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## EPIDEMIC INTELLIGENCE MODELS IN AIR TRAFFIC NETWORKS FOR UNDERSTANDING THE DYNAMICS IN DISEASE SPREAD - A CASE STUDY

Anbalagan Bhuvanewari

Vellore Institute of Technology,  
Chennai, India

[bhuvanewari.a@vit.ac.in](mailto:bhuvanewari.a@vit.ac.in)

### ABSTRACT

Aim/Purpose	The understanding of disease spread dynamics in the context of air travel is crucial for effective disease detection and epidemic intelligence. The Susceptible-Exposed-Infectious-Recovered-Hospitalized-Critical-Deaths (SEIR-HCD) model proposed in this research work is identified as a valuable tool for capturing the complex dynamics of disease transmission, healthcare demands, and mortality rates during epidemics.
Background	The spread of viral diseases is a major problem for public health services all over the world. Understanding how diseases spread is important in order to take the right steps to stop them. In epidemiology, the SIS, SIR, and SEIR models have been used to mimic and study how diseases spread in groups of people.
Methodology	This research focuses on the integration of air traffic network data into the SEIR-HCD model to enhance the understanding of disease spread in air travel settings. By incorporating air traffic data, the model considers the role of travel patterns and connectivity in disease dissemination, enabling the identification of high-risk routes, airports, and regions.
Contribution	This research contributes to the field of epidemiology by enhancing our understanding of disease spread dynamics through the application of the SIS, SIR, and SEIR-HCD models. The findings provide insights into the factors influencing disease transmission, allowing for the development of effective strategies for disease control and prevention.
Findings	The interplay between local outbreaks and global disease dissemination through air travel is empirically explored. The model can be further used for the evaluation of the effectiveness of surveillance and early detection measures at airports and transportation hubs. The proposed research contributes to proactive and

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	evidence-based strategies for disease prevention and control, offering insights into the impact of air travel on disease transmission and supporting public health interventions in air traffic networks.
Recommendations for Practitioners	Government intervention can be studied during difficult times which plays as a moderating variable that can enhance or hinder the efficacy of epidemic intelligence efforts within air traffic networks. Expert collaboration from various fields, including epidemiology, aviation, data science, and public health with an interdisciplinary approach can provide a more comprehensive understanding of the disease spread dynamics in air traffic networks.
Recommendations for Researchers	Researchers can collaborate with international health organizations and authorities to share their research findings and contribute to a global understanding of disease spread in air traffic networks.
Impact on Society	This research has significant implications for society. By providing a deeper understanding of disease spread dynamics, it enables policymakers, public health officials, and practitioners to make informed decisions to mitigate disease outbreaks. The recommendations derived from this research can aid in the development of effective strategies to control and prevent the spread of infectious diseases, ultimately leading to improved public health outcomes and reduced societal disruptions.
Future Research	Practitioners of the research can contribute more effectively to disease outbreaks within the context of air traffic networks, ultimately helping to protect public health and global travel. By considering air traffic patterns, the SEIR-HCD model contributes to more accurate modeling and prediction of disease outbreaks, aiding in the development of proactive and evidence-based strategies to manage and mitigate the impact of infectious diseases in the context of air travel.
Keywords	epidemiology, SIS-SIR model, SEIR-HCD models, disease dynamics, air traffic networks, disease transmission

## INTRODUCTION

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Air traffic plays a crucial role in facilitating the rapid spread of infectious diseases across different regions. The interconnectedness of air traffic networks creates pathways for the dissemination of pathogens, posing significant challenges to public health authorities and policymakers. Understanding the dynamics of disease spread in air travel settings is therefore essential for effective disease control and mitigation strategies. The SEIR-HCD model, when coupled with air traffic network data, allows researchers to analyze the impact of travel patterns and connectivity on disease transmission. By considering the flow of individuals through air travel networks, the model provides insights into the risk of disease dissemination, identifying high-risk routes, airports, or regions that contribute significantly to disease spread. Air travel has helped spread infectious illnesses worldwide in recent years. Walters et al. (2018) discussed disease monitoring, management, prevention, and knowledge of air traffic network disease dynamics. Mathematical models, such as the Epidemic Intelligence SIS, SIR, and SEIR models, are useful for studying disease transmission dynamics in complex networks. This study uses Epidemic Intelligence SIS, SIR, and SEIR models to analyze illness propagation in air traffic networks. This study examines connection patterns, passenger movement, and travel behavior to determine disease transmission variables and establish effective control and preventive techniques. In recent years, the integration of epidemic intelligence models with air traffic network data has gained significant attention in understanding the dynamics of disease spread. One such model, the

Susceptible-Exposed-Infectious-Recovered-Hospitalized-Critical-Deaths (SEIR-HCD) model, offers a comprehensive framework for disease detection and epidemic intelligence research in the context of air travel. This model extends the classic SEIR model by incorporating additional hospitalization, critical care, and deaths, providing a more realistic representation of disease transmission, healthcare demands, and mortality rates.

Government interventions play a crucial role in managing disease spread in air traffic networks and ensuring public health and safety. Governments may impose travel restrictions or bans on specific routes or countries that are experiencing disease outbreaks. These restrictions can include suspending flights to and from affected regions. Some countries may require proof of vaccination against specific diseases before granting entry or exit, such as the yellow fever vaccine requirement for travel to certain regions. Governments conduct public awareness campaigns to educate travelers about health and safety measures, including proper hand hygiene, mask-wearing, and social distancing. Governments may require travelers to undergo mandatory testing before or upon arrival. Negative test results may be a prerequisite for entry. It is possible to implement contact tracing measures to identify and notify individuals who may have been exposed to a confirmed case. This helps in isolating potential carriers of the disease. Developing and implementing comprehensive emergency response plans for airports and airlines to manage disease outbreaks effectively. Enhanced health screening procedures at airports, including temperature checks and health questionnaires, can be used to identify potentially infected travelers. These government interventions and health and safety protocols are vital for controlling the spread of diseases in air traffic networks and mitigating the impact of outbreaks on public health. The specific measures taken can vary depending on the nature of the disease, its transmission characteristics, and the level of risk associated with travel.

Quarantine measures may be enforced for travelers coming from high-risk areas or those displaying symptoms of infectious diseases. Isolation protocols are in place for confirmed cases. Governments may require travelers to undergo mandatory testing before or upon arrival. Negative test results may be a prerequisite for entry. It is possible to implement contact tracing measures to identify and notify individuals who may have been exposed to a confirmed case. This helps in isolating potential carriers of the disease. Enhanced health screening procedures at airports, including temperature checks and health questionnaires, can be used to identify potentially infected travelers. Travelers may be required to complete health declaration forms or provide information about their recent travel history to assess their potential exposure to diseases. Some countries may require proof of vaccination against specific diseases before granting entry or exit, such as the yellow fever vaccine requirement for travel to certain regions. Governments conduct public awareness campaigns to educate travelers about health and safety measures, including proper hand hygiene, mask-wearing, and social distancing. Airports and airlines are often required to implement strict cleaning and sanitization protocols to reduce the risk of surface transmission of infectious agents.

This information is invaluable for designing targeted interventions, implementing travel restrictions, and optimizing screening measures at airports. Jiang et al. (2023), as well as Pastor-Satorras and Vespignani (2002), identified the SIS model when applied to air traffic networks that allow individuals to transition between susceptible and infectious states multiple times, reflecting the continuous exposure and recovery patterns observed in real-world scenarios. This model enables the investigation of the potential for recurrent outbreaks within air travel networks. The SIR model extends the SIS model by incorporating 'recovered,' representing individuals who have gained immunity after recovery from the disease. This model is applicable to diseases that confer long-term immunity and can help assess the impact of recovered individuals on disease spread within air traffic networks. 'Exposed' represents infected but non-infectious people in the SEIR paradigm. Başpınar et al. (2023) proposed a model that allows for illness incubation, improving disease propagation dynamics in air traffic networks. Choi et al. (2022) study attempts to improve epidemiology by understanding disease propagation dynamics in air traffic networks using these models. The data will illuminate disease transmission variables such as airline connection, passenger numbers, travel limitations, and control

methods. Guevara et al. (2023) studied the understanding, which may help design focused measures to reduce disease transmission inside these networks and limit airborne illness spread.

