

SEIR Model for Tracking Covid-19 Outbreak

¹Pasam PrudhviKiran, ²Dr. E. Laxmi Lydia, ⁴Dr.T. Pavani

¹Assistant Professor, Vignan's Institute of Information Technology

²Professor, Department of Computer Science and Engineering, Vignan's Institute of Information Technology (A), Visakhapatnam (Andhra Pradesh), India.

⁴Gokaraju Rangaraju Institute of Engineering & Technology, Hyderabad, India

ABSTRACT

China was identified as the initiative of 2019-2020 Coronavirus a widespread disease. The first case in India was reported on 30 January 2020. Scientists and doctors signify that the testing rate in India was low when compared to the large number of infections all over the world. India has accounted COVID-19 infected rate to 1.7, very much lower to worst affected countries. The emergence of Simulation studies is set to transform almost every aspect of daily life by provoking us to develop various prediction algorithms with best possible computation time, without significantly sacrificing the output accuracy. Here in this proposed system, Simulation studies are going to play a big role in our effort to define a pandemic disease such as covid-19 scenario prediction. It is very important to understand the severity and containment of pandemics, to achieve this we focus on developing an efficient simulation model which uses techniques of Artificial Intelligence to learn and accurately predict.

Keywords: Artificial Intelligence, Covid-19, Pandemic.

I. INTRODUCTION

China was identified as the initiative of coronavirus a widespread disease. The first case in India was reported on 30 January 2020. Scientists and doctors signify that the testing rate in India was low when compared to the large number of infections all over the world. India has accounted COVID-19 infected rate to 1.7, very much lower to worst affected countries. This was identified similar to the act that existed in 1897 as Epidemic Diseases Act. Due to the outbreak of COVID-19 from china to dozen of states and most of the union territories, educational institutions, transportations by suspending all visas from other countries and from India to other countries, commercial investigations of businesses have been shut down in India as most of the active cases were connected to other countries.

Indian Prime Minister, Narendra Modi declared curfew on 22nd of third month in 2020 for 14 hours to take attention of people over COVID-19. 75 districts, with all its major cities implemented Government's order. Later on 24th of third month, observing the nation's situation of virus spread over 1.3 billion population of India, Prime minister ordered 21 days lockdown.

Michael Ryan chief executive director in health emergencies programme from World Health Organisation stated that India being second largest country in population has tremendous capacity to deal with Coronavirus through lockdown. Various Indian sectors from agriculture, economy, enterprises, self-employed people got affected devastation through lockdown. Lockdown was implemented as the primary pre-emptive source to all people to reduce the life loss. Shiv Nadar University studied that 31,000 virus cases were recorded without lockdown from 24th March to 14th April of 2020.

Despite remarkable advances in modern medicine, Infectious disease pandemics still remain the most serious threats to worldwide wellbeing and can conceivably affect national security [1] by pushing us deeper into chaos. We can observe that growth of Infectious disease incidence during recent decades. Asia-Pacific is seen to be hotspot for emerging infectious diseases as illustrated by emergence of Nipah virus, new cholera and dengue variants among others. As biodiversity loss is thought to be a first-rate explanatory element of the boom in emergence of these infectious diseases, Asia-Pacific seems a key region in which to research the hyperlinks among biodiversity, and its loss, at the styles of infectious sicknesses. Also we have to observe that, increased population density and mobility, i.e.

Mass gatherings of people in confined spaces, is playing important role in the spread of emerging infectious diseases [2] and could potentially lead to future pandemics. Especially in urban areas these disease spread rates are higher when compared to suburban areas due to differences in population density, lifestyle and behavioural factors [3].

