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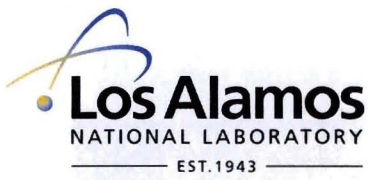

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Simulation to assess the efficacy of US airport entry screening of passengers for pandemic influenza

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Abstract: We present our methodology and stochastic discrete-event simulation developed to model the screening of passengers for pandemic influenza at the US port-of-entry airports. Our model uniquely combines epidemiology modelling, evolving infected states and conditions of passengers over time, and operational considerations of screening in a single simulation. The simulation begins with international aircraft arrivals to the US. Passengers are then randomly assigned to one of three states — not infected, infected with pandemic influenza and infected with other respiratory illness. Passengers then pass through various screening layers (i.e. pre-departure screening, en route screening, primary screening and secondary screening) and ultimately exit the system. We track the status of each passenger over time, with a special emphasis on false negatives (i.e. passengers infected with pandemic influenza, but are not identified as such) as these passengers pose a significant threat as they could unknowingly spread the pandemic influenza virus throughout our nation.

Keywords: epidemiology modelling; false negative; pandemic influenza; passenger screening; probability of detection; process simulation.

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Biographical notes: Robert T. Brigantic is a Scientist with the Pacific Northwest National Laboratory in Richland, WA. His research initiatives include operational modelling and simulation of pandemic diseases and associated impact/effectiveness analyses; operational modelling and simulation of radiation/nuclear screening processes; statistical pattern recognition and automated imagery analysis techniques; military transportation effectiveness and supply chain management optimisation. He has a PhD in Operations Research from the Air Force Institute of Technology (AFIT), an MSc in Space Operations from AFIT and a BSc in Chemical Engineering from Oregon State University. He also serves as an Adjunct Professor of Operations Research for Washington State University and the AFIT.

John D. Malone is an Infectious Diseases Physician. He received his Medicine from Ohio State University. After 30 years of active duty military service in the US Navy Medical Corps, he obtained his Masters in Public Health from the Uniformed Services University of Health Sciences (USUHS) and joined the Pacific Northwest National Laboratory, Richland, Washington, as a Programme Manager, Center for Biological Monitoring and Modelling. In 2008, he became a member of the Center for Disaster and Humanitarian Assistance Medicine, USUHS. He is an Adjunct Professor of Medicine, USUHS, with over 50 publications, many involving bioterrorism topics. He is a Fellow of the Infectious Diseases Society of America, a Fellow of the American College of Physicians and a Certified Physician Executive, American College of Physician Executives.

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Russell Lee is a member of the Distinguished R&D Staff in the Biosciences Directorate of Oak Ridge National Laboratory (ORNL) in Oak Ridge, TN. His current research is on homeland security, including systems analysis and planning for pandemics and transportation, energy and environmental modelling and analysis. He has written over 200 books, book chapters, journal articles, research reports and project deliverables. Currently, he is a member of three committees of the National Academies. He has a PhD in geography from McMaster University, and BA and MA, also in geography, from the University of Toronto in Canada. Prior to joining ORNL, he was an Assistant Professor at the University of Iowa and at Boston University.

Jim Kulesz is a Project Manager in the Computational Sciences and Engineering Division at Oak Ridge National Laboratory (ORNL). His current

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William Woody Delp is a Mechanical Engineer with the Airflow and Pollutant Transport Group, Indoor Environment Department, Environmental Energy Technologies Division of E.O. Lawrence Berkeley National Laboratory. His specialties include understanding how real buildings are operated, and how this operation influences the transport of contaminates throughout a facility. His work includes both tracer and modelling studies; optimal indoor sensor sighting for biological detectors; threat and consequence analysis for chemical or biological hazards in buildings; modelling pandemic influenza from a building science perspective. He holds a PhD, an MSc and a BSc in Mechanical Engineering from the University of Missouri-Rolla.

Ben McMahon is a Deputy Group Leader of the Theoretical Biology and Biophysics Group in the Theoretical Division of Los Alamos National Laboratory. His research interests include the fundamental physics of protein dynamics and how this understanding can be used greatly to simplify computational models of protein function. These models include quantum chemistry of enzymic reactions, studies of hydration of proteins and models of conformational change of proteins. Additional efforts include evolutionary analysis of protein families and understanding resource requirements for biosecurity planning needs of the Department of Homeland Security.

1 Introduction

In the event of confirmed human outbreak of a pandemic influenza virus overseas, the United States National Strategy for Pandemic Influenza calls for the implementation of pre-departure screening at international origin airports, en route screening and arrival screening at the US ports-of-entry (Homeland Security Council US, 2006). To ascertain the potential efficacy of passenger screening and the resulting operational impacts, we built a stochastic, discrete-event simulation of the US airport entry screening. This model uniquely combines epidemiology modelling, evolving infected states and conditions of passengers over time, and operational impacts of passenger screening in a single integrated simulation.

Under different pandemic scenarios, subsequent analysis based on this simulation can provide insights about the possible range of benefits, costs and impacts of alternative mitigative, diagnostic and quarantine measures. These insights can help decision-makers plan for the resources needed at the port-of-entry airports, anticipate the possible developments if a pandemic emerges, and ascertain appropriate courses of action.

