Susceptible-Infected-Recovered Model of Swine Flu and Influenza

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Abstract

Epidemiology, which is a cornerstone of public health, provides critical insights into the spread, impact, and control of infectious diseases. Mathematical models such as the Susceptible-Infected-Recovered (SIR) framework play a vital role in understanding disease dynamics and guiding intervention strategies. This study explores the SIR model applied to two important infectious diseases: swine flu (H1N1) and seasonal influenza. These viral infections, characterized by high transmission rates and recurring outbreaks, underscore the importance of accurate modeling for effective public health response. The SIR model divides the population into classes—susceptible, infected, and recovered—to simulate disease progression over time. By analyzing transmission parameters, recovery rates, and basic reproduction number (R_0), the model enables prediction of the peak, duration, and required control measures of an outbreak. The topic also highlights the critical role of vaccination, hygiene practices, and behavioral interventions in reducing transmission, especially in high-risk groups such as schoolchildren. Through theoretical modeling and real-world epidemiological data, this work emphasizes how integrated SIR-based approaches support timely decision-making in resource-limited settings and contribute to reducing morbidity and mortality from infectious diseases.

Introduction

Epidemiology

The primary field of public health, known as epidemiology, focuses on understanding the factors that affect the health of many people. It guides medical care and preventive measures adopted by public health, allowing scientifically supported improvements in people's health. Epidemiology is considered the core philosophy of public health and is extremely important in finding the causes of diseases and choosing the best methods of their prevention and treatment [Allen (1994); Padma (2008)]. The aim of an epidemiological investigation is to reduce or eliminate health problems, helping a community live healthier and longer lives. Epidemiological research provides important details about the number of cases and incidences of diseases in groups, helping to understand their changes over time. As a result, it makes it possible to address the causes and risks that require targeted action. By observing diseases and their spread, epidemiology helps us to know how various diseases change and increase from one generation to the next. It helps in limiting the spread of disease as well as in the creation and evaluation of healthcare centres, public health plans and projects. Epidemiology helps in determining potential risks to both the individual and the society so that appropriate decisions can be made in healthcare, administration and resource distribution. Pathology helps in the early detection of new diseases and syndromes, allowing for a quick response to any health emergency. Overall, epidemiology plays a vital role in working towards a healthy population by providing a robust statistics-based approach to study diseases and health issues.

Understanding how diseases spread is very important to estimate the impact and severity of a disease in society. It is essential to know how a disease spreads in order to create effective public health plans and safety measures. Based on their mode of transmission, diseases are classified as communicable or non-communicable. Communicable diseases, also known as infectious diseases, are caused by various biological agents such as bacteria, viruses, parasites or their toxins. These types of diseases can spread between people, between humans and animals, or through contact with contaminated areas. Barreto et al. (2006) explain that an infectious disease develops due to a specific infectious agent and spreads through multiple routes, such as physical touch, airborne particles, contaminated surfaces or contact with living beings. Good examples of this are H1N1 influenza, Ebola, malaria, HIV/AIDS and cholera. In comparison, non-communicable diseases (NCDs) can be identified by the fact that they are non-contagious and do not spread from one person to another. In most cases, these conditions arise due to the combined effects of genetics, different environments and people's habits rather than a specific pathogenic agent. Examples of NCDs are heart disease, cancer, diabetes, chronic lung problems, autoimmune disorders and chronic kidney disease. Communicable diseases usually require immediate action to prevent them, but ongoing care and prevention efforts are necessary to tackle non-communicable diseases. Each group causes major health problems and therefore requires specific plans for monitoring, diagnosis, treatment, and policy.

Modes of transmission

Infections and epidemics can spread in many ways, all of which depend on the behavior of the pathogen and the environment. Bacteria, viruses or parasites can infect people by coming in contact with the surface of contaminated objects or with an infected person. Some infectious diseases spread when skin touches another person or when a person's body fluids come in contact with the body, while others spread through contact with contaminated surfaces, objects used by others or contaminated media. Many times, diseases spread from one host to another when biological vectors or carriers carry them. Malaria, dengue and chikungunya are diseases that are spread by mosquitoes, which transmit these infections into the bloodstream during feeding. Special attention should be given to airborne infections and sexually transmitted infections (STIs) as they have different characteristics and have a serious impact on public health. Such diseases, including influenza and SARS, are spread when infected people cough, sneeze, laugh or talk, causing tiny respiratory droplets to spread into the air. Such droplets may contain germs that either remain in the air or land on surfaces and dust and can enter the body through inhalation or contact with the mucous membranes of a susceptible person. This is most troublesome in crowded or closed environments where the chances of rapidly spreading infections are high. Proper hygiene is important when shaking hands as this can easily spread germs (Rahman, 2016).

Sexually transmitted infections are caused by the spread of germs through intimate sexual acts such as vaginal, anal and oral sex. Often, these viral infections are caused by prolonged contact with fluids such as semen, vaginal secretions or blood containing HIV, syphilis, gonorrhoea and human papillomavirus. Since this mode of transmission is very private, it is often difficult to prevent for communities with low sexual health knowledge or discrimination. Preventing both types of infections requires education, promotion of better hygiene, defined control strategies against disease vectors, and making preventive care widely available. Being aware of the different ways diseases are spread is important for controlling outbreaks and formulating useful public health strategies. Nonetheless, a major range of these diseases are transmitted through sexual activity, although people can also catch some of them from contaminated blood and bodily fluids or during the birth process. Of these issues, human immunodeficiency virus (HIV) still emerges as a major worldwide health risk, as it accounts for a large proportion of STI-related deaths. Major STIs also include HSV, syphilis, gonorrhoea, and chlamydia, which are significant causes of suffering and sometimes death worldwide [Rahman (2016)]. Such infections pose many challenges to public health as they have a huge impact on society, the economy and people's mental health. As STI infections last longer, more cases are likely to occur before someone is diagnosed and treated. People who are infected but unaware can unknowingly spread the disease to others, making it difficult to prevent these infections. The fact that some sexually transmitted infections show little or no symptoms further complicates this problem. Some infected individuals may be carriers for a long time, without any obvious symptoms. People in this infectious stage do not have any symptoms, making it possible for the virus to spread easily. For this reason, sexually transmitted diseases continue to affect public health, and their effective management requires regular testing, spreading information and making health services easily available. Using a variety of mathematical and computer models, epidemiologists try to understand and predict such diseases. These models provide important information about how diseases spread and change over time, for example, using SIR models or more advanced environmental, atmospheric and survival systems. These models can be built using deterministic methods, random processes, and may involve continuous or discrete time-frames. In addition, they can be set in space or not, deal with the same or different types of entities, and run in real time or be static and repetitive. Thanks to advanced methods of modelling [Rahman (2016)] it is now possible for researchers to analyse large amounts of data, create new strategies and predict better outcomes. These methods are essential for formulating policies with solid evidence, managing limited resources and establishing strategic approaches to combat sexually transmitted infections and other complex diseases.

Disease prevention and control

One helpful method for controlling epidemics is ensuring that people interact less which reduces the spread of diseases. Still, given that modern society has a lot of people, many cities, links to the world and more movement, making large contact reductions is hard and often brings negative economic and social impacts. Although social distancing and isolation work in some situations, they should be accompanied by other strategies to handle infectious diseases for the long term.

