N1, which arose more than a decade ago, has been limited to comparatively isolated instances of human illness in which close interaction with sick birds has arose. The H5N1 virus is highly lethal (more than half of the cases were lethal), but it has not acquired the potential for successful human-to-human transmission. The 2009 H1N1 virus, on the other side, which was spread to humans by pigs, is quickly transmitted from person to person. As a consequence of human activities, especially air travel, the H1N1 virus has spread the globe faster than any other virus in history. It was, luckily, much less lethal than the H5N1 strain. The advent of a lethal influenza virus, such as the avian H5N1 virus, which spreads as quickly as H1N1 pigs among individuals, presents a very important danger to human health (Avelino et al., 2004).

Another indication of how easily contagious diseases will propagate across the world as a consequence of air travel is the SARS and MERS outbreaks, which are severe respiratory diseases. In 2002, SARS originated in China and rapidly spread to other countries in the area and then by air to Canada. The dissemination of the causative virus was stopped by an extraordinary global reaction, but not until 8,000 persons became contaminated and 800 died. In the Arabian Peninsula, MERS, triggered by a similar virus, emerged in 2012. The original reaction was unsuccessful this time and MERS started to propagate. In countries in Europe, Asia, Africa and North America, cases involving travel originating in the Middle East have been recorded. In late spring 2015, an even more disturbing case happened when the viral transmission chain, triggered by a single tourist, affected almost 200 individuals over a span of nearly two months.

Research on Emerging Diseases

The production of vaccines, antimicrobial medications and the marked extinction of smallpox have given rise to the possibility that infectious diseases can be treated or even removed. The current understanding, however, that infectious diseases continue to evolve and resurface (including the potential for bioterrorism) underscores possible difficulties in research into infectious diseases. Study on a variety of new and chronic pathogens, including influenza, SARS, MERS, dengue, chikungunya, Zika, is being undertaken at the Baylor College of Medicine's Division of Molecular Virology and Microbiology to better address this task. HIV and tuberculosis. Humankind. AIDS. In an attempt to achieve a more comprehensive understanding of how these causes cause illness and how the human immune system reacts to these pathogens, this study involves both fundamental sciences, as well as more

research aimed at improving and testing vaccinations and other methods to deter infection with these agents. Moreover, scientists are researching the processes by which antibiotic tolerance and strategies to combat drug-resistant pathogens may be acquired by bacteria.

Emerging & re-emerging infections in India

Infectious diseases that have raised their prevalence in humans in the modern past or that intend to escalate in the immediate future are new infectious diseases (NIDs). This involves emerging diseases that were previously unspecified, as well as old diseases with new functions. These new features might involve the arrival of the disease to a new location or demographic (for example, the disease may be found in young adults, as historically seen only in the elderly); new therapeutic features, including resistance to medication available; or quickly growing the prevalence and distribution of the disease. That will be known as a recurring contagious infection by a revival of a disease that was widespread but has now been removed or regulated. A recent identification of an infectious agent in the community or the assumption that the steady state has an infectious origin can also be the cause for the emergency (Courtois & Martinez; 2019).

Over the past three decades, more than 30 different infectious agents have been found worldwide; 60% are of animal origin and more than two thirds come from biodiversity (Table). Epidemics or epidemics triggered by this developing and recurrent illness also take a severe toll on lives, and a lot of fear and panic is blamed for the rapid spread across boundaries. Emerging pathogens often face serious economic, growth, and protection challenges in addition to health. For example, the first major infectious disease to occur in the 21st century was SARS (severe acute respiratory syndrome). The latest SARS virus soon spread to 30 countries in Asia, America and Europe, with a total of 8,439 cases and 812 fatalities, over a span of 7 to 8 months, after emerging in the Guangdong province of China in 2003, likely from civet cats. It has presented a significant challenge to global health protection, to the health system's capacity to deal with areas where health workers themselves are at risk, and to economies' resilience and development. The economic losses incurred by Asian countries are projected to be between US\$ 10 billion and US\$ 30 billion.