Predictions from the simulation model can be used in pandemic influenza border planning to address questions about the numbers of passengers who will screened, the number of infected passengers that will be identified and not identified, screening times and delays, supply and personnel needs, space requirements at the airport and other related planning considerations.

2 Methodology

The screening process which our simulation models is consistent with the draft Department of Homeland Security (DHS) and Centers for Disease Control and Prevention (CDC) concept plan for pandemic influenza border planning and the concept of operations for air entry screening, in which there is primary and secondary active surveillance at port-of-entry airports (US Department of Homeland Security (DHS), 2007).

Prevalence. The analysis makes assumptions about the prevalence of pandemic influenza in foreign regions, i.e. epidemic curves, based on analysis of plausible global pandemic influenza conditions. In our model, we use four general geographic regions – Asia, Europe, Latin America and Canada. The prevalence in foreign regions affects the associated prevalence among travellers from these regions to the US. Recent US Department of Transportation data on the numbers of flights and passengers into each US airport provide estimates of the possible volume of passenger traffic. We run our simulation for 100 days of screening with the assumption that screening starts while the prevalence rates are still low in the foreign regions. During the 100 simulated days, the prevalence rates then rise and then fall back to near zero.

Illness progression and detection. The passenger screening simulation model uses these estimates, randomly determines whether a passenger is infected (based on the prevalence), and tracks the progression of the illness in each infected passenger. A key input to this part of the analysis is the estimated effectiveness of accurately detecting infected passengers at exit screening prior to departure, en route, and at primary active surveillance upon arrival at the US airport.

Mitigative and diagnostic measures for screening. The efficacy of antiviral drugs provided at the airport, the ability of health care professionals to identify that a passenger possibly has influenza of any type, and the sensitivity and specificity of diagnostic methods for determining whether a person who is suspected of being infected is actually infected are also key inputs to the analysis. Input values are based on a review of the scientific literature and on subject matter experts' estimates.

3 Passenger process simulation overview

We constructed a stochastic, discrete-event simulation of anticipated passenger screening operations, and the corresponding flow of passengers, using the Rockwell Arena Professional Edition applications software (Rockwell Automation, Inc, 2006; Kelton, Sadowski and Sturrock, 2007). The simulation starts with the generation of aircraft arrivals and passenger loads from international originating airports according to daily flight schedules. Consistent with federal plans, we assumed that these flights will be

funnelled into the 18 airports that have CDC and prevention quarantine stations. Each passenger is categorised into one of three infected states as discussed below. Passengers then pass through the screening layers (i.e. pre-departure screening, en route screening, primary screening and secondary screening) and ultimately exit the system with one of four declared outcomes.

True positive. Passenger is infected with pandemic influenza and is declared infected with pandemic influenza.

False positive. Passenger is not infected with pandemic influenza, but is declared infected with pandemic influenza.

True negative. Passenger is not infected with pandemic influenza and is not declared infected with pandemic influenza.

False negative. Passenger is infected with pandemic influenza, but is not declared infected with pandemic influenza.

We note that false negative passengers are the significant threat to our nation because they will exit the screening system and unknowingly spread the pandemic influenza virus throughout the country.

4 Passenger process simulation logic

To construct our simulation of screening and quarantine station operations, we first developed a simulation flow logic diagram as shown in Figure 1. The logic starts with the assignment of probabilities for each individual passenger entering the system, that is, the probability of being in one of three true infected states: not infected, infected with pandemic influenza or infected with other respiratory illness. The probabilities being infected with pandemic influenza or other respiratory illness are labelled as p_{ip} and p_{io}, respectively. Thus, the probability of not being infected is $1-p_{io}-p_{io}$ (this assumes that the infected states are mutually exclusive).

Next, passengers pass through an origin screening layer where they could be detected and culled out as being potentially infected with pandemic influenza, regardless of their true infected state. Of course, the probability of being culled out is related to a passenger's true infected state and present condition if infected (i.e. asymptomatic or symptomatic); passengers are also allowed to recover as the simulation proceeds as the time elapsed to recover for each passenger is tracked. Assumed probabilities for these detection rates will be provided in Section 5 for this and the other screening layers in the modelled process. As with the origin, remaining passengers can be identified during the flight to the US or after arrival as they pass through primary screening. Passengers who are identified as potentially infected en route or at primary screening are sent to secondary screening for a more thorough examination and possibly for diagnostic tests (e.g. reverse transcription polymerase chain reaction (RT-PCR) diagnosis; US Department of Health and Human Services, 2006). After secondary screening is completed, passengers are declared as either being infected or not. Lastly, the simulation tabulates simulated passenger states against their 'true' infected state as modelled when they enter the system so that each passenger falls into one of the four outcomes – true positive, false positive, true negative or false negative.