If we see the previous infectious disease outbreaks we will become aware of several objects of strategic significance. Consider SARS - 2003, first, this SARS coronavirus at medical institution wards significantly threatened the lives of healthcare workers and other patients [2]; and so it's of the utmost necessity to fast quantify the hazard of infectious disease spread within high-risk healthcare facilities to contain the outbreak at the earliest degrees. On other hand passengers related to all modes of public transportation are acting as high speed transmission hotspots for disease spread, so this is also one of the very important things to be taken in to consideration for analysis of global pandemic containment. Modelling of community interaction dynamics will definitely help us to contain this infectious threat at its origin. Traditional influenza simulations models focus on large-scale populations with a generalized and homogeneous individual contact structure. They frequently neglect important regional variations when constructing network systems and therefore are insufficient to duplicate the true contact dynamics.

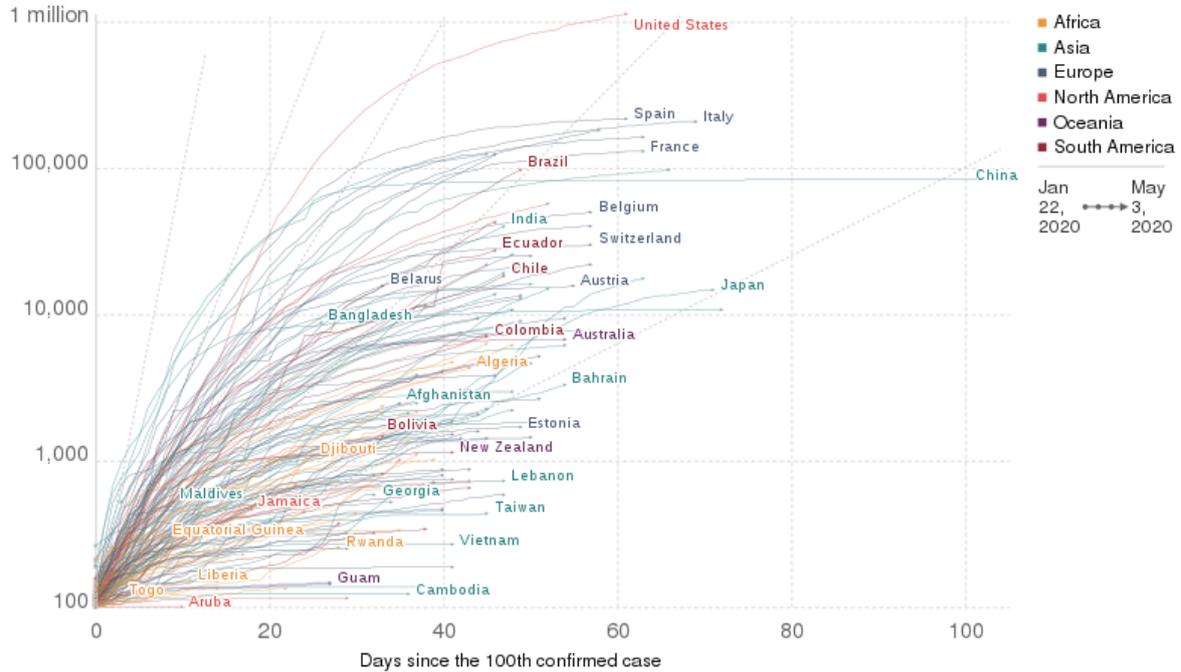
For efficient tracking of disease spread, we propose a systematic and easy to use approach, which dynamically explain true population movement, especially in urban areas. Such modeling approaches can enable pre-emptive detection, identification, and comprehension of pandemic outbreaks, as well as scientific justifications for mitigation strategies, such as social distancing, biosecurity screening, and quarantines. On other hand these approaches can also leads to development of economically viable preparedness strategies.

i. Critical Rates of Social Contacts

Consider a set of people for understanding two mixing models, homogenous & nonhomogeneous. Homogeneous models believe in that, in a certain time period all people in a set will have almost same number of contacts, with same infection transfer probability for each contact. But nonhomogeneous models constitute a variety of probabilities, where every person will have different number of contacts which maps a connection network of contacts between each member pair. Previously Dionne Aleman and her colleagues [3] have developed an algorithm, to compute probability of each person, getting infected from his contacts with in each day population. Such approach may assume different transmission probabilities depending on spatial proximity of each contact. Figure 1 demonstrates worldwide confirmed cases; image has been taken from Covid-19 service website.

