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# Risk perception and human behaviors in epidemics

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## ABSTRACT

Individuals experiencing an epidemic may change their behaviors to prevent themselves from infection by balancing the benefits and costs based on the information about the infectious disease. This study incorporated two types of information—local information, which impacts local human contacts, and global information, which impacts people's travel behaviors—into a spatial evolutionary game to determine individuals' decisions. This article constructs a new behavior-switching-based susceptible-infected-recovered (SIR) model using a spatial evolutionary game to study the impact of human behaviors and information dissemination on the spread of infectious disease. This model was evaluated and analyzed using numerical simulations for the population in the state of Kansas. In particular, individuals' perceptions of the risk based on the local information are discussed, which could help us better understand human behaviors and improve communication between policymakers and the public.

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## KEYWORDS

Disease transmission; human behaviors; risk perception; spatial evolutionary game

## 1. Introduction

The influence of human behaviors on infectious disease transmission has been a focused area of study for the past decade. Individuals often change their behaviors to prevent infection, including improving personal hygiene, taking antiviral medicine, implementing voluntary social distancing, receiving voluntary vaccination, and other protective measures (Tan *et al.*, 2004). These voluntary behaviors are referred to as spontaneous changes of human behaviors.

Funk (Funk, Salath, and Jansen, 2010) reviewed recent work on the influence of human behavior on the spread of infectious diseases. The rationality of self-protective behaviors based on information about infectious diseases has caused increased application of game theory to epidemiology (Funk, Gilad, and Jansen, 2010; Funk *et al.*, 2009; Poletti *et al.*, 2009; Reluga *et al.*, 2007; Reluga, 2009, 2010; Chen, 2004; Reluga and Galvani, 2011). However, the literature only applies game theory to a mixed homogeneous population without considering the contact pattern. Hence, a study of the combined impacts of a spatially contact structure and spontaneous behavior changes using game theory would significantly improve existing models.

In addition, information transmission about the spread of infectious disease and individuals' perception of risk must be considered in order to study human behaviors. Chen (2009) introduced a social sampling method to evaluate individuals' assessments of infectious disease prevalence based on acquired information. The model in Kiss *et al.* (2010) considers sexually transmitted infections, accounting for information transmission and individuals' responses to the infectious disease and showing that information transmission can reduce the prevalence of the infection.

A study described in Zhao, Wu, and Ben-Arieh (2015) recently investigated a methodology that combines information dissemination, contact networks, and human behavior changes to model the dynamics of infectious diseases. A spatial evolutionary game was adopted to study the impact of human behavior changes on the dynamics of disease transmission. Human responses were determined by the spatial evolutionary game, based on the balance of benefits and costs evaluated from the information related to infectious disease, such as prevalence, severity, etc. Two types of susceptible individuals were considered: risk-neutral and risk-averse (named normal individuals and switchers in Zhao, Wu, and Ben-Arieh (2015), respectively). Risk-averse individuals are typically more conservative than risk-neutral individuals and tend to protect themselves and reduce risks. All susceptible individuals collected information about the infectious diseases (particularly indicating the number of infected individuals and the number of risk-averse individuals) locally and globally and then made decisions based on that information. The impact of information on individuals' decisions (choosing to be risk-neutral or risk-averse) was referred to as the payoff in the spatial evolutionary game. Individuals could change their minds or stay with their current status quo (risk-neutral or risk-averse) based on their own and their neighbors' payoff values. Hence, the contact structures among individuals also played a key role in the spatial evolutionary game, since these contact structures heavily impact the payoff values, which explicitly determined individuals' decisions.