Figure 1 Diagram of simulation flow logic

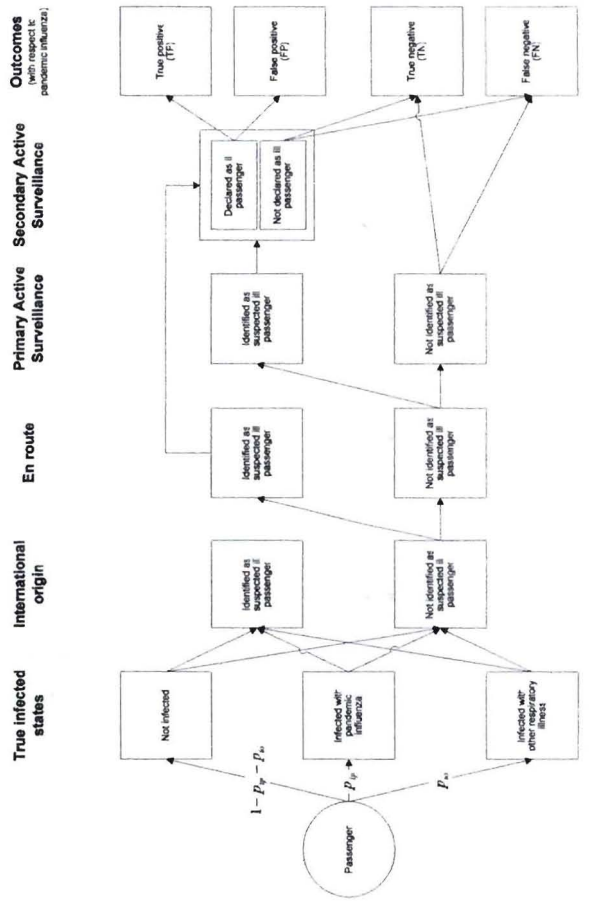
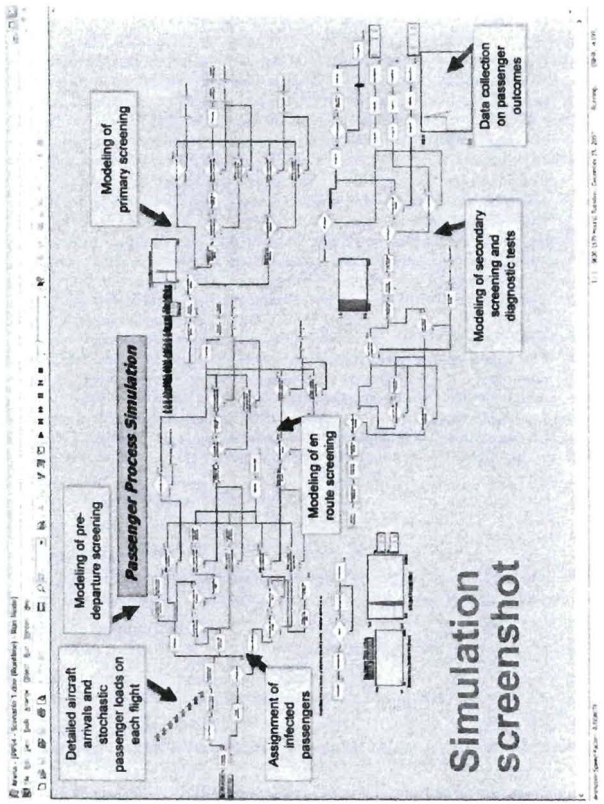


Figure 2 Screenshot of major elements (the larger blocks) associated with the passenger process simulation (see online version for colours)



5 Passenger process simulation details

This section describes the key components of the simulation. A high-level screenshot of the simulation is shown in Figure 2.

5.1 Generation of aircraft arrivals and passenger loads

The simulation starts with the generation of aircraft arrivals and passenger loads from international origins. Individual origins were grouped into one of four geographic regions – Asia, Europe, Latin America and Canada (e.g. flights from Hong Kong are in the Asia region). The modelled aircraft arrivals and passenger load distributions for San Francisco International Airport (SFO) are shown in Figure 3 (US Department of Transportation, Research and Innovative Technology Administration RITA (2006)). A portion of the Arena sub-module for the generation of these aircraft is shown in Figure 4. Passenger loads on each flight are determined by modelling historical minimum, mode and maximum historical passenger loads and then drawing a specific passenger load for each flight from a triangular probability distribution (Law and Kelton, 2000).

5.2 Assignment of infected probabilities

After passengers are generated in the simulation, they are assigned probabilities of being infected with pandemic influenza, p_{ip}, other respiratory illness, p_{io}, or not infected, $1-p_{io}-p_{ip}$. The functional form we used for p_{ip} for each region is as follows:

$$p_{ip_j} = 4c_j \frac{1}{1+10^{(-(t_s-a_j)/b_j)^2} \times 10^{(-(t_s-a_j)/b_j)}}$$

Figure 3 San Francisco international aircraft arrivals and passenger load distributions

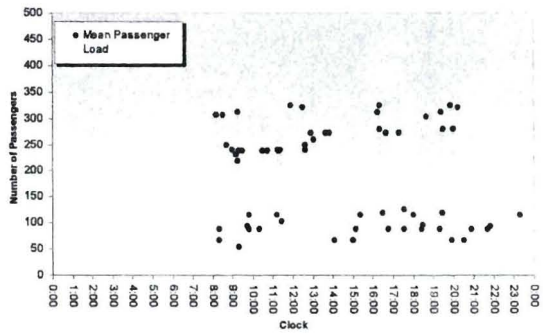


Figure 4 Screenshot of sub-module for aircraft generation and assignment of infected probabilities (see online version for colours)