Total confirmed COVID-19 cases: how rapidly are they increasing

The number of confirmed COVID-19 cases is lower than the number of total cases. The main reason for this is limited testing.



Source: European CDC – Situation Update Worldwide – Last updated 3rd May, 11:45 (London time) •

Fig.1: Increase of worldwide Covid-19 cases

Apart of this, it is important to identify and model, children and elderly people to higher estimated probabilities of becoming infected than the healthy adults. We can also model phenomenon for Super-spreaders [17] as well, an individual who is more likely to infect others, compared with a typical infected person. These kinds of varying studies will enable us to understand the importance of indirect disease transmission paths, which are very important and high risk mediums of infectious disease transmission, one of the important indirect medium is, bacteria deposited on a handrail or elevator in a busy metro station or airport. In addition we can also consider changing human behaviours, such as weekly travel schedules or visiting a hospital. All the above specified can be achieved with Flexible Modeling paradigm. Figure 2 conveys the general proposed framework.

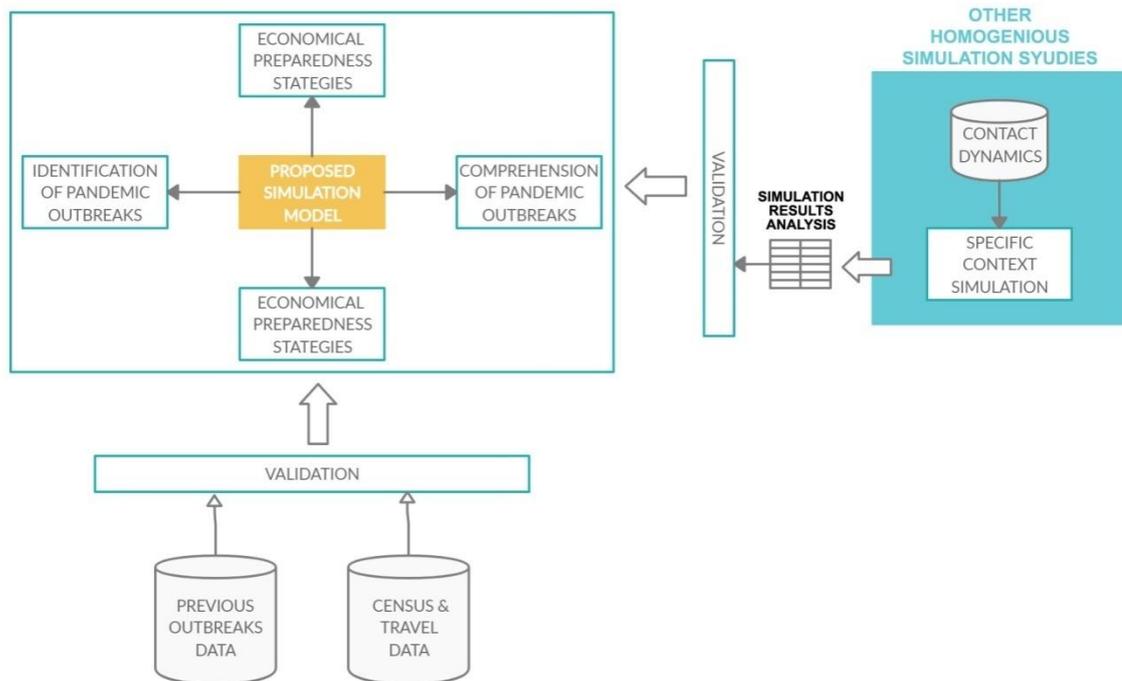


Fig.2:Flow diagram to analyze pandemic outbreaks.