The spatial evolutionary game model in (Zhao, Wu, and Ben-Arieh (2015) successfully describes impacts of changes of human behaviors and information dissemination on the spread of infectious diseases. The unstructured nature of the referenced

model in Zhao, Wu, and Ben-Arieh (2015) has the advantages of generality and flexibility, which could be applied to different levels of granularities. For example, it could be easier to extend this to an individual-level system, such as an agent-based model, or a high-level system, such as our meta-population model. In this article, we extended the classic SIR model based on the concept in the referenced model in meta-population level, validated the consistency of the results between these two models, and further extended the model to consider possible impacts on long-distance travel, spatial-temporal analysis, and memory/forgetting impacts related to risk reception. To clarify the differences of these two models, the spatial evolutionary game model is named SEGM and the modified dynamic model developed in this article is named as MDM. In addition, a new concept related to the impact of local information dissemination is introduced and discussed in this article.

## 2. Mathematical model

The basic assumptions in this article, which are identical to the assumptions in Zhao, Wu, and Ben-Arieh (2015), are briefly reviewed in this section, and the new modified dynamic model (MDM) is presented as one of the major objectives of this article. We first introduce the classic SIR model in Section 2.1. Based on the classic model, the MDM model is constructed in Section 2.2 and the extended MDM model with long-distance travel is discussed in Section 2.3.

### 2.1. Classic SIR model

Ordinary differential equations (ODEs) are commonly used to model disease transmission. One of the most classic models is

$$\frac{dS}{dt} = -\frac{1}{N}\beta SI \quad (1)$$

$$\frac{dI}{dt} = -\frac{1}{N}\beta SI - \gamma I \quad (2)$$

$$\frac{dR}{dt} = \gamma I \quad (3)$$

where  $S$  represents the number of susceptible individuals,  $I$  represents the number of infected individuals,  $R$  represents the number of recovered individuals, and  $N$  represents the number of individuals in the population. In this model,  $\beta$  is the infection rate, and  $1/\gamma$  is the infectious period. This model is the classic susceptible-infected-recovered (SIR) model without demography (Kermack and McKendrick, 1927).

### 2.2. MDM model

This section extends the classic SIR ODEs model of Eqs. (1)–(3) to a local commute model with the spatial evolutionary game based on a local contact network, which is called a modified dynamic model, or MDM. Compared to the classic SIR model, there are two types of susceptible individuals involved in the MDM. In addition, spatial structure and information dissemination, which impact susceptible individuals' decisions, are incorporated into the model. To further illustrate the concept

of each component in the MDM, information dissemination, change of human behaviors, spatial contact structure, and spatial evolutionary game are introduced in Sections 2.2.1, 2.2.2, 2.2.3, and 2.2.4, respectively, and then the MDM is developed by integrating all those concepts into the classic SIR model in Section 2.2.5.

#### 2.2.1. Information dissemination

Increasing development of transportation and communication technologies has increased the spreading rate of infectious disease and the transmission of disease information. Individuals can acquire information about the disease and current epidemics through a myriad of mediums, including news broadcasts on television or radio, social media, face-to-face communication, or education about prevention from infectious disease. The acquired amount and accuracy of information consequently impact how individuals react to disease transmission and influence their decisions during an epidemic outbreak. Chen (2009) studied how the quality of information affects the transmission of infectious disease.

In this article, we assume that individuals are well-informed, meaning that individuals always acquire complete and correct information (without rumors spread among individuals) in all locations. In addition, information about the infectious disease is characterized as local information and global information. Local information, defined as information about the disease in neighborhoods within a certain distance from an individual's location, locally impacts individuals' contacts. Global information, defined as information about disease transmission in all locations, impacts individuals' decisions and travel behaviors. Both local and global information are considered within individuals' decision-making processes.