The remainder of this research paper is organized as follows. The next section provides a comprehensive review of relevant literature on disease modeling in air traffic networks and the applications of SIS, SIR, and SEIR models in this context. Next, the state-of-the-art techniques employed in this research are described, including data collection, model calibration, and simulation experiments. The findings and analysis of the research are then presented, highlighting key factors that influence disease spread dynamics within air traffic networks. The final section presents the conclusion on the potential impact of this research on society and outlines areas for future research.

## LITERATURE SURVEY

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In this case study, we delve into the synergy between epidemic intelligence models and air traffic networks to better understand the intricacies of disease spread, using a specific case study as an example. The research investigates how air travel patterns can facilitate or hinder the transmission of diseases, providing valuable insights that can inform public health policies, disease control strategies, and air travel regulations. This study highlights the importance of interdisciplinary approaches in addressing global health challenges and the need for continuous monitoring and analysis of disease dynamics in an increasingly interconnected world. Air Traffic Networks for Understanding the Dynamics in Disease Spread (SIS, SIR, SEIR) focus on analyzing the spread of infectious diseases within the context of air travel. The literature survey details the models and provides insights into the dynamics of disease transmission, the impact of air traffic networks on disease spread, and the effectiveness of control measures. The review paper by M. Zhang et al. (2022) provides an overview of various modeling approaches used to study the spread of infectious diseases in air traffic networks. It discusses the application of SIS, SIR, and SEIR models in understanding disease dynamics within these networks and highlights the importance of considering network topology and passenger mobility patterns.

The study by Pastor-Satorras and Vespignani (2002) investigates the dynamics of disease spread within finite-size scale-free air transportation networks. It explores the impact of network structure on epidemic processes and compares the performance of SIS, SIR, and SEIR models in capturing the observed dynamics. The findings emphasize the importance of considering the heterogeneity of the network and the potential for recurrent outbreaks. This research focuses on modeling disease spread in the airport network, taking into account human mobility and social behavior. It investigates the effects of different control measures, such as quarantine and travel restrictions, on disease transmission. The study utilizes the SIS, SIR, and SEIR models to analyze the impact of network structure and control strategies on the spread of infectious diseases.

Khan et al. (2014) analyzed historical data on airline travelers departing areas of the Caribbean and South America, where locally acquired cases of chikungunya have been confirmed as of May 12th, 2014. The final destinations of travelers departing these areas between May and July 2012 were determined and overlaid on maps of the reported distribution of *Aedes aegypti* and *albopictus* mosquitoes in the United States, to identify potential areas at risk of autochthonous transmission. Mou et al. (2017) investigated the impact of air transportation networks on the spread of infectious diseases. It utilizes the SEIR model to analyze the influence of network structure, passenger volume, and control measures on disease transmission dynamics. The findings highlight the significance of targeted interventions and the potential for reducing disease spread through network-based strategies.

Li et al. (2021) discussed the optimization of epidemic control measures in airports through real-time spatial surveillance and contact tracing. It employs the SIR model to simulate disease spread and evaluates the effectiveness of different surveillance and intervention strategies. Engebretsen et al. (2023) emphasize the importance of early detection, rapid response, and targeted interventions in controlling disease outbreaks. Meloni et al. (2011) provide an overview of various modeling approaches used

to study the spread of infectious diseases in air traffic networks. They discuss the application of SIS, SIR, and SEIR models in understanding disease dynamics within these networks and highlight the importance of considering network topology and passenger mobility patterns. Ding et al. (2021) and Loske (2020) investigated the dynamics of disease spread within finite-size scale-free air transportation networks. They explored the impact of network structure on epidemic processes and compared the performance of SIS, SIR, and SEIR models in capturing the observed dynamics. The findings emphasize the importance of considering the heterogeneity of the network and the potential for recurrent outbreaks.

This research by Huber et al. (2021) focuses on modeling disease spread in the airport network, taking into account human mobility and social behavior. They investigated the effects of different control measures, such as quarantine and travel restrictions, on disease transmission. Their study utilizes the SIS, SIR, and SEIR models to analyze the impact of network structure and control strategies on the spread of infectious diseases. Boguá et al. (2003) analyze the spread of diseases in air transportation networks using real-world data. Their study explores the role of network topology and connectivity in disease transmission dynamics. The research employs the SIR model to simulate and study epidemic spreading, providing. The study by Brockmann and Helbing (2013) examines the impact of air travel on the spread of infectious diseases using mathematical models. It compares the SIS and SIR models in analyzing disease transmission within air traffic networks. The research highlights the importance of incorporating travel patterns and network connectivity in understanding the dynamics of disease spread. Colizza et al. (2007) focus on epidemic spreading in complex networks, including air traffic networks. They explore the effects of degree correlations in the network on disease dynamics. The study utilizes the SIS and SIR models to analyze the impact of network structure on the spread of infectious diseases and highlights the role of network hubs and connectivity in disease transmission.

Guimera et al. (2005) investigated the global spread of pandemic influenza and the effectiveness of containment interventions, such as travel restrictions and quarantine measures. They utilize a hybrid SIR and SEIR model to simulate disease transmission within air traffic networks. The study provides insights into the potential impact of various control strategies on mitigating the spread of infectious diseases. The study by Hufnagel et al. (2004) focuses on epidemic modeling in meta-population systems, including air traffic networks. The study explores the dynamics of disease spread across interconnected populations and analyzes the impact of network topology on epidemic processes. The research utilizes the SIS, SIR, and SEIR models to examine the effects of different coupling patterns on disease transmission. Khan et al. (2014) examined the impact of international air travel on the global spread of dengue fever. It utilizes a hybrid SIR and SEIR model to simulate disease transmission within air traffic networks. Sousa and Barata (2021) analyzed the role of different factors, including air travel patterns, population sizes, and vector characteristics, in the spread of dengue and highlighted the importance of surveillance and control measures. Overall, these studies demonstrate the application of SIS, SIR, and SEIR models in understanding disease spread dynamics within air traffic networks. They highlight the influence of network topology, passenger mobility, control measures, and intervention strategies on the transmission of infectious diseases. By incorporating real-world data and considering the unique characteristics of air traffic networks, these models provide valuable insights for policymakers, public health officials, and aviation authorities in developing effective strategies to mitigate the impact of diseases on public health and air travel.

Government intervention during difficult times acts as a moderating variable that can enhance or hinder the efficacy of epidemic intelligence efforts within air traffic networks. Different diseases have varying transmission rates, incubation periods, and modes of spread. The process of creating a generalized model is challenging. Real-world epidemiological data can be scarce, making it difficult to validate models and predictions effectively. Collaborative efforts between governments, aviation industry stakeholders, and public health organizations are essential to achieving a well-coordinated and effective response to disease outbreaks in the context of air travel. Government intervention often

includes the establishment of regulations and guidelines for airlines, airports, and travelers. These regulations can dictate requirements for health screenings, vaccination, quarantine, and reporting procedures. Compliance with these regulations is essential for epidemic intelligence because it helps in the early detection of potential disease carriers and the implementation of preventive measures. Governments can mandate airlines and relevant agencies to share critical data, such as passenger manifests, travel itineraries, and health-related information. Government intervention can facilitate the smooth flow of information, which is vital for intelligence and monitoring efforts to track and respond to potential outbreaks. Government intervention extends to international collaboration with other nations and organizations. This includes sharing information, and resources, and coordinating responses to epidemics that transcend national borders are studied. Government intervention may be influenced by political considerations, economic interests, and lobbying. These factors can sometimes lead to suboptimal or delayed responses to disease outbreaks, as shown in Table 1.