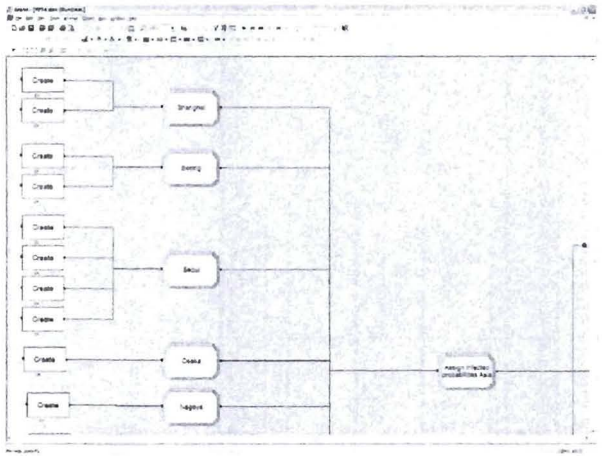
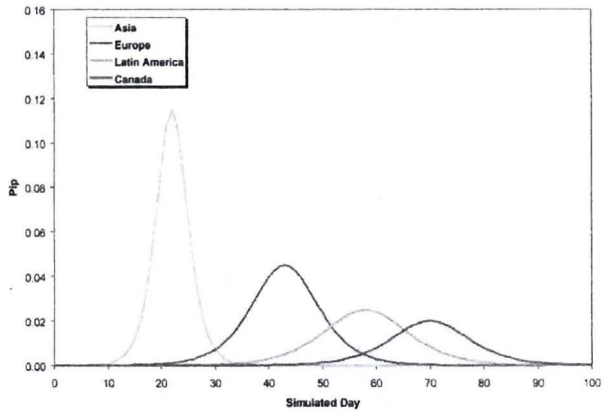


Table 1 Parameters used to compute p_{ip}

Parameter	*Asia*	*Europe*	*Latin America*	*Canada*
Approximate R_0	3.0	2.4	2.1	2.0
Center of curve	22	43	58	70
Spread of curve	4.5	9.5	12	11
Amplitude max	11.5%	4.5%	2.5%	2.0%

where $j = 1$–4 pertaining to the region of interest (i.e. Asia, Europe, Latin America or Canada), a_j is the centre of the epidemic curve, b_j is a measure of the spread of the epidemic curve, c_j is the peak amplitude of the epidemic curve and t_s is the simulation time in days (integer). The form of this curve is based on epidemic curves experienced in the 1918 influenza pandemic and presented by (though not necessarily endorsed by) M. Cetron (DGMQ, CDC) which originated with S. Barrett and MIDAS. A summary of parameter values for the different regions is provided in Table 1. These parameters yield the corresponding prevalence curves used for the probability of passengers being infected with pandemic influenza, based on their respective origin regions, as shown in Figure 5. The approximate value for the more common basic reproduction number, R_0, based on the selected parameter values for p_{ip} are also provided in Table 1 (Kretzschmar et al., 2004). For p_{io}, we assumed a constant value of 3% throughout the simulation (Malone, Madjid and Casscells, 2006). Again, we ran our simulation for 100 simulated days.

Figure 5 Probability of passenger being infected with pandemic influenza, pip, as a function of simulation day by origin region (see online version for colours)



Next, for passengers who are infected with pandemic influenza or other respiratory illness, we model the elapsed time since these passengers were first infected and when they become infectious, symptomatic and recover. In particular, using the parameters contained in Figure 6, each passenger infected is given the following attributes which are drawn independently

1 time when they first become symptomatic, $t_{ip} \sim U(12, 50)$ in hours

2 time when they would recover, $t_r \sim U(120, 384)$ in hours; the elapsed time since they were infected, $t_{ip} \sim U(0, t_r)$ in hours.

The same approach applies for those infected with other respiratory illness.

Using the parameters contained in Figure 7, we assign infected passengers with the following attributes:

1 time when passenger first becomes infectious, $t_{if} \sim \arg\min(t_{ip}, U(10, 48))$ in hours

2 period during which an infected passenger is infectious, $t_{in} \sim U(48, \arg\min(216, t_r - t_{if}))$ in hours.

Thus, a passenger is no longer infectious after $t_{if} + t_{in}$ hours. These functions ensure that a passenger cannot become symptomatic prior to becoming infectious nor be infectious after they recover.

Throughout the simulation, the elapsed time since being infected is updated so that a passenger's condition can change during the screening process and the corresponding detection parameter is applied at each screening layer.

Figure 6 Parameters and variables for asymptomatic and symptomatic times for infected passengers