#### 2.2.2. Change of human behaviors

Based on infectious disease information, some individuals may take protective measures to prevent infection and others may not, thereby revealing two distinct types of susceptible population: risk-neutral and risk-averse. Risk-neutral individuals believe very little chance exists for their infection, so they do not attempt to change their behaviors to keep themselves from getting infected. Risk-averse individuals, however, estimate the risk and assume a high probability of infection, so they change their behaviors (such as taking antibiotic medicine, wearing face masks, avoiding crowded places, etc.) to attempt to avoid infection. Although risk-averse individuals can be categorized according to the extent of their changes in behaviors, we assumed all risk-averse individuals to be identical for this study, and we did not consider multiple levels of risk-averse individuals to retain model simplicity. We modified the classic SIR model to our MDM model with two different types of susceptible individuals: risk-averse individuals and risk-neutral individuals. Susceptible individuals could be either risk-averse individuals or risk-averse individuals on each day based on their own decisions and the decision process was called a spatial evolutionary game, which will be introduced in Section 2.2.4.

In order to reduce exposure to disease, risk-averse individuals commonly use the strategy of social distancing, which

includes reducing the number of contacts, such as avoiding crowded places, limiting friend contacts, or avoiding school or work. Social distancing also includes reducing the intensity of contacts, such as receiving vaccinations if applicable, taking antiviral medicine, or wearing face masks. However, because any of these risk-averse behaviors requires increased cost (monetary cost, loss of income, or leading to inconvenience to their lives, etc.), individuals must balance their costs and benefits during the decision-making process. Moreover, individuals may routinely change their minds based on daily updates of new epidemic information.

### 2.2.3. Spatial contact structure

In reality, individuals may work in another location besides their home or visit neighboring businesses or families on a daily basis. Frequent commuting behaviors should be included in MDM. Considering population heterogeneities, the classic model could be modified to involve spatial structure. For example, as illustrated in Fig. 1, the network could be adopted to present different locations, and an index  $\mathbf{x}$  could be used to indicate the specific location on the map. Each location contains a population with four possible types of individuals: risk-neutral, risk-averse, infected, and recovered individuals. Individuals could interact with others in the same location or in connected neighborhood locations, and the contact rate depends on the distance between two locations. For example, individuals in location 2 could interact with individuals in locations 1, 2, 3, 4, or 7, with probabilities depending on distances between two locations.

### 2.2.4. Spatial evolutionary game

The spatial evolutionary game combines both classic game theory and cellular automation, in representing strategies, players, payoff function, structure of population, and an updating rule. Nowak and May (1992) first introduced the spatial evolutionary game in order to study the local cooperation phenomena for a classic problem, called the “prisoner dilemma.” This methodology analyzes various structures of populations using a regular lattice (Santos, Pacheco, and Lenaerts, 2006), scale-free networks (Lozano, Arenas, and Snchez, 2008), and real social networks (Szabo and Fath, 2007). Szabo and Fath (2007) reviewed evolutionary games on graphs. In addition, the spatial evolutionary game requires an updating policy based on the payoff function, with updating schemes such as synchronous or asynchronous updates. Newth and Cornforth (2007) reviewed several common updating schemes, and Roca, Cuesta, and Snchez (2009) summarized update rules.

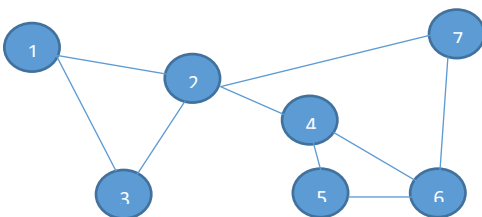


Figure 1. Network with metapopulation.

### 2.2.5. MDM model

Based on the concepts in Section 2.2.1–2.2.4, the MDM model built on the network shown in Fig. 1 for the disease transmission process could be described as:

$$\frac{dS_n}{dt}(\mathbf{x}) = -\beta_n S_n(\mathbf{x}) \lambda_n(\mathbf{x}) - (1 - \rho(\mathbf{x})) S_n(\mathbf{x}) + \rho(\mathbf{x}) S_a(\mathbf{x}) \quad (4)$$

$$\frac{dS_a}{dt}(\mathbf{x}) = -\beta_a S_a(\mathbf{x}) \lambda_a(\mathbf{x}) + (1 - \rho(\mathbf{x})) S_n(\mathbf{x}) - \rho(\mathbf{x}) S_a(\mathbf{x}) \quad (5)$$

