Modelling Influenza Pandemic, Intervention Strategies, and Food Distribution

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Based on the recent incidents of avian flu (H5N1) in Asia and the influenza pandemic cases in history (1918, 1957 and 1968) experts believe that a future influenza pandemic is inevitable and likely imminent. Evidence suggests that an efficient and rapid response will be crucial for mitigating morbidity, mortality, and costs to society. Hence, preparing for a potential influenza pandemic has received high priority from governments at all levels (local, state, federal), non-governmental organizations (NGOs), and companies. In this paper, in collaboration with the American Red Cross, we study the logistics side of the problem, specifically, food distribution logistics during an influenza pandemic. We develop a disease spread model to estimate the spread pattern of the disease geographically and over time, integrate it to a facility location and resource allocation network model for food distribution, and develop heuristics to find near-optimal solutions for large instances. We run our integrated disease spread and facility location model for the state of Georgia and present the estimated number of infections and the number of meals needed in each census tract for a one year period along with a design of the supply chain network. We analyze the impact of two intervention strategies, namely, school closure and voluntary quarantine; our results indicate that voluntary quarantine may be a better alternative due being more effective and less disruptive. Moreover, we investigate the impact of voluntary quarantine on the food requirement and the food distribution network, and show that its effect on the food distribution supply chain can be significant.

1. Introduction

Many experts believe that an influenza pandemic will hit the world in the near future given the flu cases that happened in the last few years (avian flu-H5N1) and the history of influenza pandemic (Morse et al. 2006). Epidemiologists warn that the next influenza pandemic could infect 33% of the population and kill millions (Gibbs and Soares 2005). The World Health Organization (WHO) estimates that 2-7.4 million people might die worldwide (World Health Organization 2005). Furthermore, the next influenza pandemic might cause a $71.3-165.5 billion economic impact on

the United States economy (Meltzer et al. 1999).

Increased travel volumes favor the spread of infectious diseases (Grais et al. 2003) which makes surveillance and planning activities more important. As a preparedness plan, WHO strengthened its influenza surveillance and control system, and it is operating more than 100 laboratories in 83 countries all over the world (Webby and Webster 2003). Different from other influenza pandemic cases in history, the recent cases of bird flu gave a clear warning and have been eliminated by the monitoring and intervention efforts of WHO (World Health Organization 2005).

The impact of influenza pandemic cases in history shows the extent of how governments need to prepare response plans. There have been three cases of worldwide influenza pandemic in the 20th century, namely, Spanish flu (1918), Asian flu (1957) and Hong Kong flu (1968). There are different estimates about the number of deaths during these three pandemic cases. Although the figures are a little different in different sources, they all reflect the severity of the situation. The estimates due to Smith (2006) are presented in Table 1.

Table 1   Influenza pandemic cases in history.

Past Cases	Mortality	Populations Affected
1918-19 (Spanish flu) (A/H1N1)	40-50 million (2.2-2.8%)	Persons < 65 years
1957-58 (Asian flu) (A/H2N2)	2 million (0.069%)	Infants, elderly
1968-69 (Hong Kong flu) (A/H3N2)	1 million (0.028%)	Infants, elderly

The U.S. Department of Health & Human Services and the U.S. Department of Commerce estimate that in the next pandemic 20% of working adults may become ill, and there may be a 40% workforce loss during the pandemic peak because of illness, fear of infection and the need to care for infected family members or school-aged children. The reduced active workforce level in critical services may result in secondary consequences causing greater impact than the influenza pandemic itself.

Many governments prepare for a middle-ground estimate that 25% percent of their entire nation will be infected during the course of an upcoming pandemic (Gibbs and Soares 2005). According to WHO, fifty countries have developed pandemic preparedness plans and most industrialized

countries are stockpiling antiviral drugs (Carrat et al. 2006). Although most preparation has focused on developing cell-culture vaccine manufacturing, stockpiling antivirals and vaccines, and school closing plans, designing response supply chains is also very important for meeting the various needs of the public during an influenza pandemic. Some of the infected individuals may not be able to go to grocery store to buy food, e.g., if they follow voluntary quarantine recommendations and stay home. Logistics of delivering these basic supplies to infected or quarantined households is an important operations research question (Wu et al. 2006).

In addition to governments, many NGOs have worked on response plans for a potential influenza pandemic (Morse et al. 2006, Holmes et al. 2005). For example, the American Red Cross Metropolitan Atlanta Chapter (ARC-MAC) has worked on determining ways to provide food to people who are infected and have to be treated at home (American Red Cross Metropolitan Atlanta Chapter 2006). The Ohio Department of Health and the Ohio Food Industry Foundation prepared an influenza pandemic preparedness plan for groceries (Ohio Department of Health and Ohio Food Industry Foundation 2006). The estimates about the spread pattern of the disease and the number of infected people at a given time at each location help governments and NGOs to develop detailed response plans. Thus, the modelling of the disease spread is an important step in preparing response plans for an influenza pandemic.

In this paper, we consider the problem of providing food to people who are not able to obtain it due to illness in their household during the influenza pandemic. First, we develop a disease spread model to estimate the spread of the disease geographically and over time and then construct a food distribution network based on these estimates. To the best of our knowledge, this is the first study in the literature integrating a disease spread model and a food distribution model for planning purposes. We compare the impacts of school closure and *voluntary quarantine*, i.e., the individuals in the households with an infected individual stay home voluntarily with some compliance rate limiting their peer group and community interactions, on the disease spread. Finally, we study the effect of voluntary quarantine on the food distribution supply chain. The results of our research

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have been incorporated into the manual of ARC-MAC on food distribution planning during an influenza pandemic (American Red Cross Metropolitan Atlanta Chapter 2008).

The remainder of the paper is organized as follows. In Section 2, we present the literature on the disease spread models and facility location problems. The disease spread model we developed and the simulation results follow in Section 3. We study the voluntary quarantine as an intervention policy and present the results in Section 4. Moreover, we compare its impact to that of school closure. The alternatives for food need estimation follow in Section 5. In Section 6, we provide the facility location model, propose a greedy heuristic to solve it and present the solution approaches proposed for food distribution. In Section 7, we provide the results of computational experiments and report on the performance of the heuristics proposed for food distribution logistics. We also provide insights about the impact of voluntary quarantine on food distribution. Finally, we conclude with future research directions regarding planning for an influenza pandemic.

2. Literature Review

There are two main streams of literature related to our research: (i) disease spread models, and (ii) facility location and distribution models.

The disease spread models are developed to predict the spread patterns and the effect of intervention strategies in populations with complex social and spatial structures and have been thoroughly researched for different infectious diseases such as influenza, smallpox and SARS (see Ferguson et al. (2003a) for a review of spread models for smallpox and Lipsitch et al. (2003) for SARS).