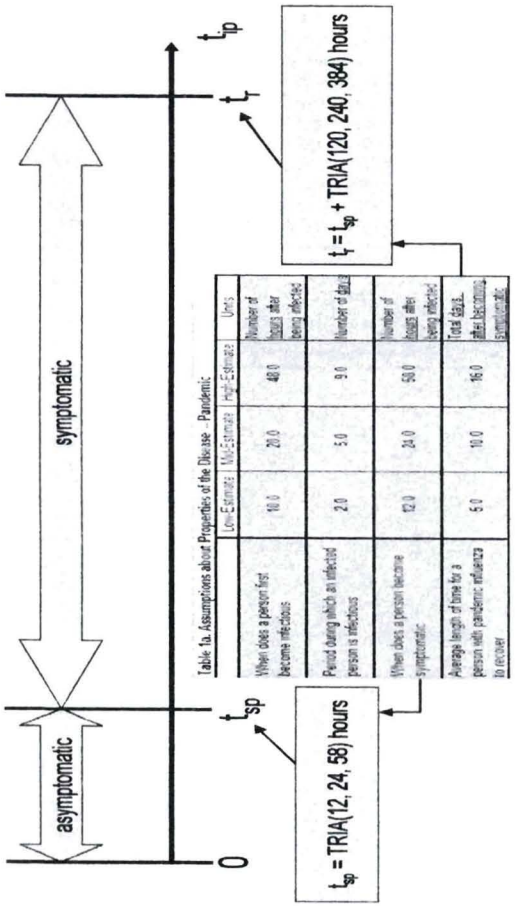
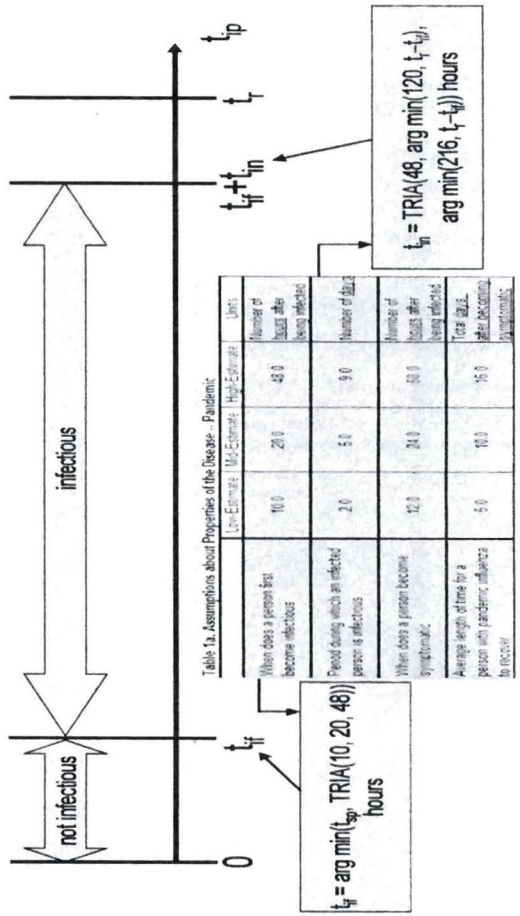


Table 1a Assumptions about Properties of the Disease – Pandemic

	Low Estimate	Mid Estimate	High Estimate	Units
When does a person first become infectious	10.0	20.0	48.0	Number of hours after being infected
Period during which an infected person is infectious	2.0	5.0	9.0	Number of days
When does a person become symptomatic	12.0	24.0	58.0	Number of hours after being infected
Average length of time for a person with pandemic influenza to recover	5.0	10.0	16.0	Total days after becoming symptomatic

Figure 7 Parameters and variables for infectious and infected times for infected passengers



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Period during which an infected person is infectious	2.0	5.0	9.0	Number of days
When does a person become symptomatic	12.0	24.0	58.0	Number of hours after being infected
Average length of time for a person with pandemic influenza to recover	5.0	10.0	16.0	Total days after becoming symptomatic

5.3 Modelling of pre-departure screening

In our model, each passenger passes through a simulated pre-departure screening layer at the originating airport. Detection parameters that determine if a passenger is denied flight depend on the passenger's true infected state (i.e. infected with pandemic influenza, infected with other respiratory illness or not infected) and the passenger's condition (i.e. asymptomatic or symptomatic). These parameters and parameters for the other screening layers are shown in Table 2. The 'gold' coloured cells indicated the baseline or Scenario 1 parameters values used in this study. We have also included model logic to allow a user specified percentage (e.g. 50%) of passengers who are infected and symptomatic, and who decide not to fly. This is akin to passenger self-screening as passengers who feel ill may decide to stay home until they feel better, especially if it is known that a pandemic has started and they may scrutinised during travel.

5.4 Modelling of en route screening

We next model the en route progression of the state of infected passengers and their potential detection by the flight crew. In this case, we also include a 2 hours pre-arrival time at the international origin for passengers. This time is accounted for in the model for disease progression. As above, passengers belonging to any of the true infected states could be identified by the flight crew, which would then require subsequent examination at secondary screening after the flight arrives in the US and the passengers are disembarked. In this case, these potentially infected passengers bypass primary screening and are sent directly to secondary screening in the model. In our model, as we track the progression of infected states and the corresponding flight durations, if a passenger ever reaches the symptomatic state en route, we use the higher en route detection probabilities as shown in Table 2 for symptomatic passengers.

5.5 Modelling of primary screening

Upon arrival in the US, all international passengers that were not identified en route as potentially infected with pandemic influenza will pass through primary screening. Again, infected passenger states are updated based on time elapsed since being infected. We model a standard 10 minute transit time to the primary area screening area. Passengers will also typically wait in line for primary screening due to finite resource levels and space. The delay time waiting in line at primary screening is accounted for in modelling passenger states and subsequent detection probabilities. At primary screening, we assumed a baseline resource level of six screeners who each monitor a single primary screening point with an assumed mean service time of 17.33 sec. To implement this in the model, we actually use a triangular distribution with minimum = 10, mode = 12 and maximum = 30 sec and draw a single occurrence from this distribution for each individual passenger upon processing at primary screening. Using the detection probabilities in Table 2, suspected ill passengers are routed to secondary screening for further examination. The remaining passengers are allowed to leave the screening system and to proceed to the federal inspection services (FIS; e.g. customs and immigration inspections).