Of all the practices, immunization and medical treatment are still widely trusted and supported by science. During the past decade, controlling infectious diseases has been achieved using different strategies like encouraging behavioral changes, expanding preventive services and giving out vaccines and antimicrobials on a large scale. People following good hygiene, having safer sexual lives and using protective clothing have been key when they are also encouraged by health education and policy rules. When applied together with treatment medicines, these changes in habits have considerably lowered the chance of the disease spreading and the number of new infections.

Infection prevention methods are considered effective because we know that doing them promptly and properly greatly lessens the risk to people's health. Unfortunately, although we have access to preventive equipment, many people are still unable to use them equally. In low-resource communities, several individuals lack access to important healthcare because of challenges with infrastructure, lack of funds or existing inequalities. Because of this difficulty, public health programs cannot function as well and, in turn, those who are highly at risk face bigger threats.

Treatment, if used as a main strategy alongside other methods, helps to decrease the effects of infectious diseases. It helps people feel better and slows down their illness and it also plays a key part in reducing the risk of more people becoming infected. Proper treatment services can cut healthcare costs, enhance individual and community productivity and reduce incidents of sickness and death among people who are prone to serious diseases. To use treatment as a key part of epidemic control, healthcare systems should be strong, orderly and able to offer top-quality care. This covers making certain there are qualified people, simple methods for administering services, quick diagnostics and healthcare that centers on the patient. Good infrastructure for treatment improves how public health systems can address and control emerging and re-emerging infections. Thanks to vaccines, efforts to control and get rid of certain diseases can continue, giving us more time to achieve our goals. So, adding treatment and immunization to behavioral and structural steps is a good way to address epidemics in all sorts of places.

Vaccination or immunization plays a key role in helping stop the spread and control infectious diseases. A vaccine assists the body in figuring out how to deal with some diseases without actually making people sick. Usually, the main part of a vaccine is a harmless version or part of the pathogen such as a protein or a toxoid which resembles the active form. Because these components of vaccines can't cause a full infection or duplicate themselves in humans, they still have enough ability to trigger a protective response in the body. When given to the body, they cause the immune system to create antibodies and activated cells that only target the exact pathogen if it's encountered again. Such protection is called acquired immunity or immunological resistance and it is formed naturally by the immune system. Vaccinations help prepare the body to protect itself from potential infections and therefore stop the disease from starting and decrease the chance of disease transmission among people. Hence, vaccinations help the individual as well as the entire community by making herd immunity possible and protecting people who have not been immunized.

There is solid evidence to show how vaccines have changed the course of history. After Edward Jenner's work on cowpox in the late 18th century, the field of immunization changed rapidly and rooted several important public health campaigns that stopped the spread of dangerous infectious diseases [Lakhani (1992)]. Since their development, vaccines have become an important part of global health programs. Earlier, especially during the 1950s, the Unites States experienced over 400,000 cases of measles each year [Rahman (2016)]. In the same way, diseases such as poliomyelitis, rubella, mumps, diphtheria and whooping cough which used to make many children seriously ill and even cause death frequently, have now been greatly reduced or eliminated in many places thanks to ongoing immunization efforts.

It is thanks to vaccines that healthcare systems experience fewer emergencies, people live longer and society as a whole develops more steadily. Even so, vaccination is most effective when immunization is applied in a fair manner, everyone trusts vaccines and there are systems in place to deliver them to all individuals in need, wherever they are. Since there are new health challenges as SARS, H1N1 influenza and COVID-19 appear, the need for reliable vaccines and their access to all becomes even clearer. All things considered, vaccination is a key aspect of current medicine used to defend both individuals and communities against infections.

Vaccines have greatly reduced the spread of influenza which is considered one of the most common and contagious illnesses across the globe. Thanks to its rapid spreading and increased mutations, early efforts to control pandemics failed. It is still clear from the Spanish flu that if a virus is not controlled, it can result in millions of deaths. However, the H1N1 pandemic of 2009–2010 saw much fewer deaths globally, proving that vaccination and proper public health help to greatly reduce the disease's severe effects. Flu vaccines are recommended every year since the virus undergoes a significant change every season. Every year, the seasonal influenza vaccine is changed to match the strains that are currently affecting people, so individuals are protected and the community as a whole gains some immunity. Regular flu vaccinations for people in a community help prevent illnesses and deaths, plus they offer stress relief even for healthcare services.

Still, even though flu vaccines have been shown to be effective, there are many difficulties related to logistics, economics and ethics in low- and middle-income countries. One major obstacle is that there is not enough vaccine available and it is not given out smoothly. It becomes very important to find the best approach to directing resources to achieve the greatest results for public health. Even the most well-intentioned public health teams can have trouble with vaccination because of social gaps, lacking access to places, money difficulties faced by many and the tricky process of choosing who gets the vaccine [Medlock and Galvani (2009)]. It is difficult to decide on vaccination strategies because susceptibility to disease changes among different people. According to studies, young people in school are most likely to catch influenza and tend to spread it among other community members [Foy et al. (1976); Longini and Halloran (2005); Jordan et al. (2006); Loeb et al. (2010)]. Since they have a lot of contact with others and travel much, these people contribute more to COVID-19 transmission, so they are a priority for early vaccination during a pandemic. For this reason, policies regarding vaccinations should take into account both data about diseases and patterns of society, paying special attention to what risks are involved, who will be first to receive them and how fair the allocation will be.

Basic compartmental models

Deterministic models in epidemiology frequently apply compartmental modeling, because this method makes it simpler to study how a disease travels in a community. These models split the population into parts that stand for the disease process stages, also known as susceptible, exposed, infected and recovered people which are denoted by S, E, I and R. Differential equations are used to model the transfer of people among compartments, depending on the disease's biological and social features. The status of a disease and how quickly it spreads and recovers can decide when someone moves to a different compartment. A person likely to get infected may end up being infected, move to the infection group and then either recover or succumb. Besides, if someone is born or enters the country through immigration, they enter the susceptible class and leaving the population might be because of natural reasons or illnesses. The activity of a compartmental model depends on the entry, transfer and exit steps.

Perhaps the most basic epidemiological models are the SI, the SIR and the SEIR models that are used as a foundation for more complex ones. Even though it is assumed in classical models that the population is well mixed and stays at a constant pace, this is not always how things work in reality. People may add additional areas to the model [for example, separated by whether they are vaccinated, hospitalized or quarantined], change parameters based on time or state [for instance, recovering from illness or moving from one area to another] or include variations in how the disease spreads because of different ages or areas. Regardless of how complex today's compartmental models are, the basic idea has not changed: individuals are part of the system, progress through its various disease stages due to epidemiological reasons and eventually leave the system. They are helpful for predicting the direction of epidemics, gauging the number of cases expected, deciding on approachable prevention and management steps and supporting public health policy. Thus such models are used frequently in epidemiology to examine infectious disease outbreaks and develop solutions based on reliable data.