There are four common ways to model the spread of an infectious disease in a population: (i) using differential equations (Cahill et al. 2005, Fraser et al. 2004), (ii) simulation modelling (Ferguson et al. 2006, Germann et al. 2006, Wu et al. 2006), (iii) random graphs (Carrat et al. 2006), and (iv) difference equations (Rvachev and Longini 1985, Grais et al. 2003). In differential equation models, every individual is assumed to be in one of the disease stages, e.g., susceptible (S), infected (I), or recovered (R) in an S-I-R model, and the cumulative number of people in each stage is used to define the instant changes on the cumulative numbers. In simulation models,

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the entire population is identified by individuals and social contact networks, e.g., households and peer groups, and the spread of the disease is predicted by discrete event simulation modelling. In random graph models, random graphs are used to construct the contact network, and the disease spread is predicted accordingly. In the models that use difference equations, the entire time horizon is identified by a sequence of time intervals, and the disease spread is predicted recursively. The spread in each time interval is defined as a function of the spread in previous intervals. Another feature that distinguishes disease spread models is the mixing assumption. In homogeneous mixing every individual has the same chance to get infected, while in heterogenous mixing the chance of getting infected for an individual depends on the number of contacts s/he makes during the day, which varies from person to person. Thus, disease spread models with a heterogenous mixing assumption capture more aspects of a real life setting, but as expected they are more complex when compared to homogeneous models. Table EC.1 in the e-companion summarizes the literature about the modelling of influenza pandemic and annual influenza.

There are two performance measures commonly used to evaluate the effectiveness of intervention policies, namely, *peak infectivity* and *infection attack rate (IAR)*. *Peak infectivity* is the percentage of the infected (symptomatic or hospitalized) population at the peak, and *IAR* is the cumulative percentage of people who have been infected (can be symptomatic or asymptomatic) during the course of the disease. School or workplace closure and other social distancing measures such as travel restrictions and quarantine during the peak can reduce the *peak infectivity* but may not significantly affect *IAR* (Ferguson et al. 2005, Germann et al. 2006, World Health Organization 2005). For example, social distancing measures only delayed the spread in the 1918 and 1957 pandemics (World Health Organization 2005, World Health Organization Writing Group 2006) but had little impact on *IAR*. Nevertheless, delaying the spread and the peak is desirable for planning purposes, since it provides more time to get prepared, and a flattened spread (with a smaller peak) decreases the probability of interruption of services and is less likely to result in capacity being the bottleneck in a response activity.

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We develop a simulation based disease spread model with *heterogeneous* mixing to predict the spread pattern of the disease *geographically* and *over time*, and test the effectiveness of voluntary quarantine as an intervention policy. Different from other papers in the literature, we consider the case when voluntary quarantine is active for a limited period of time. The comparison of the relevant models in the literature and our model is provided in Section 3 where we provide full details of the disease spread model.

Given an estimate of the disease spread over time and geographically, we need to determine the location of food distribution facilities and how to open and close them over time. This is a capacitated multi-period hierarchical facility location problem (FLP) with two levels of facilities between supply and demand nodes.

Capacitated and uncapacitated multi-period FLPs have been extensively studied in the literature (Roy and Erlenkotter 1982, Shulman 1991). Erlenkotter (1981) provides a comparison of the solution approaches for the multi-period FLP. A popular solution approach for dynamic FLP is to generate the alternative solutions for the single period problem and look for the best combination of these alternative solutions by dynamic programming (Sweeney and Tatham 1976, Ballou 1968).

Hormozi and Khumawala (1996) propose an exact algorithm to solve the uncapacitated dynamic FLP integrating mixed-integer and dynamic programming methods. They reduce the size of the state space for the algorithm proposed by Sweeney and Tatham (1976). Canel et al. (2001) study the capacitated multi-commodity multi-period hierarchical (two-echelon) FLP and develop a 2-stage solution method. First, they use a branch and bound algorithm to generate a set of candidate solutions for each period. Then, they use dynamic programming to find the optimal sequence of candidate solutions over the multi-period horizon. Their algorithm is effective when facility opening and closing costs are high. Hinojosa et al. (2000) also consider the capacitated multi-commodity multi-period hierarchical FLP, and propose a Lagrangean relaxation scheme with a heuristic algorithm for finding feasible solutions.

We formulate the *capacitated multi-period hierarchical* FLP for food distribution (CMPH-FLP) as a mixed integer linear program different from other papers in the literature (Canel et al. 2001,

Hormozi and Khumawala 1996), which propose a nonlinear formulation to solve a similar problem. Due to the size of CMPH-FLP in real world applications, algorithms that require solving a mixed integer program at each step cannot solve the problem efficiently. Even the single period version of CMPH-FLP cannot be solved optimally using a commercial solver such as CPLEX 9.0 for large instances. Thus, using the information about the demand pattern (as discussed in Section 5), we develop a heuristic to solve CMPH-FLP and propose an integrated solution approach that links the disease spread model and the facility location model with disease spread updates.

3. Disease Spread Model, Results, and Validation

We construct an individual-based continuous time stochastic model for influenza transmission. In the base model, we do not apply any intervention strategy. We investigate the effect of voluntary quarantine (or social distancing) and school closure on the spread of the virus in Section 4. In addition to food distribution planning, this model may also be useful for other purposes such as estimating the region-based hospital capacity needs for local governments for planning purposes.

The disease spread model is composed of two parts: (i) the progress of the disease within an infected individual, and (ii) the spread of the disease among the members of the population.

In our model, an infected individual goes through the stages of the disease according to the natural history for influenza pandemic in Wu et al. (2006) (see Figure 1(a)). Each individual is assumed to be in one of the following stages at a given time: susceptible (S), exposed (E), presymptomatic (I_P), asymptomatic (I_A), symptomatic (I_S), hospitalized (I_H), recovered (R) or dead (D). p_A is the probability of not developing symptoms, p_H is the probability of hospitalization for a symptomatic individual, and p_D is the probability that a hospitalized individual dies. We summarize the values of the natural disease history parameters and the relevant references in Table EC.2 in the e-companion.

The spread of the disease among the members of the population can be modelled via a contact network. Population heterogeneities such as age, density and geography are important in predicting the disease spread (Grais et al. 2003); thus, we construct a disease spread model that takes into
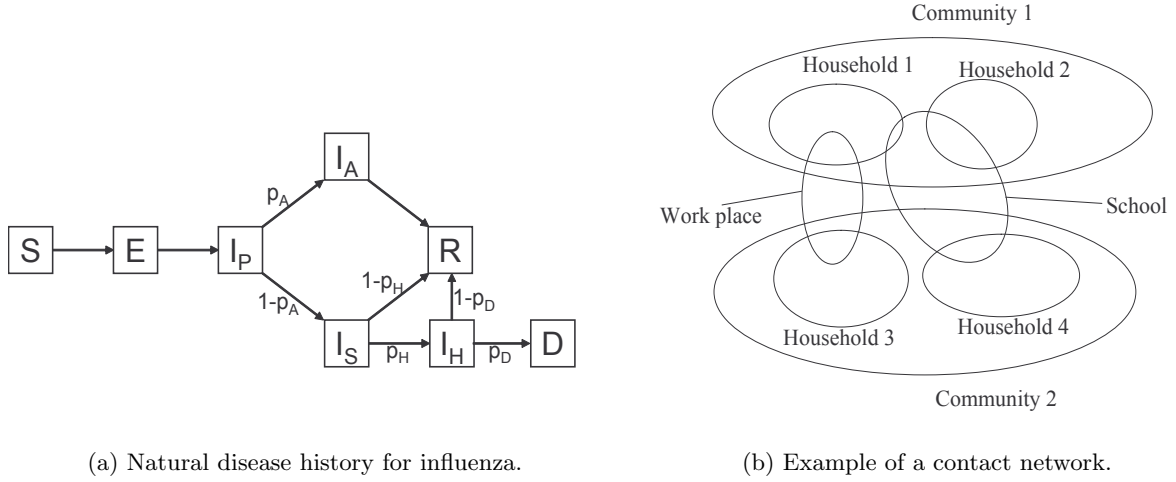
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(a) Natural disease history for influenza.

(b) Example of a contact network.