Transmission of disease spread can be maximised when the population who is at risk of becoming infected, by a disease, is more vulnerable [4]. For example disease spread can be easier when are hospitalised or when they are sick and lack of disease resistance, working or travelling with infected people around. There are proven studies that have showcased exposure and infection risk models in local healthcare facilities and special settings such as an isolation ward or general hospital ward [5][6].

Carline Van den Dool and her colleagues adapted influenza transmission, a previously developed model, in a long-term care nursing home and studied the effects of the vaccination of healthcare workers in hospital wards [14][15]. Carline clearly proposed a matrix of healthcare worker-to-patient contact probabilities, numbers of contacts, and times of each contact in hospital settings. One of our team has designed a four-state model to study each stage of contagious disease through human infection described as Susceptible Exposed Infected Removed model. It is tested through crosscheck of the symptoms of virus for every individual who have infection and who have no infection. The cumulative infection rate of isolated patient results 10 percent better than others. For the future advancement of diagnosing affected people on observing severity of illness for all hypothetical disease scenarios, healthcare professionals categorize patients depending of the type of infection. The study of hospital workflow simulation can be accurately designed for patients and workers as well based on the intensity of contact between the people.

Up to good extent, one can quantify the probable intensity of infection spread by observing spatiotemporal features of contacts between infectious and normal persons in mass transportation activities. Our studies over passenger flow in public transportation, using agent-based microscopic models [7-10], enabled us to understand the probabilities that each individual is in close contact (within 1 meter) or long-distance contact (more than 1 meter and less than 3 meters) with an infected individual [11]. We are aware that Infectious Disease spread chances are high in both the above distance cases. Using recording and surveillance systems available in public transport locations enabled us to capture passenger movement activities, such as passenger density and and travel patterns. Considering age, sex, and the traveller's place of origin, travel duration, and proximity of each contact can efficiently model the disease spread.

II. METHODOLOGY

i. Space - Time Simulation Models

Usually for infectious disease dynamics, we use random probability distribution (which may be analysed statistically but may not be predicted precisely) models [12][13][14-16], which are not efficiently applicable on large, homogeneous populations. Efficient simulations can be done using models, formulated by nonlinear systems of differential equations which are deterministic in nature. On other hand, keeping an eye on every individual's behavioural patterns for massive populations is definitely a big challenge and also requires extensive computation capabilities. Appropriate computational intervals of 100ms time step size was modelled and suggested for one metro station through frequent testing of agent-based continuous pedestrian model. Making use of parallel computing methods to run these simulations can be a solution up to some extent. It's out of great concern to program efficient sampling algorithms to simulate the scope of large population through domain subset of heterogeneous data over various inclusion probabilities.

An efficient algorithm obtained accurate results on modelling and applying over 23 million population of Taiwan using an agent model performing heterogeneous subset sampling by Meng-Tsung and his colleagues. A stochastic simulation and transmission probability of susceptible persons were identified by Ira Longini and his colleagues using all infectious contacts. Testing analysis were also made using Bayes' rule by enabling the simulation algorithm that reduces the computational time without any external significance of output results (accuracy). 15 preliminary results were computationally performed heterogeneous transmission rate for the reasonable execution time on laptop.

ii. SEIR Model

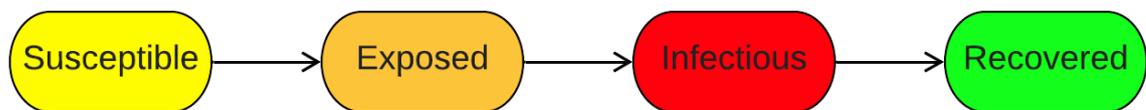


Fig.3: Flow Diagram representing SEIR Model

The SEIR models the flows of people between four states: susceptible (S), exposed (E), infected (I), and resistant (R) as shown in Fig.3.

Each of those variables represents the number of people in those groups. The parameters alpha and beta partially control how fast people move from being susceptible to exposed (beta), from exposed to infected (sigma), and from infected to resistant (gamma). This model has two additional parameters; one is the background mortality (mu) which is unaffected by disease-state, while the other is vaccination (nu). The vaccination moves people from the susceptible to resistant directly, without becoming exposed or infected.