Epidemic models

Back in the 18th century, Daniel Bernoulli was a leader in introducing mathematical models to epidemiology. His breakthrough work involved building a mathematical model to judge the impact of variolation on smallpox which led to quantitative ways of managing infectious diseases [Benenson (1995); Hethcote (2000)]. The first model of mathematical epidemiology achieved a lot for its age, but the field saw major changes in theory during the 20th century because of the achievements of Kermack and McKendrick. By publishing their work in 1927, they established how to divide people into three groups—S, I and R—and used signs like the basic reproduction number ($R0$) to decide if diseases would grow into epidemics [Kermack and McKendrick (1927); Hethcote (2000)].

Biological sciences experienced rapid growth in the use of mathematical models after World War II. It was made possible by more scientists working together and a growing appreciation of models in studying different biological and epidemiology systems. By merging biology into basic models and paying close attention to the irregular changes of disease spread [Anderson and May (1982)], researchers such as Anderson and May extended what epidemic modeling could achieve [Hethcote (2000)]. As a result, various models were developed to illustrate how diseases can affect people by describing infection times, many kinds of transmission, different types of insects, how people of various ages are involved and mixing behaviors such as sex. In order to manage different health problems and biological issues, today's epidemiological models are more advanced than ever before. Among the factors they include are uneven geographic conditions, changing seasons, a decline in immunity, unpredictable changes, quarantine actions and different ways of treatment such as chemotherapy. They have greatly contributed to understanding how different infectious and non-infectious diseases are spread. A number of diseases that medical science has focused on modeling are vaccine-preventable ones, including measles, rubella, chickenpox, diphtheria and smallpox and also diseases spread by insects such as malaria and rabies. Other significant infections such as cancer, herpes, syphilis and HIV/AIDS have been studied in detail by researchers to find out how interventions might work over an extended period and support control policies [Anderson and May, (1982); Usher (1994); Hethcote (2000); Grassly and Fraser (2008); Longini and Halloran (2005)].

The ways in which these compartments are set up make it possible to build different models that fit the requirements of diverse diseases. For example, under the SIS model, a person is infected, then recovers and returns to being susceptible which could represent diseases that lose immunity quickly, like certain bacterial infections? Measles and smallpox which leave those who recover immune for life are diseases the SIR model is designed for. Less straightforward options like SEIR and SIRS add steps to show how individuals may become immune for some time before they recover. SEIS assumptions state that individuals who have recovered may eventually not be immune anymore and move back to the exposed group if infected again. A main idea behind most classical compartmental models is that individuals from different age groups or communities are equally likely to meet and interact. Moreover, it is commonly believed that the rate at which people move between the infection, incubation and recovery phases does not change. Even though these assumptions are useful for analysis, they may not always show all the real-world challenges. Consequently, these models are now advanced to consider variations in meetings among people, areas of the disease, unexpected changes, changing seasons and the actions of individuals as factors. With compartmental models, it is possible to approach disease outbreaks, anticipate how an epidemic will progress and assess the outcome of actions like recommendations to vaccinate quarantine or treat people. When researchers change their models to suit the characteristics of various infectious diseases, they can make better suggestions for public policies and more effective use of resources.

A basic way of studying epidemics is using the classical Susceptible–Infected–Recovered model, as originally formulated by Kermack and McKendrick in 1927 using ordinary differential equations.

$$\frac{dS(t)}{dt} = -\,\beta S(t)I(t)$$

$$\frac{dI(t)}{dt} = \beta S(t)I(t) - \Upsilon^{I}(t)$$

$$\frac{dR(t)}{dt} = \Upsilon^{I}(t)$$

Here, S (t) is the number of people who can get the disease, I(t) is the number infected at any given time and R(t) is the number recovered at that same period. The value of β captures the chance that a person will pass on the disease during a contact and γ stands for the rate at which infected people recover. Basically, the model expects no births, deaths or migration, so it does not consider demographic factors. The main concepts of how epidemics spread are well understood through the model, even though it is not complicated. βS(t)I(t) is called mass action incidence rate or bilinear incidence and it assumes new infections happen when susceptible and infected people interact in proportion to what is shown in the equation. It means that when both groups come into close contact with each other, the rate of spreading the virus increases. This assumption depends on homogeneous mixing which means everyone has the same chance of interacting with any other individual in the population. Bilinear form comes from the product of how many people meet and the possible outcome of passing the disease through contacts [Park (1997)]. However, in most situations, this idea does not work because there are too many behaviors, not enough time for contacts or other reasons that slow down or stop growth.

Consequently, numerous researchers have upgraded the SIR model by using different types of nonlinear incidence functions which better match how epidemics happen and how people change their behavior [Murray (1989); Diekmann and Heesterbeek (2000); Guo and Li (2006); Dubey et al (2013; 2016)].

These assumptions broaden the system's functionality, but they also help make the system harder to analyze efficiently. So, epidemic modeling has to find a way to keep the models biological enough and yet still manageable mathematically. It is important to select the model's form and set its parameters carefully to make sure the model is still easy to understand and suitable for making decisions. Afterwards, we focus on several different nonlinear ways of describing incidence rates and consider their meaning in infectious disease modeling.

Basic reproduction number

An important number in mathematical models of infectious diseases is the basic reproduction number which is called R0. It contains important aspects of how the disease is transmitted such as the frequency of contact among individuals, the length of their infectious period and the virus's natural ability to spread. Driessche and Watmough (2002) define R0 as, "the average number of people an infected person will spread the virus to, during the entire time that the person is contagious, if all people are unprotected] Using R0, people can estimate the chance of a disease outbreak and see how severe its spread is expected to be. The frequency of meetings between infected and susceptible people is largely decided by the contact rate which greatly impacts R0. If more people come into contact, the chances of transmission become higher and so does the value of R0. On the other hand, the pattern of contacts is very different and complicated, depending on what people do in society, their culture, how densely populated an area is and people's mobility. Unlike most other model parameters, how humans contact each other is not fixed, so this makes it hard to accurately predict the spread of disease and its trend..

Another vital part that affects R0 is how long someone can spread the illness after being infected. Staying infectious for a period makes it more likely for the infected person to come in contact with more susceptible people, resulting in larger numbers of secondary infections. Therefore, if diseases are infectious for a long period such as tuberculosis or chronic viruses, they are likely to spread unless people are quarantined or treated.

Historical Spread and Comparison of Swine Flu (H1N1) vs. Influenza

Observing the history of Swine Flu (H1N1) and seasonal influenza helps us better understand how such viral infections behave, the effect they have and how they should be handled. Even though both cases involve the influenza virus, their ways of spreading, how they are handled and the results globally are not the same.

Origins and Initial Outbreaks

People have talked about seasonal influenza from very early times, as there are traces from ancient writings. Annual falls of influenza often happen in the coldest seasons and cannot be avoided by many individuals which make it an ongoing health concern. The reason is mainly due to frequent changes in the A and B flu viruses which force the need for new vaccines every year to protect people. The appearance of new influenza types during every flu season is due to regular mutations, so the world has to consistently check for new strains and adjust vaccines. Unlike other seasonal strains, H1N1 (Swine Flu) in 2009 involved the appearance of a new influenza A virus. It was formed when segments from North American swine influenza, North American avian influenza, human influenza and Eurasian swine influenza joined together. Before this case such a hybrid strain had not been found in either humans or animals, revealing just how uncertain influenza virus changes can be. In early April 2009, public health authorities in Veracruz, Mexico, discovered unexplained flu-like symptoms in a group which were the first H1N1 human cases. A few weeks after the virus appeared, it was found in the United States and soon started to spread all over the continents. The virus spread so quickly due to traveling by air, a large number of people moving worldwide and because nobody knew how to keep away from it since it was a new virus. On June 11, 2009, the World Health Organization (WHO) decided that H1N1 had developed into a global pandemic, marking it as the first influenza pandemic to appear in the 21st century. Since the pandemic was spreading very fast across the globe and the disease's seriousness was uncertain, many governments and health organizations quickly launched their pandemic plans.