Figure 1 **Two main components of the disease spread model.**

account such population heterogeneities. First, the whole population is divided into communities that correspond to neighborhoods. The communities are linked to each other via peer groups, which account for the inter-community spread of the disease. The progress of the disease depends on the age of the individual (Wallinga et al. 2006), which determines their contact groups. For example, children are considered to play a major role in the transmission of influenza (Viboud et al. 2004) because they are assumed to be more susceptible due to lower immunity (although it depends on the virus type) and to have more daily contacts through schools and play groups than adults have in work places. Hence, we divide the population of each community into five age groups, namely, 0-5, 6-11, 12-18, 19-64, 65+. In our model, we consider three levels of mixing: (i) community (day/night) (ii) peer group (day) and (iii) household (night) (see Figure 1(b)). All the individuals mix in the community during the day by visits to common areas such as grocery stores, churches, theaters, etc. The children in the first three age groups (0-5, 6-11, 12-18) mix with other children in kindergarten, elementary, and secondary schools. People in the age group 19-64 are considered as working adults, and they mix in work places with other adults. We assume 50% of adults and 100% of children do not mix in their peer groups when symptomatic, which is consistent with Wu et al. (2006) and Ferguson et al. (2005). The elderly are assumed to not mix in peer groups. To summarize, a susceptible individual in the community can get infection from the

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other individuals in his/her household, peer group or in the community with different probabilities (contact rates) in each. We assume a constant import rate (1.5 infected individuals per day per 100,000 people) for each community, which represents the infected people coming from outside the contact network (Wu et al. 2006).

Our disease spread model is generic and can be applied to any geographical area. Given our collaborations with ARC-MAC, Georgia Department of Education, and Georgia Department of Human Resources, we take the state of Georgia as the test case and construct our model accordingly. There are 159 counties and 1615 census tracts in the state of Georgia, and the total population is 9,071,756. We consider each census tract as a single community and use census data (U.S. Census Data 2000) to form the households and peer groups and to identify the sizes of the age groups.

Table 2 compares the most relevant models in the influenza pandemic literature and our disease spread model. To summarize, we develop a detailed SEIR (Susceptible-Exposed-Infected-Recovered) disease spread model with a spatial (geographical) component, age-based structure, heterogenous mixing, and night/day differentiation. The spatial component enables us to predict the spread geographically over an area, night/day differentiation helps us differentiate the type of interactions people have during the day and night. Finally, age-based structure and heterogenous mixing provide a more realistic model because of the differences in the susceptibility and infectivity of the individuals as well as their social interactions due to their ages.

Table 2   **Comparison of the proposed model with the ones in the literature.**

Reference	Natural History	Spatial Component	Age-Based	Night/Day Differentiation
Wu et al. (2006)	Detailed SEIR	No	No	No
Ferguson et al. (2006), Ferguson et al. (2005), Patel et al. (2005), Longini et al. (2005)	SEIR	Yes	Yes	No
Germann et al. (2006)	SEIR	Yes	Yes	Yes
Our Model	Detailed SEIR	Yes	Yes	Yes

Our model also differs from the papers listed in Table 2 in the implementation strategy of the

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voluntary quarantine. We consider a limited time voluntary quarantine since prolonged quarantine times may have a negative impact on the public morale. Social distancing measures such as voluntary quarantine isolate people and limit public gatherings, which are indicators of normal life and help maintain public morale (Department of Health, Social Services and Public Safety 2008). According to a survey (Hawryluck et al. 2004) and empirical research (Cava et al. 2005) based on the SARS experience in Toronto, people may develop emotional problems during and after the quarantine. Thus, it is in the public officials' interest to obtain maximum benefit out of voluntary quarantine by keeping the disruption in people's normal lives at a minimum. When voluntary quarantine is encouraged (or promoted via educational materials) for a limited time, the start time and the duration are important decision variables.

The details of the disease spread model and the relevant parameters are explained in Section EC.3 of the e-companion. An important parameter in the model is the basic reproductive number (R_0), which is the average number of secondary cases caused by an infectious individual and determines the infectivity of the virus. For example, R_0 for Spanish flu in 1918 is estimated to be around 1.7-2.0 (Ferguson et al. 2006) or 2-3 (Mills et al. 2004). On the other hand, R_0 for the 1957 and 1968 pandemics are estimated to be around 1.5-1.7 (Ferguson et al. 2006) and 1.89 (Rvachev and Longini 1985), respectively.

We ran the simulations for a range of R_0 values to account for low ($R_0 = 1.5$), medium ($R_0 = 1.8$) and high ($R_0 = 2.1$) infectivity. Figure 2 shows the spread of the disease over time among the population of Georgia for different R_0 values. Table 3 summarizes the simulation results in the absence of intervention policies. *Peak infectivity* and *IAR* (*infection attack rate*) are defined above. *Peak day* is the time when the percentage of the infected population is at its maximum. *CAR* (*clinical attack rate*) is the cumulative percentage of the people who have been symptomatic, and *death ratio* is the percentage of the people who died because of influenza during the course of the disease.

In planning for food (or other resource) distribution, the spread of the disease over area and time is important since the time and the location of the food need determines the location and
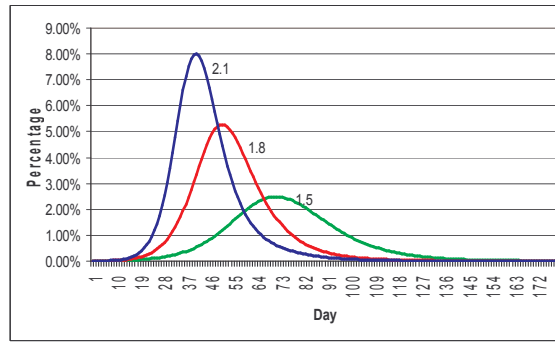
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Figure 2   Percentage of symptomatic or hospitalized individuals under no intervention.

Table 3   Results of the disease spread model with no intervention policy.

R_0	Peak Infectivity	Peak Day	CAR	IAR	Death Ratio
1.5	2.48%	70	32.50%	49.65%	0.57%
1.8	5.27%	50	44.20%	67.49%	0.80%
2.1	8.01%	40	51.27%	78.27%	0.93%

opening/closing time of the facilities. Figure 3 shows the spread of the disease for two different disease initializations (seeds) over time (for days 10 and 50) and area for $R_0 = 1.8$ (see Figure EC.1 in the e-companion for the spread of the disease between days 10 and 90). The shades are on a logarithmic scale, and darker shades represent higher number of infections in the relevant area. In the first case, the infection starts from **Atkinson** county which is a rural area in the southeast part of Georgia. In the second case, the infection starts from **Fulton** county which is in the Metropolitan Atlanta Area. As the maps in Figure 3 show, the spread in the Metropolitan Atlanta Area is not affected much by the location of the initial seed; these areas are always highly infected around day 50. However, the spread in the rural areas can depend on the location of the first infection (see Figure EC.1 in the e-companion).