II. Review of Literature

Moore et al. (2020), Global transport and communication networks allow the dissemination of knowledge, ideas and infectious diseases at a far faster pace than has traditionally been feasible. It is important to forecast the speed of a unique infection in a given network and differentiate between nodes that are more likely to become infected sooner or later during an outbreak in order to efficiently track, design, or participate in epidemic-like processes. In the case of simple infections in tree-shaped networks, our principle has been established and clarified, but we may also see how the approach applies well to complicated infections and strongly clustered networks.

Khatun et al. (2018), Because of the rising dangers of infectious diseases and the mortality rate, the provision of sufficient medical treatment to the growing population of Bangladesh has become a major concern. Providing optimal medication for evolving infectious disorders has become a problem for healthcare professionals. In this paper, we discuss some of the recent developments in modelling leukemia immunotherapy's nonlinear actions utilizing adoptive T cells. In certain situations, optimum management strategies may be valuable as a special edge for having the right approach. To demonstrate the effects, a computational procedure is conducted.

Meehan et al. (2018), Explicit expressions of the specific reproductive amount of each strain are obtained and stress its significance in controlling the complexities of the environment (e.g., possible occurrence of a pandemic) and the existence of non-negative endemic solutions. Importantly, even under fairly broad hypotheses as to what the contagious cabin pairing looks like, we observed that the primary breeding number for and strain was independent of the mutation rates between strains. In addition, we confirmed that the word paired supported strain coexistence (as an extension of the concept of competitive exclusion) and identified that it is not inherently the most prevalent strain with higher reproductive ability. Finally, the consequences of our results for public health policies and preparation are quickly addressed.

Li et al. (2020), This paper deals with two models of SIS epidemiological spread interaction that focus on frequency in a heterogeneous setting, with the word cross-spread illustrating the influence by which sensitive individuals appear to migrate away from the greater concentration of individuals affected.

Kong et al. (2020, January), conducted suitability tests of interest in three broad collections of Twitter post data and tested the probability of a retention record of self-excitation processes with three exponential infection cores, the rule of authority, and the exponential Tallies Q. We demonstrate that the modelling utility of the infection kernel differs with regard to the temporal broadcasting systems, as well as with regard to user actions, such as the possibility of becoming a bot. By integrating two models that were established as complementary by trapping quality controls, we also enhanced the prediction of popularity.

Park et al. (2020), many disease models concentrate on characterizing the basic process of transmission, but make clear assumptions about how infection is reported, and perhaps naive ones. On this note, in order to equate two standard ideas regarding disease occurrence reporting, we use a basic deterministic knockdown infection (SIR) model: people should disclose their infection as soon as they are hurt or healed. We demonstrate that incorrect baseline observation assumptions skew base breeding number estimates and result in very tight confidence intervals.

Rabajante et al. (2020) Suggested model-based techniques are often discussed for how to avoid the transmission of illness in the immediate community, such as during major social events. The model indicates that a significant element in disease transmission is exposure period. An infectious person who lasts more than 9 hours in a situation will infect other persons with a base replication number of 2 and a contagious duration of 14 days. The model recommends that anyone attending a social event receive security in excess of 70%, considering an exposure period of 18 hours.

Sameni et al. (2020). The model shows that the duration of exposure is a significant component of disease transmission. An infectious entity that remains in a circumstance for longer than 9 hours can infect other individuals with a base frequency of 2 and an infectious period of 14 days. The model advises that, given an exposure span of 18 hours, someone who joins a social function obtain insurance greater than 70 percent.

Ito et al. (2020), the goal of this paper is to establish a theoretical approach to a system of standard differential equations that critically explain the dynamics of the epidemic's spread. Provides valuable unit-based process tools that incorporate product systems properties. The basic features of vaccine and infectious disease models in the vocabulary of the is and ISS are expressed in this paper. It is anticipated that systematic therapy can promote the creation of appropriate systems to manage disease transmission via atypical Lyapunov functions.