**Table 1. List of associated challenges**

No.	Challenges	Associated Parameters
1	Data Challenges	<ul style="list-style-type: none"> <li>• Limited Data Sharing</li> <li>• Data Quality</li> </ul>
2	Network Modeling Challenges	<ul style="list-style-type: none"> <li>• Disease Variability</li> <li>• Lack of Ground Truth</li> </ul>
3	Disease Modeling Challenges	<ul style="list-style-type: none"> <li>• Disease Variability</li> <li>• Lack of Ground Truth</li> </ul>
4	Government Intervention Challenges	<ul style="list-style-type: none"> <li>• Policy Variability</li> <li>• Political and Economic Considerations</li> </ul>
5	Communication and Coordination Challenges	<ul style="list-style-type: none"> <li>• Information Flow</li> <li>• International Collaboration</li> </ul>
6	Resource and Capacity Challenge	<ul style="list-style-type: none"> <li>• Resource Allocation</li> <li>• Healthcare Infrastructure</li> </ul>
7	Ethical and Privacy Challenges	<ul style="list-style-type: none"> <li>• Data Privacy</li> <li>• Ethical Considerations</li> </ul>
8	Timeliness Challenges	<ul style="list-style-type: none"> <li>• Rapid Response</li> <li>• Integration of Multiple Data Sources:</li> <li>• Uncertainty and Model Validation</li> </ul>

In summary, existing works in the field of epidemic intelligence in air traffic networks face a range of challenges related to data, network and disease modeling, government intervention, communication and coordination, resource and capacity limitations, ethical and privacy considerations, timeliness, data integration, and model validation. Addressing these challenges is crucial for improving the effectiveness of epidemic intelligence and response efforts within the context of air travel networks.

## **STATE-OF-THE-ART TECHNIQUES**

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### ***AGENT-BASED MODELING***

Agent-Based Modeling (ABM) is a powerful technique by W. Wang et al. (2011) and used in the study of disease spread within air traffic networks. ABM allows for the representation of individual agents, such as passengers or airports, with specific characteristics and behaviors. This approach enables the simulation of realistic interactions and mobility patterns, capturing the dynamics of disease transmission more accurately than traditional models.

### ***NETWORK THEORY AND COMPLEX NETWORK ANALYSIS***

Network theory and complex network analysis techniques by X. Wang et al. (2015) have been extensively employed to understand the structure and characteristics of air traffic networks. These techniques enable the identification of key airports, routes, and hubs that play crucial roles in disease spread. By analyzing network connectivity, centrality measures, and community structures, researchers gain insights into the pathways and potential hotspots for disease transmission within these networks.

### ***DATA-DRIVEN APPROACHES AND MACHINE LEARNING***

Advancements in data availability and computational power have enabled the use of data-driven approaches, including machine learning techniques, in the analysis of disease spread within air traffic networks. By leveraging the large-scale approaches proposed by Wu et al. (2011) using data on passenger flows, travel patterns, and historical disease outbreaks, these approaches can provide more accurate predictions and a better understanding of the underlying dynamics. Machine learning models can also be trained to identify patterns and correlations between network features and disease transmission, aiding in the development of targeted control strategies.

### ***STOCHASTIC MODELING AND MONTE CARLO SIMULATIONS***

Stochastic modeling techniques, such as stochastic differential equations and Monte Carlo simulations, are employed to capture the inherent uncertainty and randomness in disease spread dynamics within air traffic networks as discussed by Hufnagel et al. (2004). These approaches consider stochastic parameters and random events, allowing for the generation of multiple scenarios and the assessment of the variability and robustness of control strategies. Stochastic modeling provides valuable insights into the potential outcomes and uncertainties associated with disease transmission.

### ***HYBRID MODELS AND INTEGRATION OF MULTIPLE APPROACHES***

To address the complexity of disease spread in air traffic networks, researchers have developed hybrid models that integrate multiple modeling techniques developed by Balcan et al. (2010). These hybrid models combine SIS, SIR, or SEIR with agent-based modeling or network analysis approaches, providing a more comprehensive understanding of disease dynamics. By combining the strengths of different techniques, hybrid models can capture both global network-level effects and local individual-level interactions, resulting in more accurate predictions and insights.

### ***REAL-TIME DATA INTEGRATION AND FORECASTING***

The integration of real-time data, such as flight schedules, passenger itineraries, and health surveillance information, into epidemic intelligence models, has become crucial for effective disease monitoring and control. Real-time data integration allows for more timely and accurate assessments of disease spread, enabling authorities to implement proactive measures promptly given by Chinazzi et al. (2020). Forecasting techniques, such as epidemic prediction models and data assimilation methods, can provide early warning systems and support decision-making in disease control strategies (Khan et al., 2014; Perra et al., 2011). These state-of-the-art techniques – namely W. Wang et al. (2011), Ruan and Wang (2003), Choi et al. (2022), and J. Zhang et al. (2015) – have significantly advanced the understanding of disease spread dynamics within air traffic networks. By incorporating more realistic assumptions, considering network structures, leveraging large-scale data, and integrating multiple approaches, researchers can provide valuable insights for policymakers, public health officials, and aviation authorities to mitigate the impact of infectious diseases and develop effective strategies for disease control and prevention.

## A CASE STUDY – CITY INFECTION SPREAD EVALUATION

The spread of infection within a specific city is typically modeled using a homogeneous Susceptible-Infectious-Recovered/Removed (SIR) model, which is based on a set of assumptions. The model's simplicity is a notable characteristic, but it demonstrates a reasonable ability to approximate the spread of COVID-19 infections. There are multiple factors contributing to this efficiency. The SIS model allows for scenarios where infected individuals do not develop immunity after being infected, resulting in their return to the susceptible population.

One potential modification involves incorporating a latent stage to accommodate individuals who have been infected but are not yet capable of transmitting the infection to others (during the incubation period). The presence of a direct transition from the Susceptible to the Infectious stage, bypassing the Exposed step, is observed in the SEIR model. Due to the absence of a vaccine currently, the implementation of traditional herd immunization strategies for preventing the spread of the disease is not feasible. The SIR model assumes that the entire population of a city is susceptible to the disease unless a strict quarantine is implemented. The extended incubation period, typically around 14 days, combined with the lack of symptoms in most infected individuals, enables the disease to spread without being detected until the first symptomatic cases are identified and tested. The statement is consistent with the original principles of the SIR model.

One of the key strategies we have employed to tackle the fluctuations in infection rates resulting from social distancing and quarantine measures is the implementation of dynamic modeling. The concept is simple: modify the value of  $R$  based on the implementation of preventive measures. We analyzed the preventive measures implemented in a city and their respective timelines as a reference point. In the initial stages, the infection has a high potential for spreading without being easily detected, resulting in a close-to-maximum  $R$ -value. Typically, social distancing measures are implemented after a median incubation period of 14 days, which results in a decrease in the effective reproduction number ( $R$ ) to its average values. Figure 1 shows the air traffic from City A, City B, City C, and City D.