As discussed before, our disease spread model parameters are in line with what have been used in the literature by several authors. To further validate our model, we calibrated the model parameters to obtain the age-specific clinical attack rates for the 1957 influenza pandemic reported by Chin et al. (1960). The calibrated and the original values are listed in Table EC.3 in the e-companion. We obtained similar age-specific clinical attack rates for an R_0 value of 1.58, which is also consistent with the estimated R_0 value of 1.5-1.7 for 1957 pandemic (Ferguson et al. 2006). The age-specific

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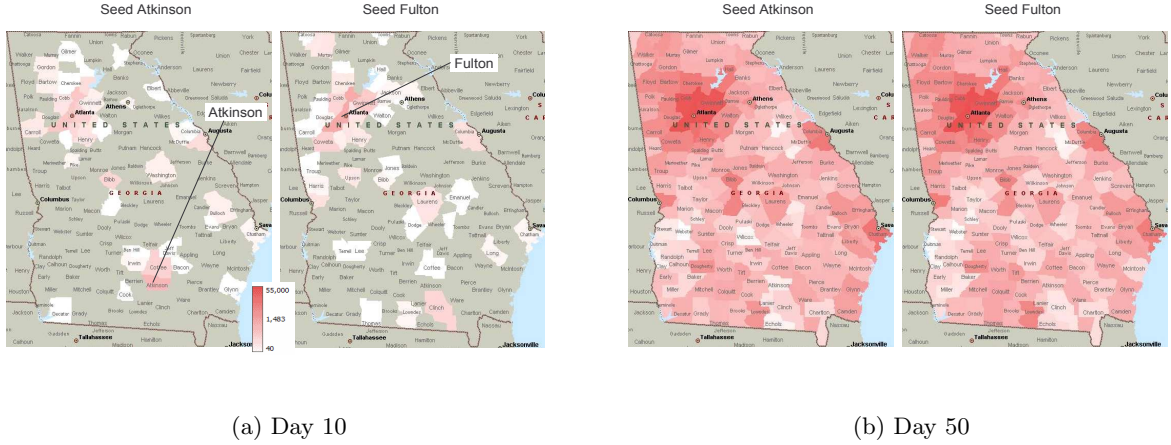
| (a) Day 10 | (b) Day 50 |

Figure 3 Comparison of the disease spread when the pandemic starts in a rural, less populated county (Atkinson) versus a central, densely populated county (Fulton). Darker shades indicate higher infection rates.

and total clinical attack rates obtained using our model and the realized values in 1957 pandemic are summarized in Table EC.4 in the e-companion.

4. Intervention Policy: Voluntary Quarantine vs. School Closure

In this section, we investigate the effect of a voluntary quarantine for several R_0 values. In addition, we compare voluntary quarantine and school closure in terms of their impacts on the disease spread. Since quarantined people interact with other individuals in their households, the risk of getting infection within the households is doubled for quarantined households, consistent with Wu et al. (2006), Longini et al. (2005) and Ferguson et al. (2006). It is a voluntary quarantine where we assume 50% compliance, that is, individuals in the quarantined households comply with the quarantine independently with probability 0.5. (We also ran experiments with other compliance rates and observed that while higher compliance decreases both the *peak infectivity* and *IAR*, there are diminishing returns.) A household may be quarantined if an individual from that household develops symptoms or the individual is hospitalized. Once a household is quarantined, if no other individual in the quarantined household develops symptoms or gets hospitalized for a week, the quarantine is released. Otherwise, the quarantine is extended for another week for that household. The quarantine is active for a limited period of time (2-12 weeks).

Both the timing and the length of the quarantine are important in order to obtain the maximum benefit. We are particularly interested in the impact of voluntary quarantine on *peak infectivity*, which relates to the maximum capacity for the resources that governments and NGOs may need to serve the needs of the public, and the *IAR*, which relates to the total amount of resources during the course of the disease. Figure 4 shows the effect of the quarantine on the *peak infectivity* and *IAR* for $R_0 = 1.8$ as a function of the start time and length. For a 2-week quarantine, the *peak infectivity* is lowest (3.40%) when the quarantine starts at the beginning of the sixth week. On the other hand, for a 12-week quarantine, the best start time in terms of *peak infectivity* is the beginning of the third week, and in this case the *peak infectivity* is 1.79%. From Figure 4(a), even a 12-week quarantine has no effect on the *peak infectivity* if the timing of the quarantine is not appropriate. From Figure 4(b), *IAR* is 59.71% if a 2-week quarantine is implemented at the beginning of week 7. For a 12-week quarantine, *IAR* is lowest (47.32%) if it is implemented at the beginning of week 5. *In general, as the length of the quarantine increases, the optimal start time (for minimizing the peak infectivity or IAR) decreases.* Note that the optimal start time of a quarantine is also related to the timing of the peak of the disease, which depends on R_0. As R_0 increases it is best to start the quarantine earlier to reduce *peak infectivity*.
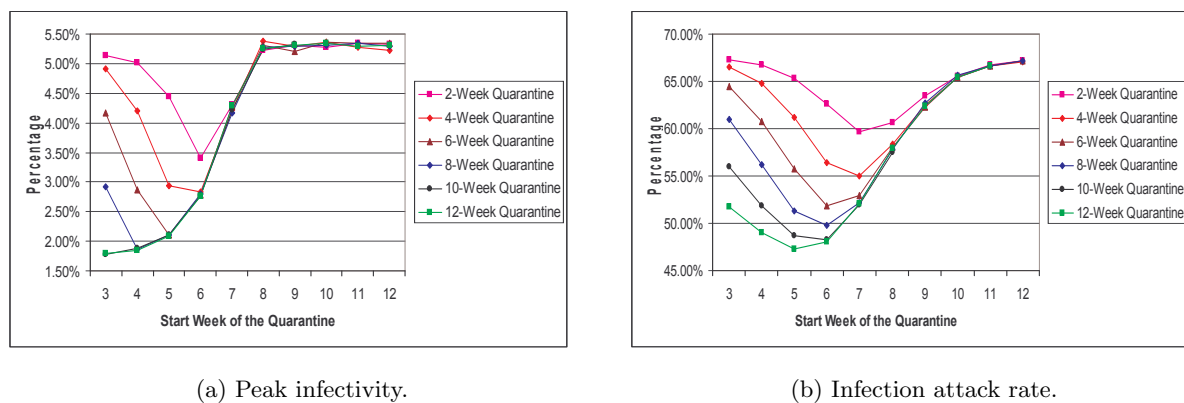

(a) Peak infectivity.   (b) Infection attack rate.

Figure 4   **Effect of timing and length of quarantine on the peak infectivity and infection attack rate.**

Both the peak infectivity and IAR decrease as the length of the quarantine increases, but there

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is a diminishing rate of return. The *peak infectivity* (in Figure 4(a)) in an 8-week quarantine is almost equal to that of a 12-week quarantine.

For different R_0 values, Table 4 summarizes the results for an 8-week quarantine (with the objective of minimizing the *peak infectivity*), which is the break point where the diminishing rate of return is clearly observed for the *peak infectivity* and *IAR* (for $R_0 = 2.1$, even a 6-week quarantine is as effective as an 8-week quarantine in terms of *peak infectivity*). We observe that for moderate to high R_0 values, i.e, 1.8 and 2.1, an 8-week quarantine has about the same impact on *peak infectivity* compared to a quarantine that is in effect during the entire course of the disease. Imposing the quarantine during the entire course of the disease versus for only 8 weeks versus no quarantine result in *IAR* of 42%, 56%, and 67.5%, respectively, for $R_0 = 1.8$ and 58.5%, 63%, and 78%, respectively, for $R_0 = 2.1$. That is, for moderate to high R_0 values, an 8-week quarantine captures most of the benefits in reducing the *peak infectivity* and *IAR*. However, for $R_0 = 1.5$, there is a significant reduction in *peak infectivity* (from 0.80% to 0.30%) and *IAR* (from 40.5% to 17.4%) if the quarantine is imposed during the entire course of the disease instead of an 8-week time interval. Hence, for low R_0 values (where the disease spread is smoother even under no intervention), a longer quarantine can be more beneficial.