Pang et al. (2020), believe that infection happens at a patch-dependent pace geographically, as well as the state of various classes of people in the patch, and the infectious cycles have a general distribution and do not shift as people switch from one patch to another.

III. Research Methodology

Epidemic management

The original or endemic degree of the disease is named the quantity of a certain illness generally present in the population. This amount is not actually the level necessary, and could in effect be zero, but the level observed. In the absence of action and the presumption that the level is not too high to overpower the susceptible population, illness may continue to exist indefinitely at this level. Consequently, the reference level is also assumed to be the predicted disease frequency. While certain viruses are so uncommon in a single community that an epidemiological examination (e.g., rabies, plague, and polio) is needed in one instance, some diseases arise more commonly, so only anomalies from the standard need investigation. Intermittent refers to an illness that arises both occasionally and irregularly. Endemic applies to the continuing occurrence of a disease or infectious agent in a community within a specific region and/or its habitual distribution. Persistent elevated levels of illness are demonstrated by excessive endemicity.

Analyzing an epi curve

The epi curve will tell researchers a variety of other details regarding an epidemic, in addition to a visual description of the spread of cases over time. They include: scale, direction of time, outliers, and pattern of propagation.

Outbreak analytics

(a) An overview of the outbreak analytics toolbox

In order to refer to a range of resources and methods used to gather, pick, simulate, interpret, model and report outbreak results, we use the word "outbreak analysis." In a standard workflow seen in Fig., these instruments and their interrelationship are summed up. Originating from lines of study used in previous influenza pandemics, MERS-CoV and Ebola virus outbreak. In other pandemic situations, be mindful that job flows will differ greatly. For e.g., foodborne epidemic research might concentrate on tracer data, whereas vector-borne disease analysis may concentrate heavily on modelling the environmental state of vectors

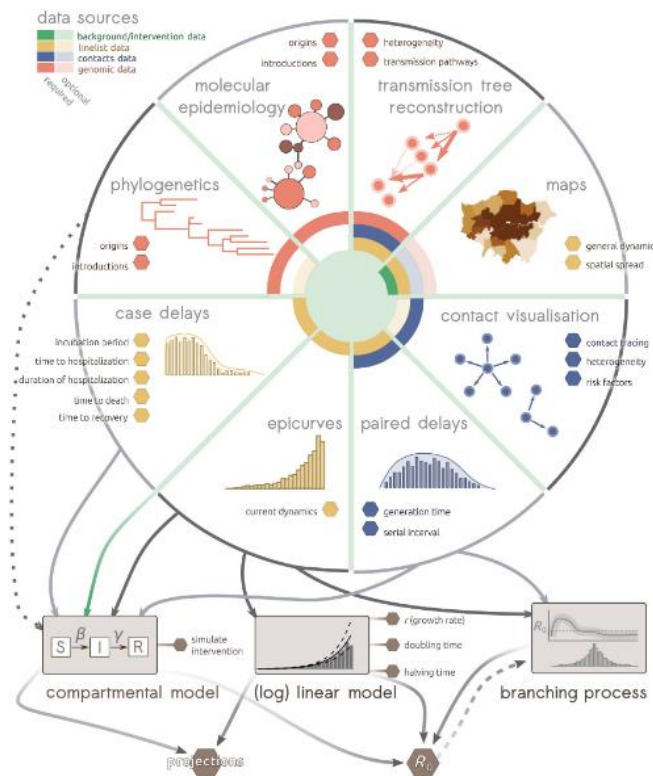


Fig. Example of an outbreak analysis workflow.

This chart represents eight general analyzes that can be made from the outbreak data. Results containing actionable information for operations are represented in hex. The data required for each analysis is represented as a different coolant in the center, using simple and light shading of the required and optional data, respectively. (Online version in the cooler).

First, after an epidemic, most pathogens do not gather adequate genetic diversity to allow reliable transmission chain reconstruction, and thus need numerous data sources, which implies that methods require more data than most other approaches to outbreak analysis. Moreover, the dynamic nature of the issue involves the use of the methods of Bayes to create the model, rendering it impossible for non-experts to interpret these methods.