The SEIR differs from the SIR model in the addition of a latency period. Individuals who are exposed (E) have had contact with an infected person, but are not themselves infectious.

The parameters are Beta and the parameter control how often a susceptible-infected contact results in a new exposure. Parameter Gamma reflects the rate of infected recovery and moves into the resistant phase. Parameter Sigma reflects the rate at which an exposed person becomes infective. The natural mortality rate (this is unrelated to disease).

This models a population of a constant size, Initial susceptible i.e., the number of susceptible individuals at the beginning of the model run. Initial exposed i.e., the number of exposed individuals at the beginning of the model run. Initial infected i.e., the number of infected individuals at the

beginning of the model run. Initial recovered i.e., the number of recovered individuals at the beginning of the model run. Days Controls how long the model will run.

This program runs on computer, so some computers may run faster than others. It is probably a good idea not to set the number iterations or the initial populations too high, since it will take longer to run. It is noted that cookies must be enabled for the algorithm to function.

$$\begin{aligned}
 \frac{dS}{dt} &= \mu(N - S) - \beta \frac{SI}{N} - \nu S & 1 \\
 \frac{dE}{dt} &= \beta SI / N - (\mu + \sigma)E & 2 \\
 \frac{dI}{dt} &= \sigma - (\mu + \gamma)I & 3 \\
 \frac{dR}{dt} &= \gamma I - \mu R + \nu S & 4 \\
 N &= S + E + I + R & 5
 \end{aligned}$$

This is an ordinary differential equation model, described by the following equation:

- Derivative of S with respect to t equals The simulation uses the fourth-order Runge-Kutta algorithm to solve it numerically, with a step size fixed at 0.01, written in JavaScript.
- The plotting methods are from the plot module.

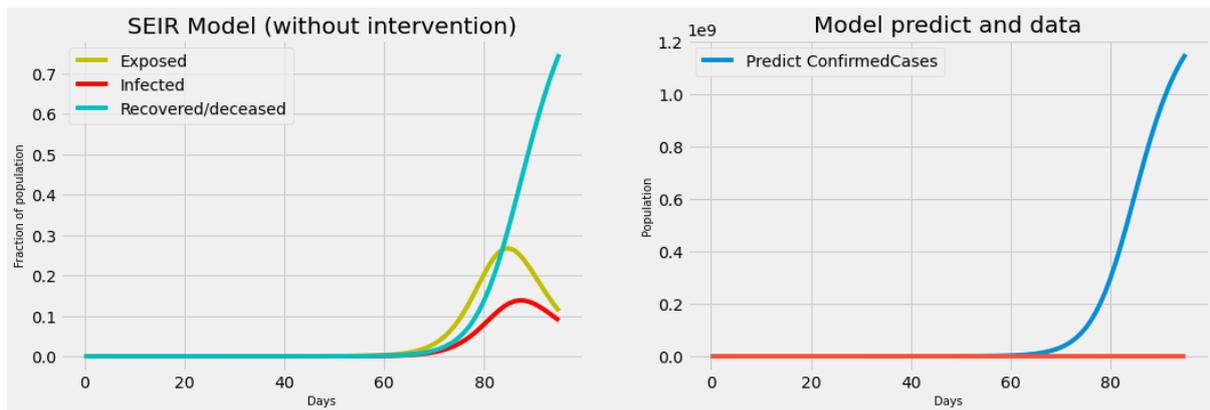


Fig.4: Graph to plot SEIR Model without intervention and prediction of confirmed cases