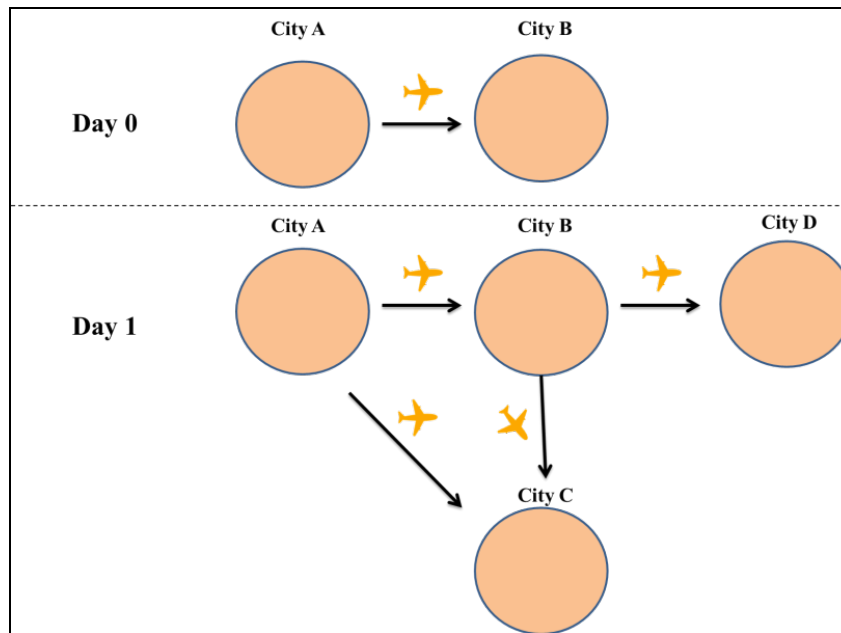


Figure 1. Airlines network connectivity – disease spread schema



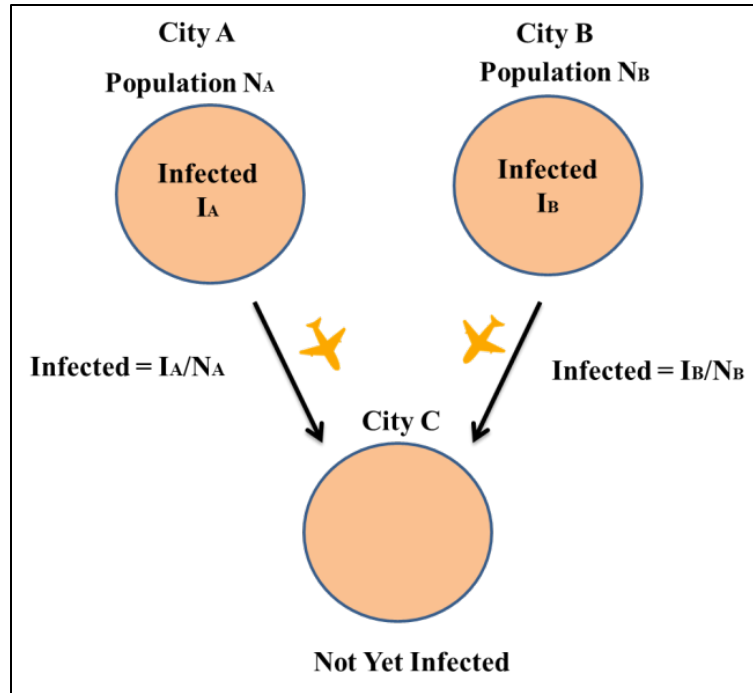


Figure 2. City connectivity – disease spread schema

The disease spread schema in Figure 2 shows the city connectivity and the infected population across the cities. In order to analyze the spread of infection through the airline traffic network, it is necessary to determine the probability of an infected city transmitting the infection to a susceptible neighboring city on any given day. The criteria for considering a city infected is the presence of at least one plane that has landed in the city and is confirmed to be infected. Therefore, it is necessary to determine the probability of the plane originating from the city with infections being infected itself.

$$P(\text{Infected Flight}) = \frac{I}{T}$$

Let us consider the variables “I” and “T” to represent the number of infected individuals in a city and the total population of the city, respectively. Afterward, we can proceed to compute the probability of the city being infected:

$$P(\text{Infected City(new)}) = 1 - P(\text{Incoming places that are healthy})$$

$$P(\text{Infected City(new)}) = 1 - \left[ \left(1 - \frac{I_M}{T_M}\right) F_M * \left(1 - \frac{I_N}{T_N}\right) F_N * \dots \right]$$

where F is the number of flights from the city per day. So, we have to recalculate the chances of infection spreading based on how many people are thought to be sick in each city. This method turned out to be fairly accurate and could “predict” big COVID-19 breakouts, such as in Western Europe or the United States. Finally, for each infected city, we run an SIR model to get the number of infected people for all days of simulation. After a duration of around one month, strict quarantine measures have been implemented, which include travel bans, area lockdowns, and other related actions. The decrease in the R-value leads to its minimum values. Using the Susceptible-Infectious-Recovered/Removed (SIR) model for the city-level spread, and concurrently simulating the transmission of the disease via the air traffic network, are the two broad approaches to infection modelling that are combined in this technique. The approach is based on the combination of these two fundamental tactics.

**Algorithm :****Step 1:** Start the INFECTED\_CITIES array with the city initially**Step 2:** Each day in the simulation\_days variable.**Step 3:** In the table INFECTED\_CITIES, for the city named infected:

- a. Obtain a list of all of the airports in the infected\_city.
- b. Obtain a list of all of the connections for the airports.
- c. In the context of connections, susceptible\_city:
  - Determine the likelihood that susceptible\_city will get infected.
  - If susceptible\_city does become infected, update the list of afflicted cities.
- d. The next day.

**Step 4:** Simulate SI, SIR, SEIR Model

A homogeneous Susceptible-Infectious-Recovered/Removed (SIR) model with numerous assumptions models infection transmission in a metropolis estimates COVID-19 spread well despite its simplicity. Infection begins during incubation. That indicates the Susceptible-to-Infectious transition skips the Exposed stage in the SEIR model. According to the dataset, no vaccine exists, thus herd immunization cannot prevent the disease from spreading. The SIR model implies that all city residents are vulnerable unless quarantined (more on that later). The majority of infected are asymptomatic and the disease spreads unnoticed until first symptomatic infections are found.

***PROPOSED SEIR-HCD MODEL***

The SEIR-HCD (Susceptible-Exposed-Infectious-Recovered-Hospitalized-Critical-Deaths) model is an extension of the basic SEIR model that incorporates the details for hospitalization, critical care, and deaths. The model represents the dynamics of disease transmission, detection, healthcare system demands, and mortality. Here are the equations that define the SEIR-HCD model:

- Susceptible (S):  $dS/dt = -\beta SI$
- Exposed (E):  $dE/dt = \beta SI - \alpha E$
- Infectious (I):  $dI/dt = \alpha E - \gamma I - \omega I$
- Recovered (R):  $dR/dt = \gamma I$
- Hospitalized (H):  $dH/dt = \eta \omega I - \delta H$
- Critical (C):  $dC/dt = \varphi \omega I - \kappa C$
- Deaths (D):  $dD/dt = \delta H + \kappa C$

These equations describe the movement of individuals between distinct S and the corresponding rates of change. During the implementation, we simulated various scenarios, interventions, and policy measures to understand the dynamics of disease transmission by modifying the parameter values, healthcare demands, and mortality within the SEIR-HCD framework. The proposed SEIR-HCD (Susceptible-Exposed-Infectious-Recovered-Hospitalized-Critical-Deaths) models are advanced epidemic intelligence models that incorporate additional to represent disease detection, hospitalization, critical care, and mortality. The list of symbols and abbreviations is in Table 2.