Table 2 Table of detection parameters at various screening stages (see online version for colours)

Case	Condition	Pre-Departure				En Route				Primary Arrive Surveillance			
		Likelihood of being detected as possibly having pan flu at pre-departure screening as a result of flight (percentage)			Likelihood of NOT detected at pre-departure screening as possibly having pan flu			Likelihood of being detected en route as possibly having pan flu (percentage)		Likelihood of NOT being detected en route as possibly having pan flu		If not detected en route, the likelihood of being detected at Primary Arrive Surveillance as a possibly having pan flu (percentage)		If not detected en route, the likelihood of also NOT being detected at Primary Arrive Surveillance as possibly having pan flu	
		Low-Estimate	Mid-Estimate	High-Estimate	High-Estimate	Mid-Estimate	Low-Estimate	High-Estimate	Mid-Estimate	High-Estimate	Mid-Estimate	Low-Estimate	High-Estimate	Mid-Estimate	High-Estimate	Mid-Estimate	Low-Estimate
Infected with pandemic influenza	Symptomatic	20.0%	60.0%	80.0%	80.0%	56.0%	20.0%	70.0%	56.0%	80.0%	56.0%	56.0%	10.0%	60.0%	90.0%	45.0%	10.0%
	Asymptomatic	0.0%	1.0%	2.0%	100.0%	99.0%	98.0%	2.0%	1.0%	100.0%	99.0%	98.0%	1.0%	2.0%	3.0%	99.0%	97.0%
Infected with a respiratory illness other than pandemic influenza	Symptomatic	20.0%	40.0%	60.0%	80.0%	60.0%	40.0%	60.0%	40.0%	80.0%	60.0%	40.0%	10.0%	60.0%	90.0%	55.0%	25.0%
	Asymptomatic	0.0%	1.0%	2.0%	100.0%	99.0%	98.0%	2.0%	1.0%	100.0%	99.0%	98.0%	1.0%	2.0%	3.0%	99.0%	97.0%
No respiratory illness		0.0%	1.0%	2.0%	100.0%	99.0%	98.0%	2.0%	1.0%	100.0%	99.0%	98.0%	0.0%	1.0%	2.0%	100.0%	98.0%

NOTE: The magnitude of the Low Estimate is less than that for the Mid-Estimate, which is less than that for the High-Estimate.

Use of the parameter values: Low-, Mid-, and High- values are used to define a triangular probability distribution from which simulation draws are made in the passenger screening procedure.

Case	Condition	Secondary					
		Likelihood of Receiving PCR Test			Likelihood of NOT detected at pre-departure screening as possibly having pan flu			PCR Test Outcomes (Likelihood of Infected + No False Pos)		
		Low-Estimate	Mid-Estimate	High-Estimate	High-Estimate	Mid-Estimate	Low-Estimate	Low-Estimate	Mid-Estimate	High-Estimate
Infected with pandemic influenza	Symptomatic	90.0%	95.0%	99.0%	50.0%	5.0%	1.0%	90.0%	95.0%	99.0%
	Asymptomatic	10.0%	20.0%	25.0%	50.0%	80.0%	75.0%	90.0%	95.0%	99.0%
Infected with a respiratory illness other than pandemic influenza	Symptomatic	90.0%	95.0%	99.0%	50.0%	5.0%	1.0%	25.0%	50.0%	0.0%
	Asymptomatic	10.0%	20.0%	25.0%	50.0%	80.0%	75.0%	25.0%	50.0%	0.0%
No respiratory illness		10.0%	20.0%	25.0%	50.0%	80.0%	75.0%	25.0%	50.0%	0.0%

5.6 Modelling of secondary screening and diagnostic tests

For those passengers directed to secondary processing, we update the progression of the illness in infected passengers. For passengers arriving from primary screening, we include another 10 minute transit time from primary screening. As before, passengers also have to wait in line to be seen by health care professionals at secondary screening so that this wait time is accounted for and the state of their illness is updated prior to examination so that the appropriate detection probability is applied. At this point, the medical professional can release the passenger to the FIS as not being suspected ill or can direct the passenger to undergo a formal diagnostic test. In the latter case, we modelled an RT-PCR diagnostic test with sensitivity (i.e. infected with pandemic influenza) and specificity (i.e. not infected with pandemic influenza) values as shown in Table 2. At secondary screening, our baseline assumption includes a total of eight medical professionals to process passengers and decide on passenger conditions/diagnostic tests. It is assumed that the mean service time for each passenger 7.67 minutes. To implement this in the model, we actually use a triangular distribution with minimum = 3, mode = 5 and maximum = 15 minutes and draw a single occurrence from this for each individual passenger going through secondary screening.

For the RT-PCR test, we assumed a mean processing time of 7.67 hours (triangular distribution with minimum = 3, mode = 5 and maximum = 15 hours). The estimates were based on discussions with subject matter experts in the field. These discussions indicated that even though the actual test could be done in a considerably shorter amount of time, the collection of a specimen from the passenger, its delivery to a testing laboratory (perhaps to a different part of the city from the airport) and reporting on results could cause the test to take significantly longer. After airport health screening personnel receive the RT-PCR test results, the passenger's condition is declared as either being infected with pandemic influenza or not.