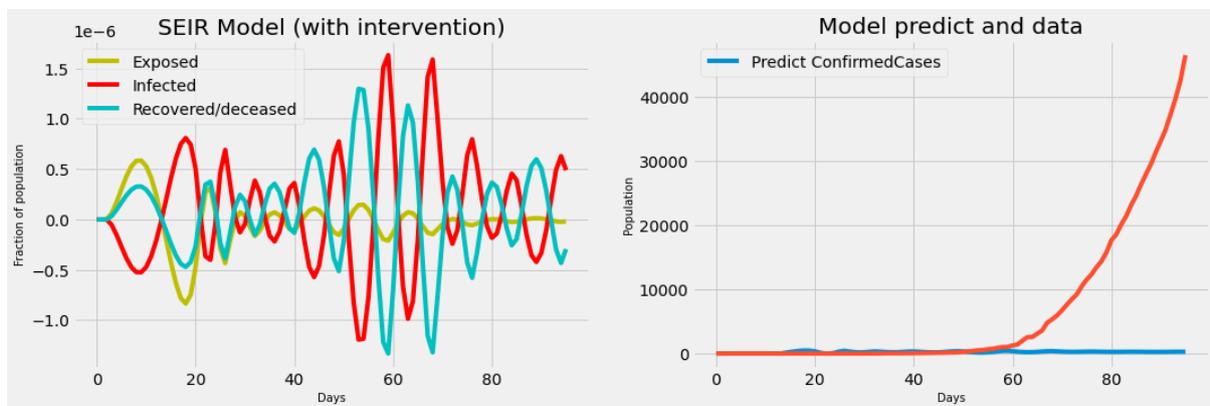


Fig.5: Graph to plot SEIR Model with intervention and prediction of confirmed cases

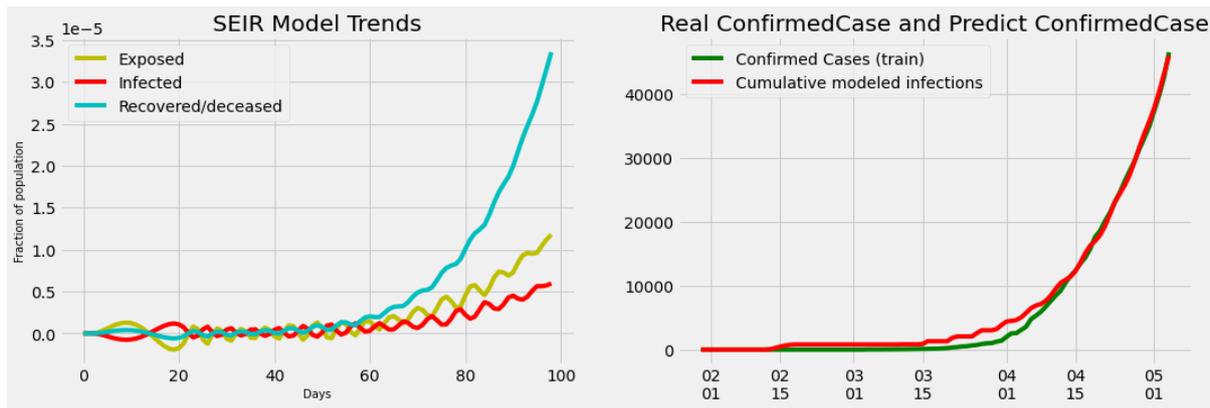


Fig.6: Graph to plot SEIR Model trends and prediction of confirmed cases

iii. Facilitating GUI

A Good GUI always facilitates Clear, Concise & Familiar, understandings. Here, displaying the results of our simulation will enable to predict over disease spread environment and also it will visualize the geographical disease spread metrics. The output figures represent the interface design developed for the simulation package of large population. Users can monitor the changes in disease parameters and intervention strategies can be taken, which directly influence the evolution of an epidemic scenario. The input parameters were adjusted based on the critical interventions that outbreak the population size, probability of virus transmission from person to person through contact, identification of vaccination coverage levels, demographic composition using GUI. The key output performance of different age group people tested through simulation interface. The expected epidemic outbreak represented to evolve through thematic map.