**Table 2. Symbols and abbreviations**

Symbol	Representation
S	Count of Susceptible Individuals
E	Exposed Yet Non-Infectious People
I	Infectious People
R	Recovered Individuals
H	Hospitalized People

Symbol	Representation
C	Individuals in Critical Condition
D	Number of Deaths
$\beta$	Transmission Rate or Contact Rate
$\alpha$	Rate at Which Exposed Individuals Become Infectious
$\gamma$	Recovery Rate
$\omega$	Detection Rate
$\eta$	Hospitalization frequency of infectious patients
$\delta$	Mortality Rate Among Hospitalized Individuals
$\varphi$	Infectious Critical Care Admission Rate
$\kappa$	Mortality Rate
S	Susceptible Individuals
E	Exposed Individuals Who Are Infected But Not Yet Infectious
I	Number Of Infectious Individuals
R	Recovered Individuals Who Have Gained Immunity

The Hospitalized rate determines the rate of people who get hospitalized, which is the chance of disease transmission between a susceptible person and an infected one:

$$H = (1 - MA) * \frac{I}{TI} + \frac{H}{TH}$$

$$C = \frac{CA * H}{TH} - \frac{CR}{TC}$$

where CA represents the average amount of time a patient spends in the hospital before either recovering or becoming critical, TH represents the average amount of time a patient spends in a critical condition (either recovering or dying), CR represents the proportion of severe cases that become critical, and TC represents the fraction of critical cases that end in death:

$$D = \frac{FA * C}{Ct}$$

The secondary spread from an infected person will occur later than it would in a SIR model, which does not account for latency since the latency delays the beginning of the individual's infectious phase. As a consequence, the initial spread of the epidemic will be less rapid if a longer latency time is accounted for. However, because deaths are not accounted for in the model,  $R_0 = 1$  remains constant. The whole progression of the epidemic is documented. After a period of rapid expansion, the disease eventually wiped off the population. Eventually, the virus runs out of hosts, or humans who are immune to it. The overall number of victims is unaffected by the addition of an incubation period.

### ***SUSCEPTIBLE-INFECTIOUS-SUSCEPTIBLE) (SI/SIS) MODEL***

The SI/SIS model is a classic epidemiological model used to understand the dynamics of infectious disease transmission within a population. In the SIS model, individuals can transition between two states: susceptible and infectious. Susceptible individuals can become infected when they come into contact with infectious individuals, while infectious individuals can recover and become susceptible again. The diagram presented below (Figure 3) illustrates the sequential progression of individuals through each stage within the SI/SIS model.

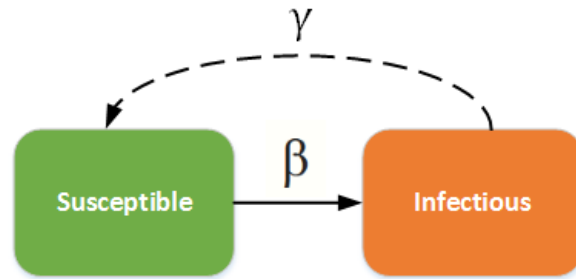


Figure 3. SI Model

The dashed line illustrates the transition of the model into a SIS (Susceptible - Infectious - Susceptible) model, wherein infection does not provide immunity or where immunity diminishes over time. Certain individuals experience recurrent or persistent infections, leading to a return to the susceptible state for previously infected individuals. The SIS model assumes that there is no long-term immunity conferred upon recovery from the disease. This means that individuals who recover from the infection can become susceptible again, perpetuating the cycle of infection within the population. The transition from susceptible to infections and vice versa is governed by parameters such as the infection rate and recovery rate. The SIS model can be mathematically represented by a set of ordinary differential equations. The equations presented in this context serve to depict the temporal dynamics of the susceptible and infectious populations, specifically by quantifying their respective rates of change. Through the process of solving these equations, researchers are able to replicate the propagation of an infectious disease within a given population and examine the intricate dynamics of the epidemic. The parameter  $\beta$  is responsible for regulating the rate of transmission, indicating the likelihood of disease transmission between an individual who is susceptible to the disease and an individual who is already infected. The recovery rate, denoted as  $R$ , is determined by the average duration, represented as  $D$  of the disease. Logistic growth describes SI model I dynamics. Without birth and death, those vulnerable will become diseased.

$$R = \frac{1}{D}$$

The simulation defaults to SEIR. Turning off incubation and putting the infectious time greater than a human lifespan turns it into an SI model:

$$\frac{df(S)}{df(t)} = -\frac{\beta SI}{T}$$

where  $T=S+I$  is identified to be the total population. The SI model can be written as the following ordinary differential equation (ODE):

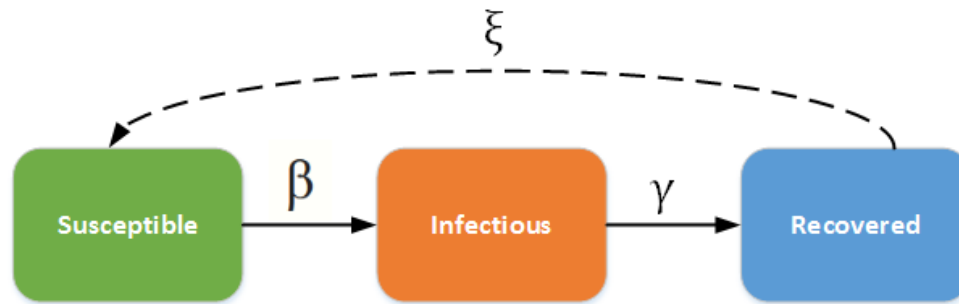
$$\frac{df(I)}{df(t)} = \frac{\beta SI}{T}$$

$$\frac{df(I)}{df(t)} = \beta I \left(1 - \frac{I}{T}\right)$$

where  $T$  is the total population. The SIS model holds significant value in the examination of diseases that do not provide enduring immunity, such as influenza or sexually transmitted infections. This method facilitates the examination of diverse facets of disease transmission, encompassing the assessment of the effects of distinct control measures and interventions.

### ***SIR (SUSCEPTIBLE-INFECTIOUS-RECOVERED) MODEL***

The SIR (Susceptible-Infectious-Recovered) model is a popular epidemiological model that helps explain infectious disease transmission in a community (Figure 4). SIR states are vulnerable, infected, or recovered. The sickness first affects everyone. An infected person may infect a vulnerable person. Infectious people may spread the illness to vulnerable others for a limited time before recovering and developing immunity.



**Figure 4. SIR Model**

The SIR model is based on the assumption that individuals who have recovered from the disease develop long-term immunity, which prevents them from being re-infected and spreading the disease further. The assumption made here is suitable for diseases that provide immunity after recovery, such as measles or chickenpox. The SIR model is typically expressed using a set of ordinary differential equations in mathematical terms. The equations provided offer a description of how the number of susceptible, infectious, and recovered individuals changes over time. Through the process of solving these equations, researchers are able to simulate and analyze the spread of an infectious disease within a population. They may investigate the epidemic's peak, longevity, and vulnerable and recovered populations. The infectious rate,  $\beta$ , determines disease transmission between susceptible and infected individuals. Let us calculate the recovery rate:

$$\mu = \frac{1}{AD}$$

The recovery rate  $\mu$  can be calculated based on the average duration,  $AD$ , of infection. In the SIR model,  $\mu$  represents the rate at which individuals who have recovered from the infection return to the susceptible state as a result of losing their immunity.

#### SIR Model Pseudocode

##### **Step 1:** Initialize:

- Set initial values for population ( $N$ )
- initial number of infected individuals ( $I_0$ )
- initial number of susceptible individuals ( $S_0$ )
- recovery rate ( $\gamma$ )

**Step 2:** Create a datastore with the values of susceptible ( $S$ ), infected ( $I$ ), and recovered ( $R$ ) individuals over time. Set the time step ( $dt$ ) and the total simulation time ( $T$ ).