Table 4   Summary of results under an 8-week voluntary quarantine with 50% compliance.

R_0	Quarantine Start Week	Peak Infectivity	Peak Day	CAR	IAR	Death Ratio
1.5	7	0.80%	52	26.52%	40.46%	0.47%
1.8	4	1.86%	63	36.82%	56.14%	0.66%
2.1	3	3.97%	49	41.26%	62.87%	0.75%

In a voluntary quarantine, the reduction in the peak infectivity is high when compared to the reduction in other performance measures. For $R_0 = 1.8$, an 8-week quarantine with optimal timing reduces the *peak infectivity* by 64.71%, *CAR* by 16.70%, *IAR* by 16.82% and the *death ratio* by 17.22%. The highest reduction is in the *peak infectivity* because quarantine decreases the number of interactions in the peak, but the reduction in the total number of interactions is limited. Keeping infected individuals at home decreases their interactions with the others outside, but in the long run

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susceptible individuals may have an interaction with other infected individuals in the community after the quarantine is released. The reductions in the *peak infectivity*, *CAR*, *IAR* and *death ratio* for different R_0 values for an 8-week quarantine with the optimal start time are presented in Table EC.5 in the e-companion.

Wu et al. (2006), Ferguson et al. (2006) and Longini et al. (2005) also study voluntary quarantine as an intervention policy. The comparison of the results are provided in Table EC.6 in the e-companion. Different from our limited time assumption, all the papers listed in Table EC.6 assume that the quarantine is active during the entire course of the disease, which may not be practical. Our results indicate that as R_0 increases, an 8-week quarantine (if started at the right time) is almost as effective as a quarantine that is imposed during the entire course of the disease.

In addition to voluntary quarantine, school closing is an alternative intervention policy which received much attention (Carrat et al. 2006, Ferguson et al. 2006, 2005, Germann et al. 2006). Georgia Department of Education prepared a report to assist school administrators in preparing influenza pandemic plans (Cox 2008) explaining local and state responsibilities, how to organize school activities, and how to communicate with staff, parents, and community. Jones (2007) explains when and for how long to close the schools in case of an influenza pandemic. 4-week closures are recommended in case of a pandemic similar to the one in 1957 and up to 12-week closures are recommended for a pandemic such as the one in 1918.

Our simulation results indicate that school closure may not be as effective as voluntary quarantine. For example, for $R_0 = 1.8$, even a 2-week quarantine with optimal timing is as good as a 12-week school closure with optimal timing in terms of reducing both *peak infectivity* and *IAR*. Thus, considering the additional disruptions in services that could be caused by school closures (if some parents have to leave the workforce to stay home to take care of their children), voluntary quarantine may be a better alternative as a social distancing measure.

5. Estimating the Food Need

In this section, we propose several alternatives to calculate the food need in case of an influenza pandemic. In the state of Georgia, the ARC-MAC has taken on a responsibility to feed people in

case of an influenza pandemic, and our research has been motivated by their planning process. While the ARC-MAC focuses primarily on Metropolitan Atlanta Area (15 counties), it is also leading the discussions on planning for food distribution at the state level.

In the remainder of the paper, we consider $R_0 = 1.8$ and perform a detailed analysis of the food distribution supply chain network in case of an influenza pandemic. We estimate the food need using the disease spread model assuming that an individual needs 3 meals a day. There are several alternatives for calculating the food need depending on who to feed: (i) serve the households with at least one infected (symptomatic or hospitalized) individual (Figure 5(a)), (ii) serve the households that are below poverty level with at least one infected individual (Figure 5(a)), (iii) serve the households with all adults infected (Figure 5(b), under no intervention and 8-week quarantine starting at the fourth week), (iv) serve the households that are below poverty level with all adults infected, and (v) serve the quarantined households in case of a quarantine.
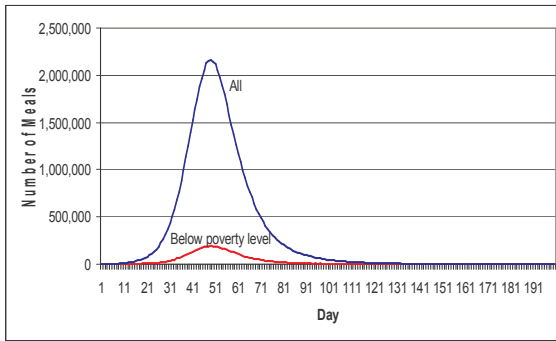
(a) The households with an infected individual are served.
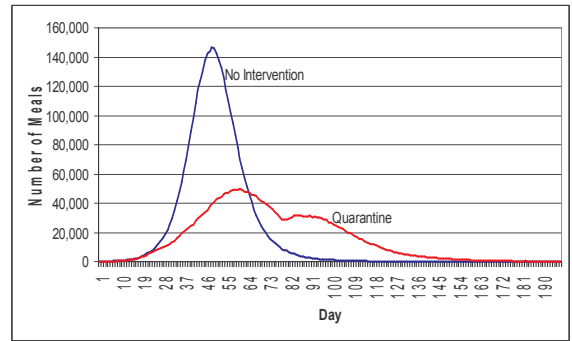
(b) The households with all adults infected are served under no intervention or an 8-week quarantine policy.

Figure 5   **Number of meals needed daily for different alternatives**

In Figure 5(a), the number of meals needed is high when compared to other alternatives since all the households with an infected individual are served in this case. In Figure 5(b), we observe two peaks for an 8-week quarantine. After the quarantine is released, there occurs another (lower) peak due to the increased number of interactions in the community.

6. Facility Location Model and Solution Approaches for Food Distribution

In this section, we explain CMPH-FLP and propose a mixed integer linear formulation. Since CMPH-FLP is NP-hard, and even medium size instances of CMPH-FLP cannot be handled using commercial solvers such as CPLEX 9.0, we propose an "Add-Drop" type heuristic, called *Add-Drop Heuristic* (ADH), which is a modification of add (Kuehn and Hamburger 1963) and drop (Cooper 1964) heuristics proposed for FLPs. An example of add-drop heuristic can be found in Narula and Ogbu (1979) in the context of determining the location of health care centers and hospitals. Furthermore, we propose two solution approaches for designing and managing the food distribution network during the influenza pandemic.

Given our discussions with the ARC-MAC, we propose a 3-tier distribution network: supply points, major facilities (where the food is processed and/or packed for easy pick-up by individuals), and points-of-delivery (PODs) (e.g., schools, churches, community centers, businesses, etc.). Individuals/households who are in need will get their food from the PODs (which we assume can be run with minimum personal contact, e.g., individuals could drive through and someone puts the food into the trunk). Other ways of distribution can be determined for those without transportation. In our food distribution network, each census tract is considered as a demand node, and the amount of demand is determined by the number of individuals/households in need. The major facilities and PODs can be opened or closed over time based on the estimates of demand across area and time. In our formulation, we consider demand updates and closing/opening decisions on a weekly basis.

The questions that need to be answered are: (i) Where to locate major facilities and PODs? (ii) How to open/close these facilities over time (e.g., on a weekly basis) as the (anticipated) food need changes? (iii) How to allocate the food among the major facilities and the PODs with the goal of minimizing the total cost of serving the target population?