A major feature of the H1N1 outbreak in 2009 was that it affected people of all ages differently. While older adults and people with other health issues often suffer from regular flu, children, teens and young adults were infected with the H1N1 virus more than expected. This pattern points out that older people might still have some protection from the past, while the young were more likely to develop severe infections.

Global Impact and Transmission Patterns

Generally, influenza occurs in seasonal outbreaks and its cases are at their highest during winters in moderate areas. According to estimates by the World Health Organization (WHO), every year these outbreaks cover thousands of severe cases and result in more than 650,000 deaths related to respiratory diseases worldwide. Because the virus is affected by climate, how many people live in one area and local health services, its impact can be predicted and controlled through vaccinations and campaigns to raise public awareness. Unlike the norm, the H1N1 Swine Flu in 2009 spread outside the usual seasons set for flu viruses. The novel coronavirus appeared in the spring, not the winter and quickly spread all around the world, moving across continents, bypassing climate, season and borders. Because of improved ways of transportation and the lack of immunity in most people, the virus spread very fast. Because of how the virus could spread unpredictably, it caused major strain for public health services across the globe.

Another important aspect of the H1N1 pandemic was that it caused unusual harm among certain groups. While seasonal influenza mainly harms the elderly and people with health problems, H1N1 was especially severe among children, adolescents and young adults. Those who were pregnant were identified as having higher risks of being hospitalized and suffering from serious problems. The need for a younger population to receive vaccines led health officials to rethink their approaches and they devised more attention and support to children and mothers. There were many sides to the influence of H1N1 such as health matters, reduces in economic output, closures of schools and offices and fewer people traveling abroad. Since the virus did not behave as seasonal flu, experts discovered that health measures should be flexible and based on real data. It made clear that sharing resources, information and border control is important in solving global outbreaks, especially when certain places had less access to vaccines.

Public Health Responses

Taking on seasonal flu, public health organizations usually have set plans, using yearly vaccinations, informing the public and giving antiviral drugs to the most at-risk people. These strategies use past epidemiological research to deal with seasonal outbreaks in a controlled way. Despite the normal procedures, the H1N1 Swine Flu pandemic was a quick and significant disease that made the world need to take immediate action. In response to the pandemic, many governments used emergency plans, adding careful observation, fast reporting and clear directions for the public. An important feature of the response was creating and bringing out a vaccine especially for H1N1 quickly. A swift identification of the virus genome by scientists meant that pharmaceutical companies began making vaccines in only three months after the initial outbreak—this was considered a real advancement in the vaccine development sector. Worldwide, countries started major immunization efforts focused on protecting pregnant women, children and individuals who had ongoing health problems. In addition to giving vaccines, guidelines for traveling, closing schools, encouraging better hygiene and holding extra stocks of the drug oseltamivir (Tamiflu) were introduced to control the virus.

Although great efforts were made, the H1N1 pandemic exposed important problems with how prepared the world was for pandemics. Those regions which had limited access to health services, diagnostic tools and vaccines, exposed the big differences between rich and poor nations regarding health. The imbalance in access to vaccines demonstrated how important it is to have worldwide fairness in who gets them during emergencies. In addition, the pandemic showed that calling for clear and ongoing risk communication helps people trust information, follow health instructions and avoid false facts. Getting accurate information to the public became a problem for some nations which then hampered the use of preventive strategies and getting vaccinated.

Comparative Mortality and Morbidity

The 2009 H1N1 pandemic caused millions of people worldwide to catch the virus, but it had a lower fatality rate than major deadly influenza pandemics of the past, especially the 1918 Spanish Flu. More than 2% of those who caught the 1918 pandemic died, causing the loss of an estimated 50 to 100 million lives, with many who passed being young and healthy. However, the estimated case fatality rate of H1N1 in 2009 was from 0.01% to 0.08% and was not as high as that of the Spanish flu, yet it was considered serious because many people were affected overall. Though fewer lives have been lost than expected, the pandemic cannot be overlooked, since it still spread fast and caused major stress to healthcare services, leading to many deaths in high-risk groups. While people are often concerned about major outbreaks, seasonal influenza continues to be a serious problem each year for public health. According to the World Health Organization, seasonal flu causes about 290,000 to 650,000 deaths worldwide each year and mainly strikes elderly, very young and medically ill people. Some of the serious consequences linked to seasonal influenza are being admitted to the hospital, developing pneumonia or heart health issues and loss of work time due to the disease. Even with seasonal flu recurring each year, its mark on health and medical institutions cannot be ignored.

There are noticeable variations in how seasonal influenza and H1N1 affect people. Most of the time, when there is seasonal influenza, serious cases are more common among the elderly and those who already have medical conditions. Unlike other types of flu, the 2009 H1N1 case was notable because it mostly affected children, young adults and pregnant women. Since COVID-19 cases increased in certain areas, it put pressure on pediatric intensive care units and services for mothers.

Objectives of the Chapter

1. To develop a Susceptible-Infected-Recovered (SIR) model that mathematically represents the transmission dynamics of Swine Flu and Influenza in a closed population.
2. To derive and analyze the system of differential equations governing the model, and to interpret the biological significance of key parameters such as the transmission rate (β) and recovery rate (γ).
3. To implement the SIR model computationally using numerical methods for solving differential equations and simulate the spread of both diseases under real and hypothetical scenarios.
4. To perform sensitivity analysis and parameter variation to assess the impact of different public health interventions, such as reduced contact rates or increased recovery rates, on the epidemic outcome.

5. To compare the modeling results with real-world epidemiological data for Swine Flu and Influenza, thereby validating the model and drawing practical conclusions about their respective spread patterns.

Model Formulation

One of the main models in mathematical epidemiology is the Susceptible-Infected-Recovered (SIR) model which shows how an infectious disease spreads in a population. It is especially helpful for studying diseases that lead to immunity, for example Swine Flu (H1N1) and Seasonal Influenza, so this study will make use of it.This model implies that people move from one distinct health state to another in a set order.