##### **Step 3:** Set initial conditions:

- $S[0] = S_0$
- $I[0] = I_0$
- $R[0] = N - S_0 - I_0$

##### **Step 4:** Simulate the epidemic:

- for  $t$  in range(1,  $T$ ):
- # Calculate the rates of change

```

dS = -beta * S[t-1] * I[t-1] / N
dI = beta * S[t-1] * I[t-1] / N - gamma * I[t-1]
dR = gamma * I[t-1]
Step 5:
# Update the values
S[t] = S[t-1] + dS * dt
I[t] = I[t-1] + dI * dt
R[t] = R[t-1] + dR * dt
Step 6:
List the results:
# Plot the values of S, I, and R over time
    
```

The SIR model helps analyze infectious illness transmission and evaluate control options. When the infection is short-lived, such as during an emergent outbreak, and the disease does not result in death, it is possible to disregard vital dynamics, which include birth and death rates, as they have minimal impact on the overall course of the infection. The SIR model can be expressed as an ordinary differential equation (ODE) in its deterministic form:

$$\frac{df(S)}{df(t)} = -\frac{\beta SI}{T}$$

where  $T=S+I$  is identified to be the total population. The SI model can be written as the following ordinary differential equation (ODE):

$$\frac{df(I)}{df(t)} = \frac{\beta SI}{T} - \omega I$$

$$\frac{df(R)}{df(t)} = \omega I$$

The equation  $T = S + I + R$  represents the total population. In a population that is closed and lacks vital dynamics, the eventual extinction of an epidemic is attributed to an inadequate number of susceptible individuals capable of maintaining the transmission of the disease. The introduction of infected individuals at a later stage will not initiate a subsequent epidemic owing to the presence of life-long immunity within the current population. The SEIR-HCD, SIS, and SIR models are mathematical models used in epidemiology to simulate and analyze the dynamics of infectious diseases. Each of these models has its own merits and weaknesses, and their appropriateness depends on the specific characteristics of the disease and the context in which they are applied. Table 3 summarizes the merits and weaknesses of the SIR, SIS, and SEIR-HCD models.

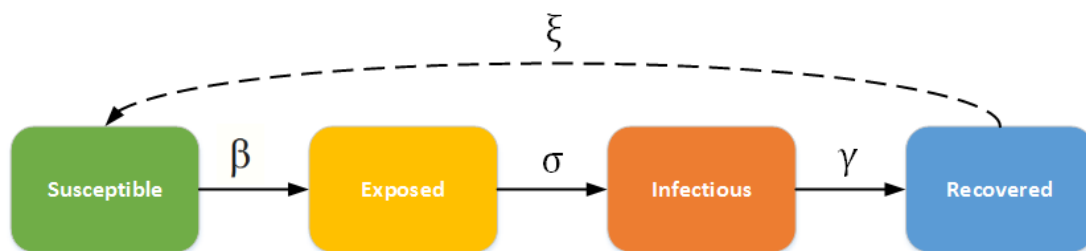
**Table 3. Merits and weaknesses of model**

Model	Merits	Weaknesses
SIR Model	- Simplicity and ease of understanding	- Lack of complexity
	- Well-defined parameters	- No re-susceptibility
	- Useful for endemic diseases	- Doesn't account for carriers
SIS Model	- Simple dynamics	- Limited applicability
	- Suitable for short-term infections	- Doesn't account for removed cases
SEIR-HCD Model	- Incorporates exposed individuals	- Complexity
	- Detailed health status	- Data requirements
	- Flexibility for disease-specific compartments	- Sensitivity to assumptions

The choice of model for the proposed work depends on the specific disease, available data, research objectives, and computational resources. More complex models like SEIR-HCD are suitable for modeling the dynamics of diseases with severe outcomes and resource-intensive healthcare needs, while simpler models like SIS or SIR may be useful for quick assessments and initial insights into disease spread. Governments may face resource limitations, leading to challenges in allocating sufficient resources for epidemic intelligence, response, and healthcare infrastructure. Intensive government intervention can raise concerns about civil liberties and data privacy, especially when enforcing measures such as contact tracing and quarantine. Coordinating government interventions at various levels (local, regional, national, and international) can be logistically challenging and may result in delayed responses. Government interventions may sometimes result in communication gaps and misunderstandings between relevant agencies and stakeholders, potentially hampering the efficiency of the response. Decisions on government intervention, such as isolation and quarantine, may involve ethical dilemmas, particularly regarding the balance between public health and individual rights. Government policies may lag behind the rapid spread of diseases, especially in the early stages of an outbreak. Delays in policy implementation can impact the effectiveness of epidemic intelligence.

### ***SEIR-SEIRS MODEL***

The infectious rate determines the rate of spread, which is the chance of disease transmission between a susceptible person and an infected one. It is controlled by the infectious rate. The pace at which dormant people become infectious is referred to as the incubation rate (the typical length of the incubation period is denoted by  $1/D$ ). The average duration,  $D$ , of infection, is what determines the recovery rate, which is written as  $1/D$ . Within the framework of the SEIRS model, the term in question pertains to the rate at which individuals who have recovered from the infection lose their acquired immunity and transition back to a susceptible state. Figure 5 illustrates the progression of individuals through each compartment in the SEIR/SEIRS model. The dashed line illustrates the transition from the SEIR model to the SEIRS model, wherein individuals who have recovered from infection can once again become susceptible to the disease due to the absence of lifelong immunity conferred by recovery. During the dormant phase of many diseases, the person is sick, but they are not yet spreading the disease to other people.



**Figure 5. SEIR-SEIRS Model**

This gap between getting sick and being contagious can be accounted for in the SIR model by adding a latent/exposed population,  $E$ , and letting people who are infected but not yet contagious move from  $S$  to  $E$  and from  $E$  to  $I$ .

SEIR Model Pseudocode:

**Step 1:** Initialize:

- Set initial values for population ( $N$ )
- Set initial number of infected individuals ( $I_0$ )
- Set initial number of susceptible individuals ( $S_0$ )
- Set initial number of exposed individuals ( $E_0$ )

```

- Set infection rate (beta)
- Set recovery rate (gamma)
- Set the time step (dt) and the total simulation time (T).
Step 2: Create arrays to store the values of susceptible (S), exposed (E), infected (I), and recovered (R) individuals over time.
Set initial conditions:
    S[0] = S0
    E[0] = E0
    I[0] = I0
    R[0] = N - S0 - E0 - I0
Step 3: Simulate the epidemic:
for t in range(1, T):
    # Calculate the rates of change
    dS = -beta * S[t-1] * I[t-1] / N
    dE = beta * S[t-1] * I[t-1] / N - sigma * E[t-1]
    dI = sigma * E[t-1] - gamma * I[t-1]
    dR = gamma * I[t-1]
Step 4: Update the values
    S[t] = S[t-1] + dS * dt
    E[t] = E[t-1] + dE * dt
    I[t] = I[t-1] + dI * dt
    R[t] = R[t-1] + dR * dt
Step 5: Simulate the results:
# Simulate the values of S, E, I, and R over time
    
```

This will allow the model to take into account the time between getting an illness and becoming infectious. In a population that is closed off, meaning there are no new births or deaths, the SEIR model becomes the following:

$$\frac{df(S)}{df(t)} = -\frac{\beta SI}{T}$$

where  $T=S+I$  is identified to be the total population. The SI model can be written as the following ordinary differential equation (ODE):

$$\begin{aligned} \frac{df(E)}{df(t)} &= \frac{\beta SI}{T} - \varphi E \\ \frac{df(I)}{df(t)} &= \varphi E - \beta I \left(1 - \frac{I}{T}\right) \\ \frac{df(R)}{df(t)} &= \varphi I \end{aligned}$$

where  $T=S+E+I+R$  is the total population.