6.1. Mixed Integer Linear Model

We develop a mixed integer linear formulation for CMPH-FLP (Table 5 summarizes the notation) assuming that the demand, i.e., the number of meals needed for each week/period in the time horizon for each census tract, is deterministic (we obtain demand estimates by running the disease spread model). To the best of our knowledge, a linear formulation has not been proposed for CMPH-FLP.

Table 5   Notation used in the formulation.

T	:	number of weeks (time horizon)
N_1, N_2, N_3, N_4	:	sets of supply points, major facilities, PODs, and demand nodes
S_i	:	amount of meals that can be supplied by supply point i for $i \in N_1$
F_j	:	fixed cost incurred if facility j is open during a week for $j \in N_2 \cup N_3$
f_j, g_j	:	cost of opening and closing facility j for $j \in N_2 \cup N_3$
c_o^1, c_o^2	:	unit material (meal) handling cost at a major facility, and POD
C_j	:	capacity of the facility j for $j \in N_2 \cup N_3$
D_{kt}	:	demand of demand node k in week t for $k \in N_4$, $t \in T$
d_{ij}	:	distance (in miles) between node i and node j for $i \in N_k$, $j \in N_{k+1}$, $k \in \{1,2,3\}$
c_u^1	:	unit transportation cost from a supply point to a major facility per mile
c_u^2	:	unit transportation cost from a major facility to a POD per mile
$c_{individual}$	:	unit transportation cost from a POD to a demand node per mile

The objective in our model is to minimize the total cost while satisfying the demand. The decision variable definitions and full formulation is available in Section EC.7 of the e-companion. Commercial optimization software such as CPLEX 9.0 can handle only small instances of CMPH-FLP. To find (near-)optimal solutions for large instances, next we propose heuristic approaches.

6.2. Heuristics for CMPH-FLP

In this section, we explain ADH and a variant of it, namely, *Hybrid Heuristic* (HH). The pseudocode for ADH is provided in Section EC.8 of the e-companion. The idea behind ADH is as follows: In each period, to determine which PODs and major facilities to open, we solve two single period FLPs. That is, for period t, first we solve a single period version of CMPH-FLP assuming that the demand of node k is a weighted average of future demands (with weights decreasing over time) as follows:

$$\overline{D}_{kt} = \frac{D_{kT}}{2^{T-t}} + \sum_{j=t+1}^{T} \frac{D_{kj}}{2^{j-t}} \qquad (1)$$

The solution to this problem helps us predict the major facilities and PODs that will be open in the future. Then, combining the solution of this problem with the information about the PODs and major facilities that were open in the previous period, we solve the same problem assuming that the demand of node k is D_{kt} to determine which major facilities and PODs to open in period t.

Next, we explain the subroutine for solving these two single period problems. First, we assign all the demand nodes to the nearest POD(s) considering the capacity constraints on the PODs. Then, for each POD, we calculate the savings achieved by closing it and assigning its demand to other nearby PODs. Then, we close the POD with the highest positive savings. Note that while calculating the savings achieved by closing a certain POD or major facility, the PODs and major facilities that were open in the previous period (period $t-1$) have an advantage since the opening and closing costs for these facilities are already incurred. We continue these steps until there are no other PODs with positive savings. Next, assuming that the remaining open PODs represent the demand nodes, we apply similar steps to determine which major facilities to open.

To summarize, in ADH, we solve a single period version of CMPH-FLP for the (weighted) average of the future demand estimates, and then, for the current period's demand using the subroutine explained above. In an alternative heuristic, namely, *Single Period Heuristic* (SPH), we solve both of these two single period problems optimally. SPH will have larger run times but may improve the performance. As a third alternative, we combine ADH and SPH such that in each period, we solve the first problem with the (weighted) average of future demand using the subroutine explained above and solve the second problem with the current period's demand optimally. We call this the *Hybrid Heuristic* (HH) which reduces the solution time required compared to SPH. We test ADH, SPH and HH for a set of instances and compare the solution times and the optimality gap of the solutions found by them in Section 7.

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6.3. Solution Approaches for Constructing the Food Distribution Network

In this section, we discuss two solution approaches to the food distribution logistics problem during influenza pandemic. The first one is called the *Deterministic Approach (DET-A)* where the food need is estimated using the disease spread model and input to the CMPH-FLP, which is solved by the heuristics proposed in Section 6.2. The demand estimate may be the average of multiple simulation runs. In this approach, the network is not updated over time with new disease spread estimates. The advantage of this approach is its simplicity of implementation (i.e., the decisions about when and where to open/close facilities are made at the beginning). However, the decisions can be improved with more information about the spread of the disease over time.

The second approach is called the *Dynamic Update Approach (DYN-A)*. At the beginning of each week, we update our estimate on the amount of food need by using the information about the up-to-date spread of the disease. In this approach, we implement only the decisions for the current period and then rerun the simulation in the next week for the remaining time horizon by providing the status of the real-world spread as an input to the simulation. This rolling horizon approach decreases the deviation of the estimates from the real-world situation. To the best of our knowledge, we are the first to propose and implement such a dynamic update algorithm in the context of determining the location of distribution facilities during a large-scale disease spread.

7. Computational Results

In this section, we provide the results of the computational experiments. First, we test the performance of the proposed heuristics to solve CMPH-FLP. Then, we compare the performances of the *DET-A* and the *DYN-A*. Finally, we present the analysis about the impact of voluntary quarantine on food distribution.

In the computational experiments, we consider the case of serving households with all adults infected, but the approach is valid for any alternative used for calculating the food need. In real life, the event of influenza pandemic will be recognized some time after the occurrence of the first infection. During that time, some part of the population will be infected, and then, governments

and NGOs will consider supplying the basic needs to the infected people/houesholds. We assume that we serve food to people when more than 0.5% of the population is infected at a given time, and this corresponds to an 8-week time interval (between weeks 5 and 12) for $R_0 = 1.8$. Although the exact percentage is hard to estimate, the assumption is reasonable because the NGOs and/or governments will not construct a large food distribution network if the number of infections is under some threshold value. For example, Germann et al. (2006) consider initiating the intervention strategies 7 (or 14) days after the pandemic alert, and they assume that a pandemic alert is triggered when the total number symptomatic individuals reach to 10,000. This corresponds to day 24 for $R_0 = 1.9$ in their results.

7.1.   Performance of the Heuristics

To evaluate the performance of the heuristics, we consider Gwinnett county, Fulton county and the Metropolitan Atlanta Area as the test cases. There are 71, 167, and 603 census tracts in Gwinnett county, Fulton county, and the Metropolitan Atlanta Area, respectively. The number of periods is 8 (weeks) in the test instances, corresponding to the length of the time interval during which more than 0.5% of the population is infected at a given time.

Based on the estimations provided by ARC-MAC, the capacity of a typical POD is assumed to be around 10,000 meals per week. The total capacities of the major facilities and supply points are equal to the total capacity of the PODs. The supply points, major facilities and PODs are randomly assigned to the relevant areas. The opening/closing/fixed operating costs of the PODs and the major facilities are proportional to the square root of the capacity of the relevant facility since facility related costs are usually represented by a concave function of capacity due to economies of scale (Feldman et al. 1966). The opening, operating and closing costs of a major facility is 10 times that of a POD of the same size since most of the food processing/packing operations will be performed in major facilities. The opening cost is assumed to be two times the closing cost and four times the fixed operating cost. The shipments from supply points to major facilities and from major facilities to PODs will be in large amounts and done by trucks. However, for the shipments

from PODs to households, either an individual from the household will drive to a POD or a small truck will distribute to households. Based on this observation, the unit shipment costs from supply points to major facilities (c_u^1) and from major facilities to PODs (c_u^2) are assumed to be equal to each other and 50% of the unit shipment cost from PODs to demand nodes $(c_{individual})$. Finally, we assume three different settings for the shipment costs, namely, low, medium and high. In the "low" setting, the facility related costs dominate the objective function, in the "medium" setting the shipment costs and facility related costs are comparable, and in the "high" setting, the shipment costs dominate.