- **Susceptible S(t):** Individuals who are at risk of contracting the infection but have not yet been exposed.
- **Infected I(t):** Individuals who have contracted the disease and are capable of transmitting it to susceptible individuals.
- **Recovered R(t):** Individuals who have recovered from the infection and are assumed to have gained full immunity, thus no longer participating in disease transmission

Model Assumptions

In this study, the SIR model is formed using some primary assumptions that reduce the complexity of disease spread to a form that can be studied with mathematics. It is assumed that in this model, every person has an equal possibility of contacting any other person, regardless of where they are from or their social group. Because of this assumption, the amount of transmission for everyone in the population is the same. The model assumes the total population size which is denoted by N, to stay the same throughout the study. During the epidemic process, births, deaths, immigration and emigration are not considered. This supposition helps us study the spread of disease without interference from other demographic situations. A further assumption is that there are fast and continuous changes from one compartment to another. People are assumed to transfer from the group of people susceptible, to the group that is infected and from there to the recovered group, in a regular process explained by differential equations without any sudden jumps. Furthermore, according to this model, a person who recovers should not be affected by the illness again. When a person heals from the infection, they are handled like someone in the recovered class and cannot be re-exposed to the infection during the model's time frame.

Under the SIR model, both the infection rate and the recovery rate are assumed to be constant despite how the disease progresses. In this basic model, the rates remain unchanged no matter the time, changes in the environment or public health policies.

System of Differential Equations and Their Interpretations

The SIR model can be written mathematically as three linked ordinary differential equations (ODEs) which show the rate of change in the Susceptible (S(t), Infected (I(t) and Recovered (R(t)) groups. Based on the main idea that disease is spread via contact between those who are infected and those who are vulnerable, it is also assumed that recovery gives someone immunity for life.

$$\frac{dS(t)}{dt} = -\beta S(t)I(t)$$

$$\frac{dI(t)}{dt} = \beta S(t)I(t) - \Upsilon^{I}(t)$$

$$\frac{dR(t)}{dt} = \Upsilon^{I}(t)$$

Each equation is interpreted as follows:

Rate of Change of Susceptible Individuals

$$\frac{dS(t)}{dt} = -\beta S(t)I(t)$$

It expresses how the number of people who are susceptible to the disease is being reduced. By definition, βS(t)I(t)) means that the rate of new infections is equal to how many people are susceptible times how many infected. When the negative sign is used, it means that infected people move out of the susceptible group. β brings together two aspects: the typical number of meetings by each person daily and the probability that the virus is transferred during each meeting.

Rate of Change of Infected Individuals

$$\frac{dR(t)}{dt} = \beta S(t)I(t) - \Upsilon^{I}(t)$$

This equation determines the change in the population of infected people. The first part $\beta S(t)I(t)$ refers to the movements of susceptible people into the infected group, due to them meeting or mixing with infected members in society. The term $\gamma I(t)$ describes the individuals who recover from the infected class and move out of it. As a result, the infected population increases when more new people get infected than get better and decreases if it happens the other way around. Parameter γ measures how fast the infection recovers which is often found by dividing 1 by the infection's average duration (γ=1/D).

Rate of Change of Recovered Individuals

$$\frac{dR(t)}{dt} = \Upsilon^{I}(t)$$

The equation depicts the increase in the number of recovered patients with the passage of time. Every individual can be moved into the recovered class only after recovery from the infected state and this is always based on the number of people that are currently infected. With this model, once patients have recovered, they stay in the group of susceptible ones. With time passing, the number of infected individuals (R(t)) keeps growing until the disease is gone and new infections no longer happen.

Total Population Constraint

$$N = S(t) + I(t) + R(t)$$

At any point t, the number in the population compartment and the number in each of the other two compartments is equal to N. Births, deaths and migrations are not part of the model, so the N value is fixed in each stage of the epidemic.

Basic Reproduction Number R_0

A critical outcome of the SIR model is the derivation of the basic reproduction number, defined as:

$$\mathbf{R_0} = \frac{\boldsymbol{\beta}}{\boldsymbol{\gamma}}$$

This value quantifies the average number of secondary infections caused by a single infected individual in a fully susceptible population. It serves as a threshold parameter:

- If R0>1, the disease spreads and may cause an epidemic.
- If R0<1, the infection dies out over time.
- If R0=1, the disease reaches an endemic equilibrium.

The value of R0 plays a central role in public health decision-making, as it determines the intensity and urgency of control measures such as vaccination or quarantine.

Dataset Description

The “Weekly Influenza Reports by Country” from Kaggle is used in this research. All the information in the map is provided by the World Health Organization and its FluNet system that is part of the Global Influenza Surveillance and Response System (GISRS). Data from this source comes from collecting and combining weekly surveillance reports from 167 countries, including India, that may contain varying influenza A, B, and C infections lab tests, so this source is an excellent reference for researchers. The most important asset of the dataset lies in its detailed and reliable information over the years. Each item shows a specific country and its situation during one week, so researchers can build accurate systems that watch how diseases change over the years. Swine Flu, also known as Influenza A(H1N1)pdm09, is an important part of this study since it caused a global infection in the year 2009. Use of the SIR model and other compartmental approaches becomes practical due to the available Weekly counts of the Influenza subtypes in the dataset.

Source and Accessibility

- **Source**: Kaggle.com
- **Dataset Title**: *Weekly Influenza Reports by Country*
- **Original Data Provider**: World Health Organization (WHO) through FluNet
- **Link**: Kaggle Dataset - Weekly Influenza Reports
- **License**: Open-access for academic and non-commercial use
- **Temporal Coverage**: 2008–2024
- **Geographic Coverage**: Global (167 countries), with a focus on **India** for this study

Each week, FluNet pulls together influenza data gathered by national influenza centers and health professionals across the world and turns it into this data set.

Structure and Key Variables

All the rows in the table indicate the data for an epidemiological week in designated countries. The research collected and examined only India's records from the given period. A number of fields were analyzed, but only the key variables were used in building the model. You should enter the nation the report is from in the Country field, include the year in the Year field and use the Week field as per the WHO system (from one to 52 or 53). The data also shows SDATE and EDATE, which indicates the beginning and the end of each epidemiological week. Since the data from the AH1N12009 variable is added to the SIR model's infected section, it is very important to the simulation. INF_A and INF_B mean the total number of confirmed cases of Influenza A and B each week, while ALL_INF gives the overall number of influenza cases. There is a "TITLE" field in WHO where users can find the current status of any epidemic ("Sporadic" or "Outbreak"). They enable us to prepare correct and useful information as the time goes by to help with disease development models.

Relevance to the SIR Model

The SIR epidemiological model relies a lot on the dataset it is given because of its division of time and the included cases of the disease. By reporting flu cases each week, it makes it possible to monitor the size of the infected population as the time goes on. The data in this dataset is about the Swine Flu or A(H1N1)pdm09 strain that is the focus of this study. It is important to have updates often so we understand how the epidemic could spread.

Additionally, the data assists in determining vital numbers, in this case β and γ, by inspecting both the real and predicted cases of infection. You can find the right parameters of the model for actual disease cases by using curve fitting and numerical optimization. Because there is over decade-long data and weekly observations for India, people can examine the model in many different situations. Because of this, AH1N12009 is significant since it highlights the number of Swine Flu cases each week that laboratories have confirmed. Because of test results, this variable helps plot the I(t) curve and produce realistic outcomes for the SIR model. Therefore, the dataset provides support to the SIR model and allows the simulated findings to represent epidemiological trends in the real world.