## RESULTS AND DISCUSSION

Initially, the proposed work is to collect relevant data on air traffic networks, including flight schedules, passenger volume, and travel patterns. Additionally, data on disease-specific parameters, such as infection rate and recovery rate, should be obtained to calibrate the models accurately. We conduct a comprehensive analysis of the air traffic network to understand its structure and connectivity patterns. This analysis can include measures such as degree distribution, clustering coefficients, and centrality measures to identify key airports and routes within the network. We develop and implement epidemic intelligence models, including SIS, SIR, and SEIR, tailored to the air traffic network context. These models should incorporate the network structure, passenger mobility patterns, and disease-specific parameters to simulate the spread of infectious diseases within the network. The models are calibrated using air traffic data on historical disease outbreaks and their associated spread within air traffic networks. Validate the models by comparing the simulated results with actual outbreak data to ensure their accuracy and reliability.

We conducted scenario analysis by varying model parameters and introducing control measures to assess their impact on disease spread. We explored different scenarios, such as varying levels of passenger screening, travel restrictions, or vaccination campaigns, to understand their effectiveness in mitigating disease transmission within the air traffic network. Based on the simulation, the patterns of disease transmission and the factors that contribute to its spread within the air traffic network are explored. We examined the role of network connectivity, flight routes, and passenger mobility in shaping the epidemic dynamics. The discussion also focuses on the effectiveness of different control measures in reducing disease transmission and the potential trade-offs associated with their implementation. Additionally, we compare the performance of different models (SI, SIR) in capturing the observed dynamics and discuss the limitations and assumptions of the models used. The discussion surrounding epidemic intelligence models in air traffic network centers and their simulation is shown in Figure 6 and Figure 7.

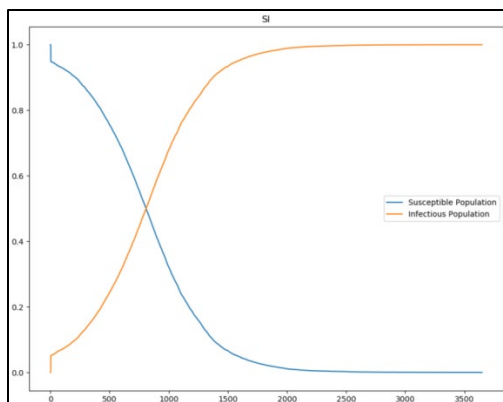


Figure 6. SI Model outbreak simulation

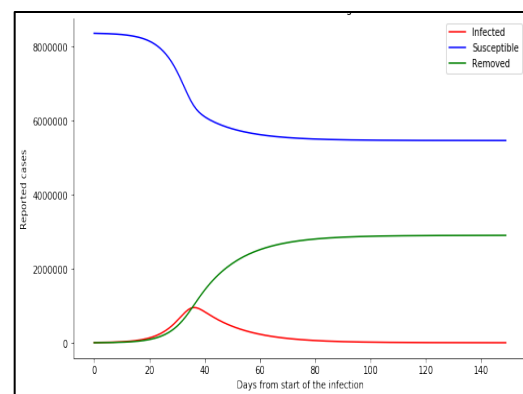


Figure 7. SIR Model outbreak simulation

The SIS model has been extensively utilized in epidemiological studies to comprehend the dynamics of disease transmission, evaluate the effectiveness of interventions, and provide insights for public health decision-making. We performed a sensitivity analysis to identify the most influential factors affecting the spread of infectious diseases in the air traffic network. This analysis can help prioritize interventions and control strategies based on their potential impact on disease dynamics. The proposed work aims to enhance our understanding of the dynamics of disease spread within air traffic networks by utilizing epidemic intelligence models. The discussion surrounding the epidemic intelligence model SEIR-HCD (Susceptible-Exposed-Infectious-Removed-Hospitalized-Critical-Deaths) in air traffic network centers and its simulation is shown in Figure 8 and Figure 9.

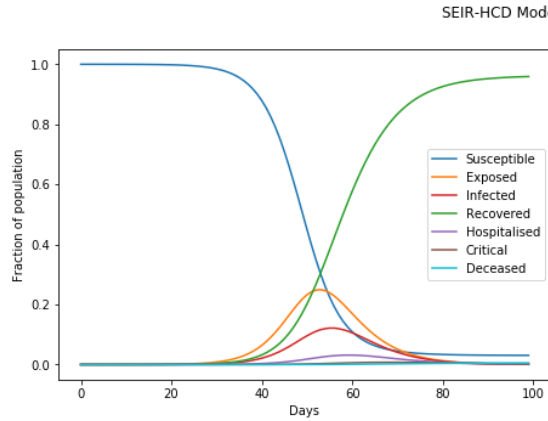


Figure 8. SEIR-HCD Model (existing)

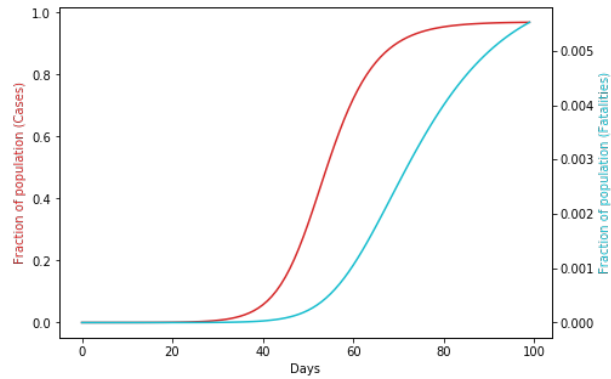


Figure 9. SEIR-HCD Model (detected)

By considering the unique characteristics of air travel and incorporating network analysis techniques, the SEIR-HCD model with an intervention on day 45 is simulated to determine the valuable insights. It informs evidence-based decision-making processes to effectively manage and control the spread of infectious diseases in air traffic networks (Figures 10 and 11).

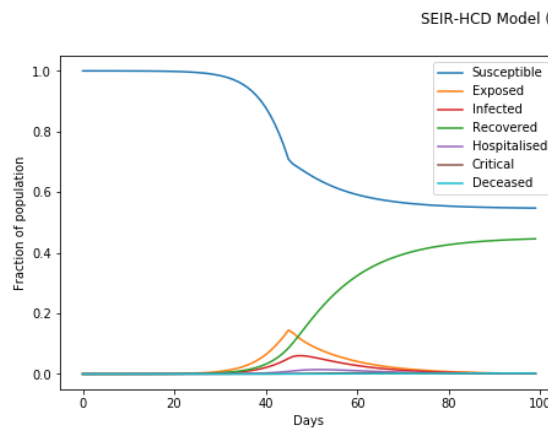


Figure 10. Proposed model (Day 1)

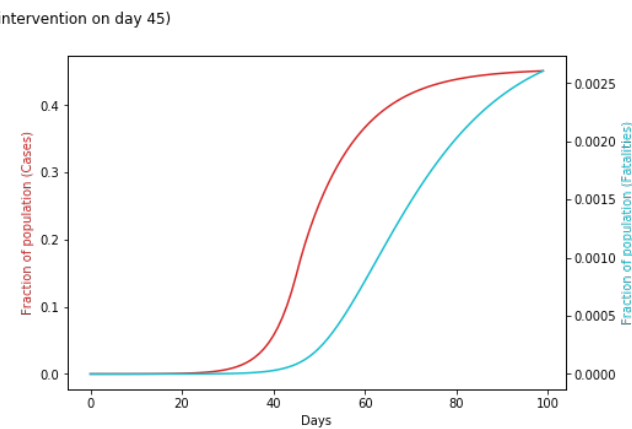
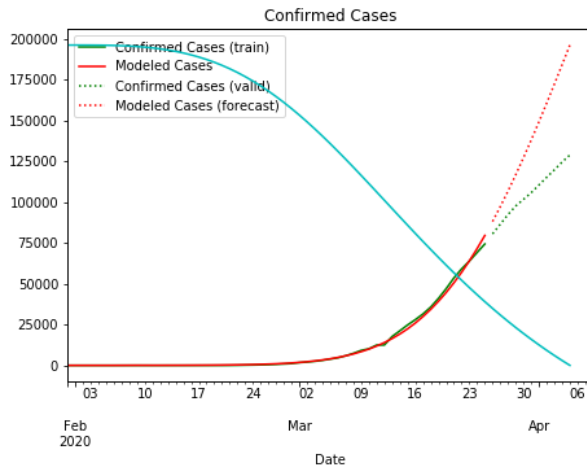