- Data Collection
- Types and sources of data
- Data analysis
- Data quality
- Performance indicators
- Recording/entering data
- Data compilation
- Data cleaning and preparation for analysis
- Analysis of weekly aggregate data
- Analysis of disease outbreak data

Cross-sectional and empirical sample architecture, implementations, strengths and weaknesses (including population, monitor, case, and related studies) and intervention tests (including randomized clinical trials). It is important to divide predominant experimental designs into observational and interventional trials. Observational experiments do not actively classify subjects to gain a particular dose, such as cross-sectional studies, case studies, and community studies, although interventional studies do. Also listed here are each of the above research designs.

IV. Mathematical Construct and Modeling

Escalation of an Epidemic to a Pandemic

When an epidemic exhibits rapid growth, the International Health Organization (WHO) will announce a pandemic, which will significantly boost the growth rate, since there are far more instances per day than the day before. The latest instance of this is the coronavirus illness (Covid-19). A community of cases of pneumonia of unknown origin was confirmed to the World Health Organization (WHO) on December 31, 2019, in Wuhan, Hubei province, China. It was eventually reported as a new virus in January 2020 and the number of cases began to escalate throughout the following months, but it was not localized in China and saw exponential development worldwide. Owing to the dramatic rise in the number of cases

worldwide, a global pandemic was announced on 11 March [9] and, internationally, at 4:22 p.m. CET, 9 December 2020, recorded 67,780,361 verified COVID-19 incidents, including 1,551,214 fatalities, reported to the World Health Organization.

Phases of the disease

Six levels have been defined by the World Health Organization to meet before announcing a pandemic. Step 1 is low risk and a full pandemic is Stage 6; the steps below can be seen:

Step 1: The virus is seen in wildlife, but there has not been an outbreak in humans.

Step 2: humans have been contaminated with a recognized livestock virus

Step 3: the appearance in humans of individual cases, isolated or limited classes of diseases; possible instances of spread from person to person, though not at the level of the population, triggering outbreaks.

Step 4: spread of infection from person to person at a pace that results in societal disease outbreaks

Step 5: in more than one region, the dissemination of the disease is now apparent in humans.

Step 6: in at least one different nation other than that seen in Stage 5, epidemics spread at the population level.

Prepare for a worldwide pandemic until you reach stage 6. To promote accountability and inform health organizations and the public, each stage includes a set of protocols to adopt. These procedures are listed in the following table.

Test Result

Methods	Accuracy on training set	Accuracy on test set
K-Nearest Neighbors	0.67	0.65
Logistic Regression	0.674	0.683
Decision Tree	0.969	0.607
Random Forest	0.674	0.683
Gradient Boosting	0.717	0.623
Support Vector Machine	0.67	0.68

V. Findings of Research

It should be highlighted that mathematical models applied to real-world systems (social, biological, economical, etc.) are only valid under their assumptions and hypothesis. Therefore, this research and similar ones that address epidemic patterns, do not convey direct clinical information and dangers for the public, but should rather be used by healthcare strategists for better planning and decision making. Hence, the study of this work is only recommended for researchers familiar with the strength points and limitations of mathematical modeling of biological systems. The python codes required for reproducing the results of this research also explored.

VI. Conclusion and Future Scope

The outbreak of the any epidemic disease has taken the lives of several thousand worldwide and locked out many countries and regions, with yet unpredictable global consequences. In this research we investigate the epidemic patterns of this virus, from a mathematical modeling perspective. The study is based on an extension of the well-known machine learning algorithms and models. It is shown how social measures such as distancing, regional lockdowns, quarantine and global public health vigilance, influence the model parameters, which can eventually change the mortality rates and active contaminated cases over time, in the real world. As with all mathematical models, the predictive ability of the model is limited by the accuracy of the available data and to the so-called level of abstraction used for modeling the problem. In order to provide the broader audience of researchers a better understanding of spreading patterns of epidemic diseases, a short introduction on biological systems modeling is also presented and the python source codes for the simulations are provided online.

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