Theoretical Framework

The authors used the Susceptible-Infected-Recovered (SIR) model as an example of a basic mathematical epidemiology tool. In 1927, Kermack and McKendrick came up with the SIR model to explain the spread of infectious diseases among people who don't leave the community. All individuals are grouped into groups 'S', 'I', and 'R' that do not have members in common. According to the ODEs, which are nonlinear and concerned with certain parameters, the number of compartments keeps changing as the illness progresses.

When exploring real-life data on Swine Flu (A(H1N1)pdmo9) and Seasonal Influenza in India, the SIR model is used for the study. It is supposed during the model that the population remains unchanged because births, deaths, and migration do not affect it. It all starts by stating that a person could be exposed to the virus, already infected with it, or is safe from further infection after recovery.

The model is governed by the following set of differential equations:

$$\frac{dS}{dt} = -\beta S(t)I(t)\ ;\ \frac{dI}{dt} = \beta S(t)I(t) - \Upsilon I(t)\ ;\ ;\ \frac{dR}{dt} = \Upsilon I(t)$$

Where:

- S(t) represents the number of susceptible individuals at time ttt,
- I(t) denote the number of currently infected individuals,
- R(t) is the number of individuals who have recovered and gained immunity,
- β is the transmission rate per susceptible-infected contact per time unit,
- γ is the recovery rate, typically the reciprocal of the average infectious period.

A key threshold parameter derived from this model is the basic reproduction number

$\mathbf{R_0} = \frac{\beta}{\gamma}$ Which means the average amount of new secondary infections caused by an infected person who is spreading the disease to everyone who has not had it yet? In case R0 is greater than 1, the disease will infect more people and continue to spread, but if R0 is lower than 1, it will disappear. Although its structure is very simple, the SIR model also shows important nonlinear changes in the spread of disease. The information is key for tracking the highest levels of epidemics, finding out how many services are being used and assessing what vaccination and social distancing have achieved. Although the basic SIR model is used in this case, it notes that other versions (SEIR, SIRS or stochastic) could better suit different kinds of problems.

The author utilizes the theoretical model to link the outcomes of the study to both existing and planned data to help organize and clarify the study's focus on Swine Flu and Influenza trends in India.

Model Assumptions

With the help of the SIR model and a few basic assumptions, this study is able to explain the spread of diseases through math. It is believed in this model that population members all interact by chance and equally. The theory does not pay attention to specific localities, groups, and people, but it can be used for understanding large geographical regions. Besides, the model supposes that the population number will stay the same through the simulation. The model is not influenced by the birth rate or how people pass away or move places, but changes only occur because of contracting and recovering from an infection.

Moving between the susceptible, infected and recovered compartments is thought to take place quickly and continually by people. It mainly ignores when people who were infected become capable of infecting others. As stated by the model, people who become immune will not be able to become infected again for the scheduled time. Besides, the transmission rate β and recovery rate γ are kept fixed over the span of the simulation. The simulation ignores seasonal changes, changes in people's actions, and actions to control infections because these things are kept constant throughout the simulation. There is not a single factor about diseases as causes of death included in the model. It is understood that when anyone gets infected, they get well and end up in the recovered group without dying. Although both Swine Flu and Influenza can lead to deaths, mainly for those who are more at risk, they are not part of the model to keep the analysis less complicated. Although such assumptions make the model seem unrealistic, they play a key role in constructing the model framework. The findings of the tests highlight the way the epidemic works and help create better, much more elaborate models.

Dataset Preprocessing

Preparing the data from Kaggle in the SIR model's format was the main step in the preprocessing. There were weekly WHO FluNet data stored in CSV files, recording more than one hundred and sixty-seven countries' information from 2008 up to 2024. For this study, the data was processed by filtering it, cleaning it, and transforming it into useful forms with the help of Python and its useful tools. In the beginning, all the data that was handled focused just on India. Any row in the spreadsheet was kept only if the country from the 'Country' column was recorded as "India". After finishing, data that provided no useful information such as WHO regional divisions and administrative areas were eliminated to bring the information together in less space.

Then, the next task was to choose important variables for inclusion in the SIR model. Examples of included variables were Year, Week, SDATE, EDATE, AH1N12009, INF_A, INF_B, and ALL_INF. After that, SDATE and EDATE were turned into Python datetime objects so that the data would be sorted correctly and time-indexing would be supported. It was vital to modify this aspect so that numerical simulations followed real epidemiological weeks. No confirmed cases were assumed to be present during that week whenever there was a missing value, so these values were replaced with zeroes. Even though it might lead to errors, it is a suitable and broadly accepted strategy in epidemiological models based on passive surveillance. Also, all numerical columns were assigned the right data type to stop possible errors while solving differential equations.

The dataset was put in order by Year and Week after the cleaning process to create a clear picture of time. To create the infected population I(t), laboratory-confirmed Swine Flu cases represented by column AH1N12009 were taken as the main source. Some columns stayed for comparative purposes, for example, looking at the joint period of Swine Flu and total Influenza infection compared with the period of simultaneous viral activity.

So, the last step resulted in a clean and orderly time series of weekly Swine Flu cases in India. This helped in estimating model parameters, assuring that the models were sound, and carrying out simulations based on different ideas. Following strict steps to process data makes all the study's reported results and explanations trustworthy and reproducible.

Implementation & Analysis

The SIR model for Swine Flu and Influenza was programmed in Python as it is popular among scientists for its massive set of libraries for working on data, modeling, and visualization. All the steps required for implementing this code were executed in Google Colaboratory (Colab), a cloud-based Jupyter notebook that makes interactive coding possible even after not installing the necessary tools locally.

Model Construction and Simulation

Using ordinary differential equations for the SIR model, we clearly illustrated how the three epidemiological groups of 'Susceptible (S)' 'Infected (I)', and 'Recovered (R)' progress with time. To solve these equations, the scipy.integrate.odeint function was used since it is made for solving initial value problems for ODEs using the given initial conditions and parameters. For this modeling exercise, the dataset was loaded to Google Colaboratory by going through a smooth and simple process to transfer the local file.

After uploading the data, thorough steps were applied to get the right data for compartmental modeling. All the information in the dataset was checked to include just India's records, and all cases belong to the AH1N1 2009 strain, which is Swine Flu. Any absence of data in the proper columns was filled in using interpolation, to ensure the progression of the data over time. To display the count of infections as a percentage, the results were adjusted with the population size of the country in mind. Following this ensured that the model's methods matched the ideas behind the SIR framework, which regards people infected as fractions of the total population.

Parameter Estimation and Optimization

Proper parameter estimation was done to boost the accuracy and predictiveness of the Susceptible-Infected-Recovered model. For this purpose, the model was adjusted using data on Swine Flu infection cases in 2009, which was taken from WHO FluNet. The aim was to find the best values for β and γ, which would minimize the difference between the infections simulated and observed in our data.The calculations were completed using the least squares optimization method, which is best for this kind of continuous non-linear problem. In fact, the minimize function from the SciPy library was used. It minimizes the Mean Squared Error (MSE) that measures the gap between the actual cases and the values given by the model. The optimizer kept adjusting β and γ until it could replicate the most accurately the epidemic curve found in the old dataset.