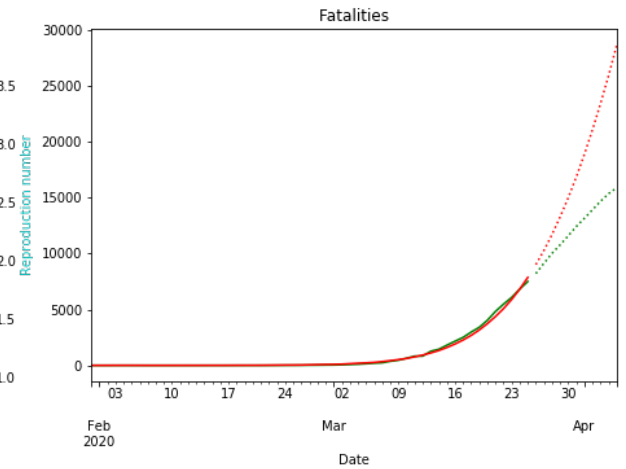
Figure 11. Proposed model (Day 45)

The SEIR-HCD models are then simulated using mathematical equations or computational simulations to analyze the dynamics of disease spread within the air traffic network. The results obtained from implementing epidemic intelligence models in air traffic networks provide insights into the dynamics of disease spread and the impact of various factors. These models help in understanding the patterns of disease transmission within interconnected populations and the role of air travel in facilitating the spread of infectious diseases. The results may include the number of infected individuals, the duration of the epidemic, the peak of infections, and the final size of the susceptible and recovered populations. Additionally, the models can be used to evaluate the effectiveness of control measures, such as pre-flight screening, travel restrictions, or vaccination campaigns, in mitigating the spread of diseases. SEIR-HCD models are advanced epidemic intelligence models that incorporate additional to represent disease detection, hospitalization, critical care, and mortality. The implementation of epidemic intelligence models in air traffic networks involves integrating epidemiological models such as SIS, SIR, and SEIR with air traffic data, network analysis techniques, and relevant parameters.

These models aim to provide a more comprehensive understanding of disease spread, healthcare system demands, and the impact of control measures. Research on SEIR-HCD models focuses on various aspects, including disease detection, epidemic intelligence, and model refinement. Here are some key points regarding research on SEIR-HCD models in the context of disease detection and epidemic intelligence. SEIR-HCD models consider the detection of infectious cases, which is crucial for timely interventions and controlling disease spread. The simulation of the number of cases of confirmed fatalities is identified in Figure 12 and Figure 13.



**Figure 12. Proposed model  
(Confirmed Cases)**

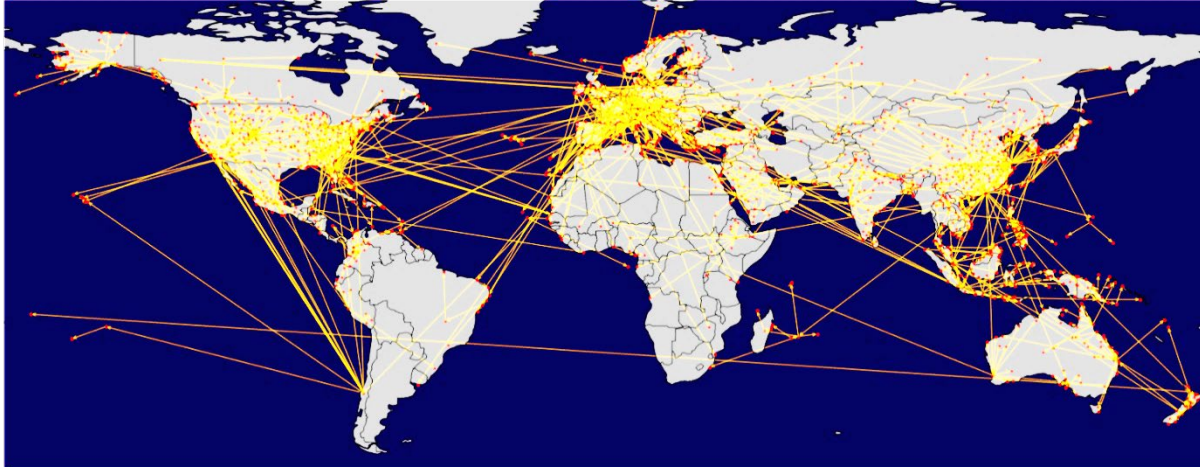


**Figure 13. Proposed model  
(Fatalities Identified)**

The integration of air traffic network data into SEIR-HCD models also enables the exploration of the interplay between local outbreaks and global disease dissemination through air travel. This understanding is vital for assessing the risk of importation and exportation of infections, especially during epidemics of global concern. In conclusion, the utilization of SEIR-HCD models with air traffic network data enhances our understanding of disease spread dynamics in the context of air travel. It offers valuable insights into the role of air traffic networks in disease transmission, the effectiveness of control measures, and the implications for public health interventions. By considering air traffic patterns, the SEIR-HCD model contributes to more accurate modeling and prediction of disease outbreaks, aiding in the development of proactive and evidence-based strategies to manage and mitigate the impact of infectious diseases in the context of air travel.

This includes data on disease transmission, hospitalization rates, critical care needs, and mortality. Researchers use statistical methods and optimization techniques to estimate model parameters accurately and validate the model against observed data. This includes incorporating heterogeneity in the population, age-specific effects, spatial variations, and other relevant factors. Variants of the SEIR-HCD model, such as age-structured models or spatial models, are developed to provide more granular insights into disease spread and healthcare demands. Figure 14 shows the proposed SEIR-HCD model for air traffic simulation.

Geospatial mapping is carried out to visualize the geographic distribution of disease cases, hospitalizations, critical care needs, or deaths. It provides a spatial perspective of the epidemic, enabling the identification of regional disparities and informing targeted interventions and resource allocation. They allow users to explore different parameters, interventions, and scenarios. In addition, the dashboards can include various visualizations, such as time series plots, heat maps, network graphs, and comparative analyses.



**Figure 14: Proposed SEIR-HCD model - air traffic simulation**

## CONCLUSION

The implementation, results, and discussion of epidemic intelligence models in air traffic networks contribute to a better understanding of the dynamics of disease spread within these networks. They provide valuable insights for policymakers, public health authorities, and aviation authorities in formulating effective strategies to mitigate the risks of infectious disease transmission through air travel. By integrating real-world data, mathematical modeling, and network analysis, these studies help inform decision-making processes and support the development of targeted interventions and control measures to minimize the impact of infectious diseases in air traffic networks. In conclusion, the application of SEIR-HCD (Susceptible-Exposed-Infectious-Recovered-Hospitalized-Critical-Deaths) models in disease detection and epidemic intelligence research, incorporating air traffic network data, holds immense potential for understanding the dynamics of disease spread in the context of air travel. By integrating air traffic network data into the SEIR-HCD model, researchers can gain insights into the role of travel patterns and connectivity in disease transmission across different regions. This enables a more accurate representation of disease spread dynamics, considering the movement of individuals through air travel networks.

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## AUTHOR

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**Dr. A. Bhuvaneshwari** is an assistant professor in the School of Computer Science Engineering, VIT University, Chennai, India. She received her B.E. degree (2010) and Ph.D. (2019) from Anna University and M.Tech. degree (2012) from Sastra University, Tamil Nadu, India, all in computer science and engineering. She conducts research and mentors students in specific research domains including social network analysis, big data analytics, epidemic intelligence, web mining, and recommendation engines.