$$\frac{dI}{dt}(\mathbf{x}) = \beta_n S_n(\mathbf{x}) \lambda_n(\mathbf{x}) + \beta_a S_a(\mathbf{x}) \lambda_a(\mathbf{x}) - \gamma I(\mathbf{x}) \quad (6)$$

$$\frac{dR}{dt}(\mathbf{x}) = \gamma I(\mathbf{x}) \quad (7)$$

where

$$\lambda_n(\mathbf{x}) = \sum_{y \in \text{local}} I(\mathbf{y}) K_n(\mathbf{x} - \mathbf{y}) / N(\mathbf{y}) \quad (8)$$

$$\lambda_a(\mathbf{x}) = \sum_{y \in \text{local}} I(\mathbf{y}) K_a(\mathbf{x} - \mathbf{y}) / N(\mathbf{y}) \quad (9)$$

and

$S_n(\mathbf{x})$	Number of risk-neutral at location $\mathbf{x}$ ,
$S_a(\mathbf{x})$	Number of risk-averse at location $\mathbf{x}$ ,
$\rho(\mathbf{x})$	Percentage of risk-neutral individuals to total susceptible individuals at location $\mathbf{x}$ ,
$K_n(\mathbf{x} - \mathbf{y})$	Kernal function of contacts for risk-neutral between location $\mathbf{x}$ and location $\mathbf{y}$ ,
$K_a(\mathbf{x} - \mathbf{y})$	Kernal function of contacts for risk-averse between location $\mathbf{x}$ and location $\mathbf{y}$ ,
$I(\mathbf{x})$	Number of infected individuals at location $\mathbf{x}$ ,
$R(\mathbf{x})$	Number of recovered individuals at location $\mathbf{x}$ ,
$N(\mathbf{y})$	Total number of individuals at location $\mathbf{y}$ ,
$\beta_n$	Infection rate of individuals adopting risk-neutral behavior,
$\beta_a$	Infection rate of individuals adopting risk-averse behavior,
$\gamma$	Recovery rate.

Eqs. (4) and (5) use two infection rates,  $\beta_n$  and  $\beta_a$ , for risk-neutral individuals and risk-averse individuals, respectively, where assuming  $\beta_a < \beta_n$ . The contact rates,  $\lambda_n(\mathbf{x})$  and  $\lambda_a(\mathbf{x})$ , are for risk-neutral individuals and risk-averse individuals in location  $\mathbf{x}$ , respectively, and they are calculated in Eqs. (8) and (9), where  $K_n(\bullet)$  and  $K_a(\bullet)$  are kernel functions that represent the possibilities that one individual may contact others in a certain location (i.e., same location or neighboring location). Individuals could interact with others in the same location or other locations with different possibilities, depending on the distance between two locations and the number of infected individuals in the location where susceptible individuals visit.

Considering individuals' decision-making processes, the payoff functions,  $F_n(\mathbf{x})$  and  $F_a(\mathbf{x})$  in Eqs. (10)–(11), for the risk-neutral individuals and risk-averse, respectively, are defined

similarly to those in Zhao, Wu, and Ben-Arieh (2015):

$$F_n(\mathbf{x}) = -\frac{\frac{m_1 \sum_{y_l \in \text{local}} I(y_l)}{\sum_{y_l \in \text{local}} N(y_l)}}{1 + \frac{c_1 \sum_{y_l \in \text{local}} S_a(y_l)}{\sum_{y_l \in \text{local}} (S_a(y_l) + S_n(y_l))}} - \frac{\frac{m_2 \sum_{y_g \in \text{global}} I(y_g)}{\sum_{y_g \in \text{global}} N(y_g)}}{1 + \frac{c_2 \sum_{y_g \in \text{local}} S_a(y_g)}{\sum_{y_g \in \text{local}} (S_a(y_g) + S_n(y_g))}} \quad (10)$$