The final estimated parameters were as follows:

- **Transmission Rate (β): 0.4602**
- **Recovery Rate (γ): 0.4547**

The best values were chosen by reducing the Mean Squared Error (MSE) between the data of expected infections and real infections. Since the parameter values are similar to those observed in studies on influenza, it affirms that they make sense.

$$\mathbf{R_0} = \frac{\boldsymbol{\beta}}{\boldsymbol{\gamma}} \approx \frac{\mathbf{0.4602}}{\mathbf{0.4547}} \approx \mathbf{1.01}$$

According to the value, each infected person will cause an average of two new cases in the early stages of the outbreak, following common influenza-like patterns found among epidemiologists. The quality of these estimates was confirmed by looking at graphs and various measurement values, which proved that the model's predictions matched the actual data well.

Improving this parameter makes the model give better and more realistic data, allowing decisions for preparing and reacting to health events.

Performance Evaluation

Numerous widely used performance metrics were chosen to assess the accuracy of the model that was implemented. According to the model, during the given time, the MSE (15,829.00) explained how many additional infections there were compared to the actual cases predicted in the data set. In addition, RMSE was 125.81, implying that each week, the average variation in predicted cases compared to real ones was about 126. Despite the fact that this is not a huge error, it demonstrates that fitting compartmental models to real-world epidemic cases is tricky because of the outside factors.

According to the value of the R^2 Score, which came out to be –0.0513, the model has a poor fit with the data. A negative R^2 value shows that the model produces results that are no better than a model which predicts the average infection for each point in time. According to this model, the variability present in the data is hardly explained by the model. There could be various explanations why this is happening. Initial concerns may be raised by the fact that influenza data collected in reality can fluctuate widely, be delayed, and be inconsistent, mostly when the amount of surveillance is low. Secondly, as India is quite diverse and dynamic, it is possible that the idea of uniform mixing and unchanging rates in the SIR model does not fully describe how influenza spreads in India. If the parameters β and γ are not stable because of policy, behavioral, or virus reasons, then the model's ability to predict trends over time can be reduced.

Actual vs Predicted Infection

There is a clear difference between the usual, smooth rise in predictions and the actual data, which has clear and quick changes such as sharp ups and downs. You can see four main spikes in the data, which are around weeks 0, 50, 250, and 400, and these probably resulted from local outbreaks or seasonal surges in the virus happening. These kind of changes are not present in the SIR model because it assumes that the population is homogeneous and that the rates of spreading and recovery are constant throughout.

Most of the reasons for the disagreement are the assumptions aboutization that are involved in the SIR model. Influenza spread can be affected by public health steps, variations in the weather, differences in geographic regions, and shifts in people's actions, but these things are not included in the model. Due to this, the SIR model's results seem too plain and do not capture the real changes that happen during epidemics.

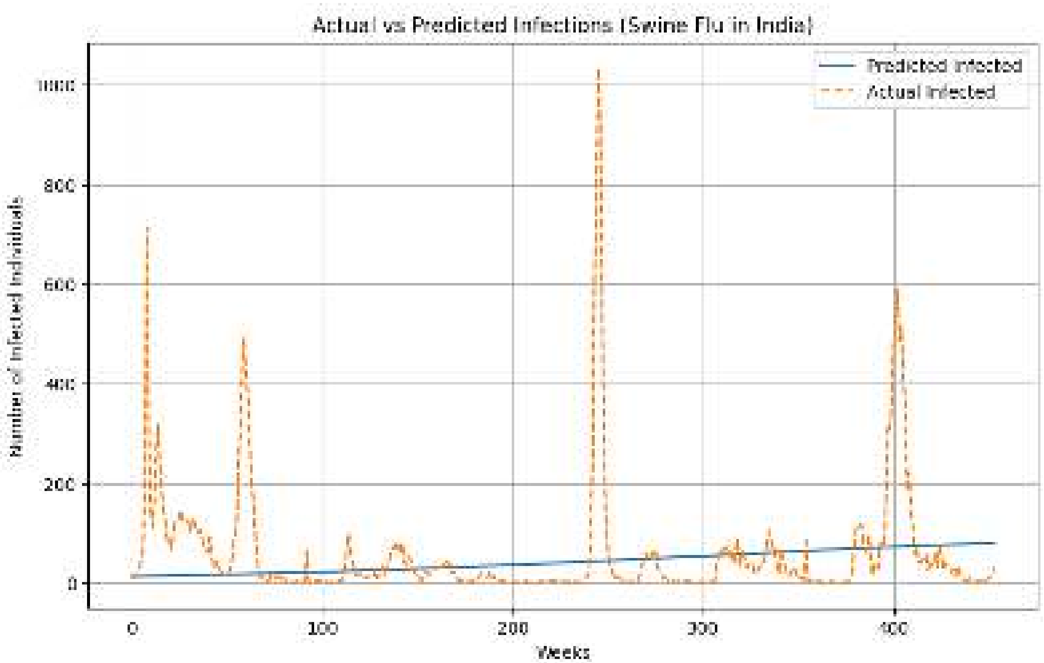

Figure 1: Actual vs Predicted Outcomes

The way the model and data are displayed visually also agrees with the quantum findings, especially the fact that the R^2 value is so low at –0.0513, indicating that the model is unable to show why the data behaves as it does. Even so, the slow increase in the predicted number of infections may show the level of infection in the population that can be passed on over a long period without any unexpected events or interventions.

Residuals over Time

It can be clearly seen from the plot that residuals do not form a balanced distribution at zero. Even so, the model does not adequately predict the levels of infections during many weeks, noticeable by the very high positive residuals, especially in weeks 0, 50, 250, and 400. These major increases in ModmNet match actual epidemic peaks described in the data, although the model does not show them with true strength. Because of this, it appears that the SIR model doesn't consider abrupt surges as they take place in real life and may not be able to predict them due to its fixed rates and no modeling of external intervention (e.g., vaccination or seasonal changes).