5.7 Data collection on passenger outcomes

Ultimately, every passenger who enters the US in our model is given one of the four outcomes discussed above (i.e. true positive, false positive, true negative or false negative). These outcomes are tracked over time in the simulation and are used for computing various metrics and results, a sample of which is shown in Section 6.

6 Sample results

Running our simulation produces a variety of pertinent output metrics, both epidemiological (e.g. number of pandemic influenza infected passengers entering the US over time) and operational in nature (e.g. passenger waiting times at the various screening layers).

Figure 8 shows a sample of a portion of the simulation output as captured in a spreadsheet. Additional sample results are shown in Figures 9–13 based on our assumptions for SFO. Figure 9 shows a comparison of false negative, true positive and false positive passengers by simulation day for SFO. Figure 10 shows a similar plot of combined false negative and true positive passengers broken out by respective origin regions. Figure 11 shows a comparison of false negative outcomes if no screening was done at all, if just origin exit screening was invoked, and then the full entry screening process as described.

Figure 8 Sample of a portion of output from passenger process simulation

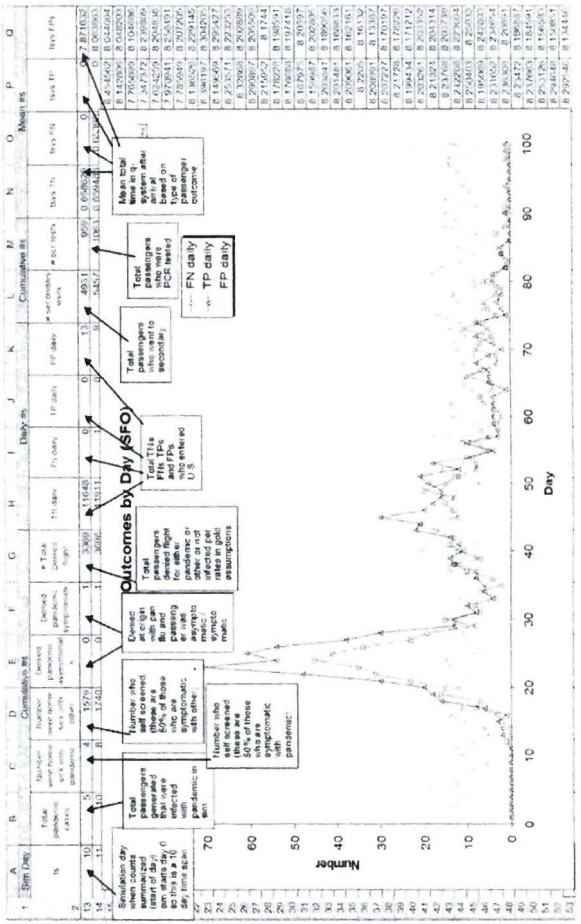


Figure 12 shows false positive outcomes by region for SFO. It is important to track and account for false positive passengers because they will consume screening process resources (both personnel and supplies like antiviral medications), add to the overall mean wait time of passengers in the airports, and cause stress to these erroneously diagnosed passengers.

Lastly, Figure 13 displays the total time in the screening system upon arrival at SFO for the different passenger outcomes. True positive and false positive passengers spend considerably longer time in the system because they are sent to secondary screening and a large percentage of these passengers then undergo RT-PCR testing.

Figure 9 Aggregate false negative, true positive and false positive summary for San Francisco international airport (mean number of outcomes by day for 30 simulation replications)

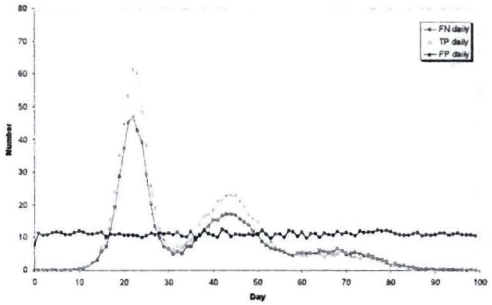


Figure 10 Aggregate false negative and true positive summary for San Francisco international airport (mean number of outcomes by day for 30 simulation replications) (see online version for colours)

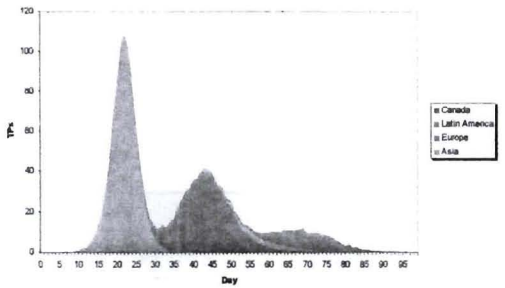


Figure 11 Comparison of false negative outcomes for different levels of screening for San Francisco international airport (mean number of outcomes by day for 30 simulation replications) (see online version for colours)