We compared the average performance of the heuristics for each of the three shipment cost settings (low, medium, high). We used CPLEX 9.0 as the optimization engine, and all computational experiments are carried out on a system with a 2.4 GHz Xeon processor and 2 GB RAM. For finding the optimal solution, we set a time limit of 8 hours for the small instances (Gwinnett and Fulton county) and 12 hours for the Metropolitan Atlanta Area instances. We set a time limit of 0.5 hour and 1 hour for each single period problem in SPH and HH, respectively, since two optimization problems are solved in SPH in each period whereas only one optimization problem is solved in HH in each period. The detailed results (CPU times and optimality gaps with respect to the best lower bound) are presented in Table EC.7 in the e-companion. Since the optimality gaps are calculated with respect to best lower bound, they are conservative estimates.

From the computational experiments, we see that CMPH-FLP becomes easier as the shipment costs dominate the objective function, where almost all of the facilities are open during the entire time horizon. One simply assigns each demand point to the closest facility. We conclude that it is the number of major facilities that makes CMPH-FLP harder (see third, fourth and fifth set of instances in Table EC.7, where we increase the number of major facilities, PODs and supply points compared to the second set of instances).

As the instances become larger, we observe that the best integer solution found at the end of the time limit is significantly worse than the solutions found by the heuristics. Even if we increase the time limit, CPLEX 9.0 cannot handle large instances due to a memory problem.

The average optimality gap of the solutions found by SPH and HH are very close to each other and is around 3%. However, the solution time of HH is around 30% that of SPH. The solution time required for ADH is negligible compared to SPH and HH, but the average optimality gap is around 4.5%. Hence, we propose using HH and ADH to solve CMPH-FLP. Furthermore, for very large instances such as the entire state of Georgia, ADH is the best alternative since in this case, even the single period problem is difficult to handle using commercial optimization software.

7.2. Deterministic Approach vs. Dynamic Update Approach

In this section, we compare the performances of *DET-A* and *DYN-A* as well as a benchmark case, "Perfect Solution", which is the solution obtained assuming that we know the real-world spread ahead of time, which is impossible to know but provides a comparison base for our solution approaches. Since large instances cannot be solved optimally using CPLEX 9.0, we consider Gwinnett county as the test case with 5 major facilities, 36 PODs and 10 supply points. We consider using both of the heuristics (ADH and HH) as well as solving CMPH-FLP optimally to compare *DET-A* and *DYN-A*.

The same experimental setting explained in Section 7.1 is used in these experiments. The benchmark case is generated by a single simulation of our disease spread model. According to the result of the experiments, if we use HH and ADH, the solutions obtained by *DYN-A* are approximately 0.33% and 0.54% better, respectively, when compared to *DET-A* in terms of total cost. In addition, the total cost of the solutions obtained by *DYN-A* are within 4% of the "Perfect Solution". Even if we solve CMPH-FLP optimally at each step of *DYN-A* and *DET-A*, the benefit of using *DYN-A* is only 0.37%. This indicates that the performance of *DYN-A* over *DET-A* is not affected by the algorithm used to solve CMPH-FLP.

The performance of *DET-A* is close to that of *DYN-A* since we assumed that we know the disease spread parameters ahead of time. If the parameters can be estimated with reasonable accuracy, because of its simplicity to implement, *DET-A* is a good alternative for designing the food distribution network. In the case where disease parameters cannot be estimated accurately, using *DYN-A* is a better choice.

7.3. Effect of Quarantine on Food Distribution Supply Chain

In this section, we investigate the effect of voluntary quarantine on food demand and food distribution supply chain both in terms of total serving cost and the quality of service, which is defined as the percentage of demand served within 10 miles. Quality of service is important both due to convenience to the public and because of potential shortages in gas supply and the risk of introducing the infection to other areas by driving a long distance.

Quarantine with optimal timing and length decreases the likelihood of capacity bottlenecks and supply chain disruptions significantly. In case of an 8-week quarantine, more than 0.5% of the population is infected between weeks 6 and 18, and the reduction in the total demand is 26.70% when compared to the no intervention case. Note that the reduction in IAR was 16.82% (see Section 4). On the other hand, the reduction in the average demand (over time) is even higher (55%) since the demand (and number of infections) is more spread over time (see Figure 6).
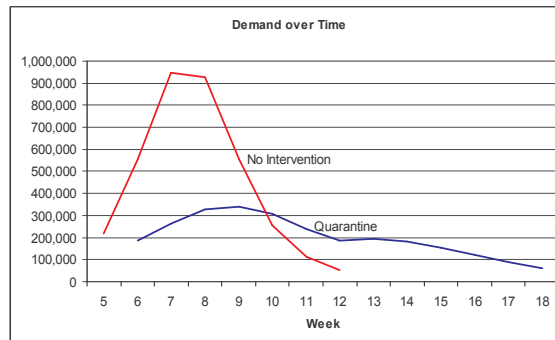

Figure 6   **Effect of quarantine on the food requirement.**

Next, we study the effect of a quarantine on the supply chain network using the results of 10 different simulation runs with 200 PODs, 10 major facilities and 20 supply points in the entire Metropolitan Atlanta Area (603 census tracts/demand nodes). The supply points and PODs are randomly assigned, but the major facilities are assigned to most crowded census tracts of the 10 densely populated counties.

Table 6 shows the cumulative effect of quarantine on the supply chain network. The reduction in total cost is higher when the shipment costs or facility related costs dominate since the reduction

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in total demand is almost fully reflected in the total cost in these settings. On the other hand, in the "medium" shipment cost setting, since both shipment costs and facility related costs comprise the total cost, the reduction in total demand is not fully reflected in the total cost.

From the third and fourth columns of Table 6, quality of service decreases as the shipment costs decrease. This is intuitive because lower shipment costs increase the amount of demand served from a long distance. On the other hand, the quality of service is better under the no intervention case (assuming all of the facilities can indeed operate at the estimated capacities). Since the average demand is lower under quarantine, fewer number of facilities are operated in a given period, and this decreases the percentage of the demand served within 10 miles.

Table 6   Comparison of 8-week quarantine with no intervention case.

Shipment Cost	Cost Reduction in an 8-Week Quarantine Compared to No Intervention	Demand Served within 10 Miles	
		8-Week Quarantine	No Intervention
High	22.35%	99.79%	99.85%
Medium	18.74%	97.86%	99.66%
Low	25.97%	85.29%	94.99%

There are 15 counties in the Metropolitan Atlanta Area, and 70% of the population lives in four counties, namely, Cobb, DeKalb, Fulton and Gwinnett (see Figure EC.2 in the e-companion for a Metropolitan Atlanta Area map shaded according to population densities).