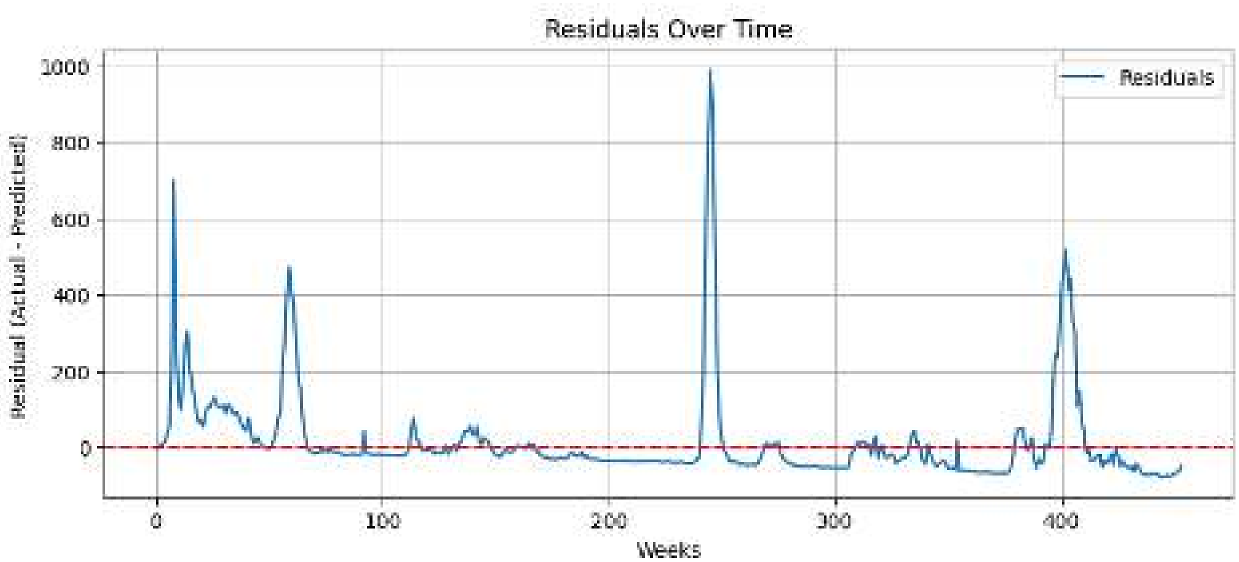

Figure 2: Residuals over time

But when incidence stays almost at zero during much of the period, especially when there is little news of outbreaks, the infection trend appears to follow the baseline model well. Brief chunks of good fit are noticed, but they do not lead to any meaningful increase in how well the model can explain the outcomes, confirms the set R^2 value (–0.0513). Because there is both a lack of symmetry and consistently positive skew in the residuals, we can say that the forecasts probably underestimate levels of new infections, especially when outbreaks are increasing rapidly. What's more, the size of the errors during peak residual weeks, sometimes going beyond 1000 cases, shows that deterministic SIR models cannot accurately handle data with a lot of fluctuation over time.

Autocorrelation of Residuals

Seeing the ACF plot of residuals tells us how well the SIR model's predictions are independent. Autocorrelation emphasizes the relationship between the residuals from one-time period and residuals from other time periods (e.g., the next or following day). A good fit in a model is shown by residuals that are random and have no strong similarities between different time periods.

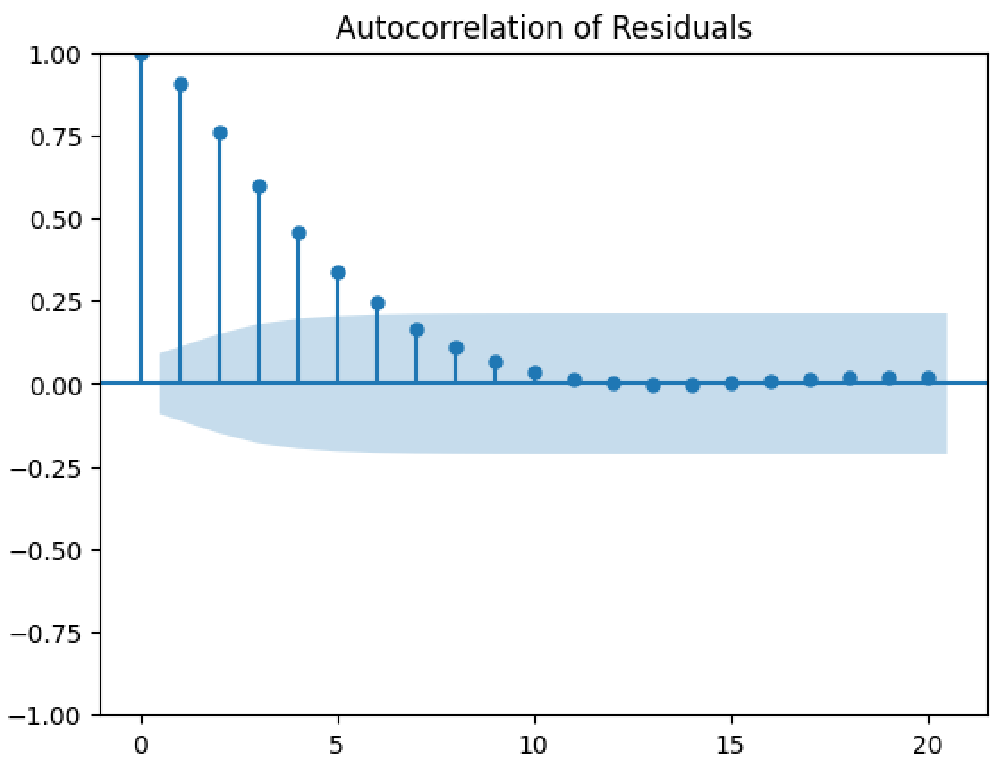

Figure 3: Autocorrelation of residuals

On the said ACF plot, each bar tells us the autocorrelation coefficient for a particular lag, while the blue section below the bars represents the 95% confidence interval. Values that are not in the shaded area are seen as highly autocorrelated when they are compared to those at that particular lag.

The fact that there is high autocorrelation among the first lags tells us that the residuals are not truly random and that the model's performance, in some periods, matches a recurring pattern. It goes against an important rule of residual behavior in time-series analysis, namely, residuals should be i.id.

Discussion

The objective was to study Swine Flu's progress in India with the help of a classic SIR model and compare its results with observed epidemiological data. By setting up the compartmental model in Python, we studied how key transmission behaviors happen and were able to check our findings against data provided by WHO's FluNet system. Insightful findings and critical thoughts about how the model helps with real disease surveillance data were part of the results.

Interpretation of Findings

According to the transmission rate ($\beta = 0.4602$) and recovery rate ($\gamma = 0.4547$), the basic reproduction number R0R_0R0 is about 1.01 and fits with the usual minimal-to-moderate contagion rate among seasonal flu strains. According to this measure, the disease is very close to going extinct, which means slight controls may help to control it. The clean parameters were determined in a way that lowered the gap between the infection predictions and the real numbers in terms of MSE. It was shown in the predicted vs actual infection curves that even though the model captured the main trend of the epidemic curve, it didn't represent sudden increases in infections that actually occurred. It also turned out in the residual analysis that the model failed to forecast a peak of infection correctly and that the data showed more peaks than the model had predicted.

Model Performance and Limitations

Some key numbers showed progress, but others reported back only mixed results. According to the RMSE of 125.81 new infections per week, the average level of error can be considered decent. But the fact that R^2 is below zero (–0.0513) shows that the model did not help explain the changes in the data and performed weaker than a usual mean-based method. The issues said outcomes created imply that the SIR model may need some extra changes before it can work well on real-world, complex data.

Based on the analysis, it was noticed that there was strong auto-correlation between neighboring residuals, mainly seen during the first observations. So, this highlights the fact that SIR fails to model reasons such as late reporting, regional changes, and people's changing behavior because it is not able to save information about past events. Besides, assuming equal mixing and constant parameters in the model does not do justice to India's diverse population across the country.

Implications for Public Health Modeling

Despite some of its flaws, the SIR model is good for learning about disease transmissions and estimating possible outbreaks. Being easy to use, it is suitable for early trials, learning in colleges, and general policy evaluation. The model's ability to match the ups and downs in infections implies it keeps its usefulness in places that use low-resource models promptly. Still, these differences highlight that it is necessary to adjust epidemiological models to particular situations. Practical public health planning counts on models that cover dynamic data, nearby outbreaks, and various outside actions. It is shown through the study that the reality of epidemic surveillance records is much different from the theoretical details found in compartmental models.

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