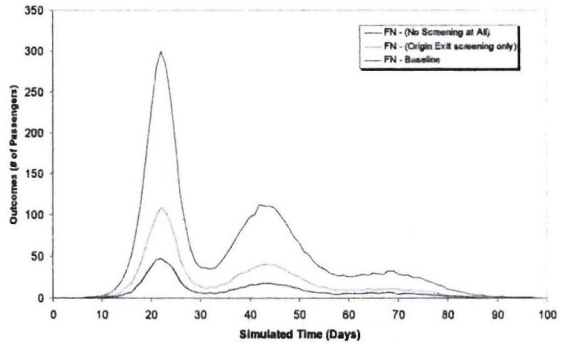


Figure 12 Comparison of false positive outcomes, by region, for San Francisco international airport (mean number of outcomes by day for 30 simulation replications) (see online version for colours)

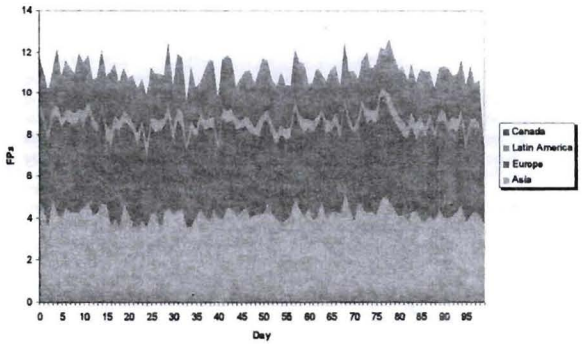
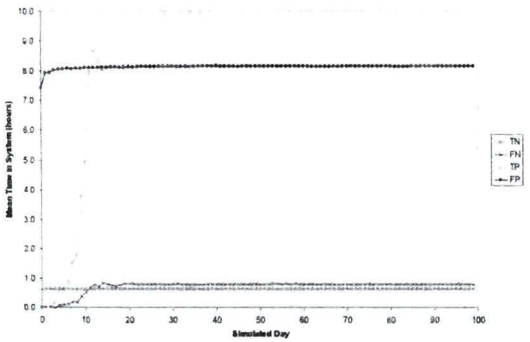


Figure 13 Comparison of total time in system by outcome for San Francisco international airport (mean number of outcomes by day for 30 simulation replications)



In our work, we focused on SFO but then applied our analysis by appropriately scaling the SFO results (i.e. different flight arrival patterns, passenger loads and region origins were accounted for) to the other US airport ports of entry for a nation wide look at passenger screening.

7 Conclusions

This simulation is quite powerful in its ability to model individual passenger infected states and conditions stochastically, incorporating epidemiologic prevalence functions directly into the simulation, and outputting an estimate on the number of pandemic influenza infected passengers entering the United States as a function of time. Detection efficacy at the various layers can be modelled to determine the overall effectiveness of the screening process. Of course, the model is highly dependent on input parameter assumptions like pandemic influenza prevalence rates at origin regions and detection probabilities at the various screening layers. Hence, care should be taken in making broad conclusions from the simulation, and sensitivity analysis on results should be conducted. In addition, at this point we have not applied high fidelity modelling of the different potential specific screening protocols for each passenger, but this is a potential area for future research as warranted. Some specific conclusions and insights based on our results are as follows.

1 *Importance of exit screening*. International agreements that enable extensive pre-departure screening could greatly reduce the number of infected passengers entering the US. In fact, based on the parameters assumed in our study, this is one of the major screening layers used to remove infected passengers from inbound flights to the United States.

2 *Effectiveness of entry screening*. Effective entry screening can reduce entry of infected people by more than 50%, but effectiveness of screening is limited by the number who are asymptomatic. This conclusion points to the need for research on technologies/methods that can be used to identify asymptomatic passengers.

3 *Effect of screening on timing of entry*. The results, indicate that the impact of entry screening is primarily on reducing the numbers of infected passengers entering the country undetected, and not so much on significantly delaying the day when the initial infected passengers enter the country.

4 *Secondary cases*. In addition to the above results and conclusions, secondary cases (i.e. those who contracted influenza during travel) are not factored into the above statistics and could be a significant source of additional, undetected infected passengers.

5 *Strain on resources*. Screening activities could require significant airport-terminal space and result in significant passenger delays. A key point here is that due to the stochastic nature of flight arrivals, passenger loads and service times, queues will build up. Resource (e.g. equipment, space and personnel) requirements might need to be planned against maximum as opposed to the mean queue lengths and holding requirements.

6 *Diagnostic advances could reduce delays*. We are able to estimate passenger processing times and queue lengths at various stages in the process, as well as resource utilisation levels based on the assumed resource staffing levels. This capability could facilitate assessments of quarantine and screening system needs, such as adequate personnel staffing levels, physical space requirements and other related infrastructure needs (Quarantine Stations at Ports of Entry Protecting the Public's Health, 2006). Development of new diagnostic tests could greatly reduce delays to airport passengers waiting for test results. The major contributor for long service times for passengers is waiting for RT-PCR test results. If such tests could be automated and/or made shorter and/or be carried out at point-of-care at the airport, wait times could be significantly reduced.

One last comment worth mentioning is that the simulation allows us to estimate each of the true positive, false positive, true negative and false negative values over time. In reality, we would only actually know the true positive values under a real pandemic since, for example, if we could identify infected passengers, then they would be true positive passengers. Knowing this, it might be possible to correlate model outputs with real world observed true positive values to estimate the false negative passengers into our country.

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