$$F_a(\mathbf{x}) = -k_c + \alpha F_n(\mathbf{x}) \quad (11)$$

The percentage for an individual to switch his/her behaviors is defined as and logistic function based on the difference between the risk-neutral individuals and risk-averse individuals:

$$\rho(\mathbf{x}) = \frac{1}{1 + e^{-\theta(F_n(\mathbf{x}) - F_a(\mathbf{x}))}} \quad (12)$$

where

- $k_c$  Fixed cost for social distancing behavior,
- $m_1$  Parameter related to estimated risk based on local prevalence,
- $m_2$  Parameter related to estimated risk based on global prevalence,
- $c_1$  Parameter related to estimated risk based on local risk-averse,
- $c_2$  Parameter related to estimated risk based on global risk-averse,
- $0 \leq \alpha \leq 1$  Parameter related to discount of estimated risk by risk-averse,
- $\theta$  Parameter related to switch rate of risk-neutral individuals based on the difference of payoff.

Local and global information of prevalence (proportion of the number of infected individuals to the total population) and the number of risk-averse individuals are considered as they relate to susceptible individuals' decisions. In Eqs. (10) and (11), we assume that risks could be a negative value; therefore, payoff values for both risk-neutral individuals and risk-averse individuals are always non-positive. However, risk-averse individuals incurred an additional cost,  $k_c$ , for the preventive measure; on the other hand, the risk-averse individuals' risk for infection is consequently less than that for risk-neutral individuals, as denoted by discount parameter  $0 \leq \alpha \leq 1$  in Eq. (11). The difference of payoff values between risk-neutral individuals and risk-averse individuals determines the percentage of risk-neutral individuals in Eq. (12).

It is worth mentioning that the assumed value of parameters are used to study the behavior of the system in the numerical simulations in Section 4; however, the real dataset is also required to determine an accurate model for the specific disease transmission.

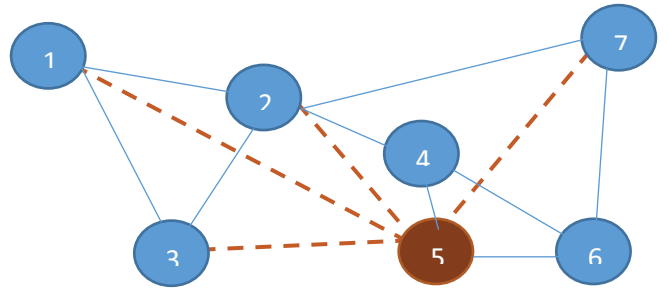


Figure 2. Network for long-distance travel.

### 2.3. MDM with long-distance travel model

In addition to local commuting behaviors, individuals may also travel to large cities or tourist resorts for shopping, vacations, business, or social engagements, causing those locations to become network centers that connect to various distant locations. Individuals may only visit the center monthly, quarterly, or yearly instead of daily. As illustrated in Fig. 1, if location 5 represents a center node, then the corresponding modified network is shown in Fig. 2. The dashed lines represent contacts resulting from long-distance travel. Considering such long-distance travel, the system of Eqs. (4)–(12) remains the same, but kernel functions  $K_n(\bullet)$  and  $K_a(\bullet)$  correspondingly change based on the probability of contacts for long-distance travel.