III. CONCLUSION

These kinds of systems allow users to understand the movement of spatial-disease spread and also user can compare dispersion patterns across different demographic dynamics and geographical features. Further these systems can be integrated with many popular and standard systems like www.globalmicrobialidentifier.org, which provides genomic information of microorganisms, linked to, metadata of those microorganisms such as epidemiological details. Exploring interoperability among different techniques for disease detection can justify foremost statistics-sharing for effective containment of infectious disease spread.

REFERENCES

1. C. Enemark and M.J. Selgelid, *Ethics and Security Aspects of Infectious Disease Control: Interdisciplinary Perspectives*, Ashgate Publishing.
2. E.S. Toner and J.B. Nuzzo, "Acting on the Lessons of SARS: What Remains to Be Done?" *Biosecurity and Bioterrorism: Biodefense Strategy, Practice, and Science*, vol. 9, no. 2, pp. 169-174
3. D.M. Aleman, T.G. Wibisono, and B. Schwartz, "Accounting for Individual Behaviors in a Pandemic Disease Spread Model," *Proc. 2009 Winter Simulation Conf.*, pp. 1977-1985.
4. World Health Organization, *Consensus Document on the Epidemiology of Severe Acute Respiratory Syndrome (SARS)*, World Health Organization
5. D.S.C. Hui et al., "Aerosol Dispersion during Common Respiratory Therapies: A Risk Assessment Model of Nosocomial Infection to Healthcare Workers," *Proc. Health Research Symp.*, pp. 49.
6. G.N. Sze To, M.P. Wan, and C.Y.H. Chao, "Evaluation of the Effectiveness of Isolation Facilities in Preventing the Nosocomial Spread of Viral Disease through Airborne Route," *Indoor Air 2008: Proc. 11th Int'l Conf. Indoor Air Quality and Climate, 2008*, pp no. 16
7. S.B. Liu et al., "Crowdedness in Metro Stations: Passenger Flow Analysis and Simulation," *Transportation Research Board 92nd Ann. Meeting Compendium of Papers*.

8. S.M. Lo, Report on the Passenger Flow in Kowloon Tong Station, report submitted to Mass Transit Railway Corporation (MTRC), unpublished, 2011.
9. M. Asano, T. Iryo, and M. Kuwahara, "Microscopic Pedestrian Simulation Model Combined with a Tactical Model for Route Choice Behaviour," *Transportation Research Part C: Emerging Technologies*, vol. 18, no 6, 2010, pp. 842-855.
10. M. Moussaïd, D. Helbing, and G. Theraulaz, "How Simple Rules Determine Pedestrian Behavior and Crowd Disasters," *Proc. Nat'l Academy of Sciences*, vol. 108, no. 17, 2011, pp. 6884-6888.
11. G. Brankston et al., "Transmission of Influenza A in Human Beings," *The Lancet Infectious Diseases*, vol. 7, no. 4, 2007, pp. 257-265.
12. I.M. Longini et al., "Containing Pandemic Influenza at the Source," *Science*, vol. 309, no. 5737, 2005, pp. 1083-1087.
13. B. Sander et al., "Economic Evaluation of Influenza Pandemic Mitigation Strategies in the United States Using a Stochastic Microsimulation Transmission Model," *Value in Health*, vol. 12, no. 2, pp. 226-233.
14. van den Dool et al., "Modeling the Effects of Influenza Vaccination of Health Care Workers in Hospital Departments," *Vaccine*, vol. 27, no. 44, pp. 6261-6267.
15. N.E. Lizon, D.M. Aleman, and B. Schwartz, "Incorporating Healthcare Systems in Pandemic Models," *Proc. 2010 Winter Simulation Conf*, pp. 2230-2236.
16. S. Andradóttir et al., "Reactive Strategies for Containing Developing Outbreaks of Pandemic Influenza," *BMC Public Health*.
17. Super-spreaders in infectious diseases, Richard A. Stein, *International Journal of Infectious Diseases*, Volume 15, Issue 8, Pages e510-e513