We provide a detailed analysis for the "medium" shipment cost case below. The demand and the number of open PODs over time under the 8-week quarantine can be seen for 5 counties in Figure 7 (see Figure EC.3 in the e-companion for the demand and number of open PODs over time under the no intervention case). Both under no intervention and an 8-week quarantine, the number of open PODs start to increase earlier when compared to demand. Because the opening/closing costs are incurred only once, when the demand at a location is expected to increase, a nearby POD is opened earlier to utilize the benefit of shipping. This is mainly due to comparable shipment and facility operating costs. In the setting where fixed operating cost dominates shipment cost, the
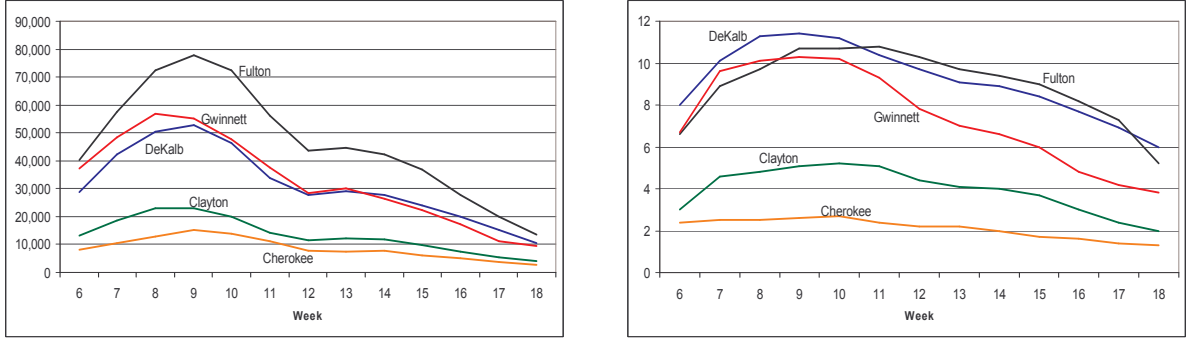
(a) Demand over time.

(b) Number of open PODs over time.

Figure 7 Demand and number of open PODs over time under the 8-week quarantine.

number of open facilities closely follows the demand curve. Finally, proportional with the number of infections, most of the PODs are operated in densely populated counties.

Figure 8(a) shows the average number of major facilities operated in each county. The major facilities in DeKalb and Cobb counties are the ones that are operated almost during the entire time horizon since they are among the most populated counties, and they have a better combined location than other alternatives.

Figures 8(b) and 8(c) show the minimum, average, and maximum open durations of the PODs for each county. The minimum open duration of the facilities is higher in the quarantine case because of smoother demand. In the no intervention case, some of the PODs are open when the demand peaks, and then they are closed when the demand decreases. The deviation in the open duration of PODs is higher in the densely populated counties (Cobb, DeKalb, Fulton and Gwinnett) because the demand curve in these counties has a higher peak, increasing the number of opening/closing decisions.

8. Conclusions and Future Directions

In this paper, we construct a disease spread model with a spatial and an age-based structure for influenza pandemic that is helpful for developing intervention strategies and for preparedness planning. With the goal of designing a food distribution supply chain network during an influenza pandemic, we link the disease spread model to a facility location and resource allocation model and
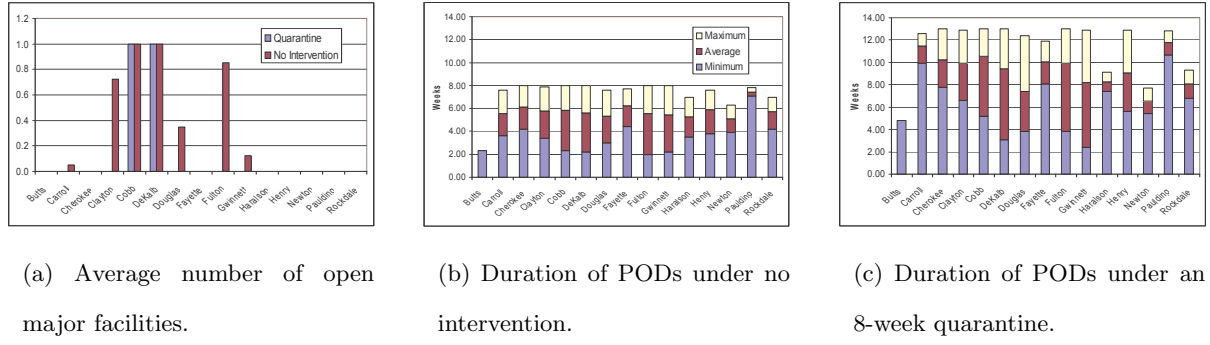
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(a) Average number of open major facilities.

(b) Duration of PODs under no intervention.

(c) Duration of PODs under an 8-week quarantine.

Figure 8   Average number of open major facilities and minimum, average and maximum duration of open PODs.

propose two solution approaches, namely, *Deterministic Approach* and *Dynamic Update Approach*. In the *Deterministic Approach*, the disease spread is estimated only at the beginning, and the food distribution network is constructed according to this estimate. In the *Dynamic Update Approach*, the estimates on the disease spread as well as the food distribution facility location and resource allocation decisions are updated over time. Since the corresponding facility location problem is hard to solve for large instances, we design efficient algorithms to find near-optimal solutions. Our computational results indicate that the *Hybrid Heuristic* performs better when compared to the *Add-Drop Heuristic*, but for very large instances that cannot be handled by commercial optimization software, the *Add-Drop Heuristic* is the best alternative.

Models that predict the spread of the disease accurately help public health officials in developing efficient response plans ahead of time before the influenza pandemic hits. Estimating the disease specific parameters is one of the key issues in developing efficient response plans. While models like *Deterministic Approach* using estimates from earlier influenza pandemic cases can be used for advance planning purposes, dynamic approaches such as *Dynamic Update Approach* which generate updated estimates after the pandemic begins can be used to implement response plans.

We study voluntary quarantining as an intervention policy and find the best timing and length of the quarantine for different R_0 values. We conclude that an 8-week quarantine is equivalent to a 12-week quarantine (or a quarantine that is in effect during the entire course of the disease) in terms of reducing the *peak infectivity* for high R_0 values. For lower R_0 values, an 8-week quarantine may

still be a good choice given the negative effect of prolonged quarantine times on public functions and morale, and the diminishing rate of benefits from long quarantines on peak infectivity and the infection attack rate (IAR). The optimal start time of a quarantine decreases both in the duration of the quarantine and the R_0 value. In addition to voluntary quarantine, we study school closure as an alternative social distancing measure and find that it may not be as effective as a voluntary quarantine. Since school closures can be more disruptive on the overall services and the economy (e.g., if some parents have to leave the workforce to care for children who are out of school), we recommend limited-time voluntary quarantine as an effective intervention policy to public health officials.

Although the effect of a quarantine on IAR is limited, it can decrease the *peak infectivity* significantly which is crucial for the continuity of the supply chains of goods and services. It can also reduce the probability of having capacity problems in different infection related services during an influenza pandemic. For example, in the food distribution supply network, the number of facilities operated decreases by almost half in the case of a quarantine when compared to the no intervention case. This significant reduction has several benefits including the reduced equipment and workforce requirements to operate the food distribution facilities where the workforce is likely to be a scarce resource due to illness, fear of infection and the need to care for infected family members.

In this paper, we analyzed the food distribution supply chain during an influenza pandemic. Designing medicine/vaccine distribution supply chains and analyzing the effect of influenza pandemic in terms of supply chain disruptions are two other important problems that have to be addressed to develop efficient response plans for an influenza pandemic. In our disease spread model, we did not assume any seasonal effects or viral evolution, which may change the spread pattern of the virus. Another future direction is optimizing the intervention policies such as distribution of vaccines and antivirals. This may decrease the number of infected people as well as the amount of food need.

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