If infection cases occur in the center node, risk-averse individuals may cancel their travels for their own safety, depending on the number of cases in their destination. The probability of travel cancellations for risk-averse individuals based on the number of cases is defined as

$$p_c = \ln \left( \frac{eI(\mathbf{x}) + d}{I(\mathbf{x}) + d} \right), \quad (13)$$

where  $e$  is the natural logarithm,  $I(\mathbf{x})$  is the number of infected individuals at location  $\mathbf{x}$  (destination), and  $d$  is a constant that determines the increasing rate of cancellation. Risk-averse individuals who cancel travels are assumed to stay in their location and have contact with others in their current location, since they will not contact individuals in their planned destination for travel. The value of  $p_c$  impacts kernel function  $K_a(\bullet)$  since the contact probability distribution changes due to travel cancellations. For example, if risk-averse individuals in location 3 have probability distributions of 10%, 10%, 75%, and 5% to contacts in locations 1, 2, 3, and 5, respectively, and half the risk-averse individuals cancel their travel plans, then the modified probability distribution is 10%, 10%, 77.5%, and 2.5%, respectively.

### 3. Equilibrium analysis

The system of Eqs. (4)–(13) admits the disease-free equilibrium (DFE)  $(S_n; S_a; I; R) = (S_n^*; S_a^*; 0; 0)$  for each location  $\mathbf{x}$  with the fixed ratio of risk-neutral individuals and risk-averse individuals, thereby satisfying

$$\frac{S_n^*(\mathbf{x})}{S_n^*(\mathbf{x}) + S_a^*(\mathbf{x})} = 1 / (1 + e^{-\theta k_c}) \quad (14)$$

$$S_n^*(\mathbf{x}) + S_a^*(\mathbf{x}) = N(\mathbf{x}) \quad (15)$$



The solution of  $S_n^*(x)$  and  $S_a^*(x)$  yields

$$S_n^*(x) = N(x) e^{\theta k_c} / (1 + e^{\theta k_c}) \quad (16)$$

$$S_a^*(x) = N(x) / (1 + e^{\theta k_c}) \quad (17)$$

In the epidemiology,  $R_0$  is one significant indicator to evaluate the force of infection of the infectious disease, and it is defined as “the average number of secondary cases arising from an average primary case in an entirely susceptible population” (Andreasen and Christiansen, 1989). When  $R_0$  is less than 1, the DFE is stable, meaning that the spread of infectious disease could be controlled. When  $R_0$  is larger than 1, however, the DFE is unstable. One homogeneous population without any contact structure contained

$$R_0 = \frac{\beta_n S_n^* + \beta_a S_a^*}{\gamma N} \quad (18)$$

Considering spatial structure and one infected individuals in location  $x$ , Eq. (18) can be rewritten as

$$R_0(x) = \frac{\beta_n \sum_{y \in \text{neighbor}} S_n^*(y) K_n(x-y) + \beta_a \sum_{y \in \text{neighbor}} S_a^*(y) K_a(x-y)}{\gamma N(x)} \quad (19)$$

where  $R_0(x)$  is related to the initial location, contact probabilities, and the population in each location, meaning that  $R_0(x)$  is not fixed in this model. Usually the largest one calculated for all counties is adopted as the real  $R_0(x)$ . The calculation of  $R_0(x)$  in Eq. (19) is consistent with  $R_0(x)$  in Eq. (18) when the spatial contact structure is removed. For simplicity, Eq. (19) can be rewritten as

$$R_0 = \frac{R_n e^{\theta k_c}}{1 + e^{\theta k_c}} + \frac{R_a}{1 + e^{\theta k_c}} \quad (20)$$

where  $R_n$  is the value of  $R_0$  for the population in which all susceptible individuals are risk-neutral individuals, and  $R_a$  is the value of  $R_0$  for the population in which all susceptible individuals are risk-averse individuals. If  $R_a$  is greater than 1, the infectious disease will lead to an outbreak, even when all susceptible individuals are risk-averse individuals. If  $R_n$  is less than 1, the

infectious disease can be controlled, even when all susceptible individuals are risk-neutral individuals. Therefore, the spread of infectious disease may be stopped by a change in human behavior only when  $R_a < 1 < R_n$ . Birth rate and death rate were not included in this model, so no endemic equilibrium existed in the system of Eqs. (4)–(13). The system would stabilize until all infected individuals were recovered.

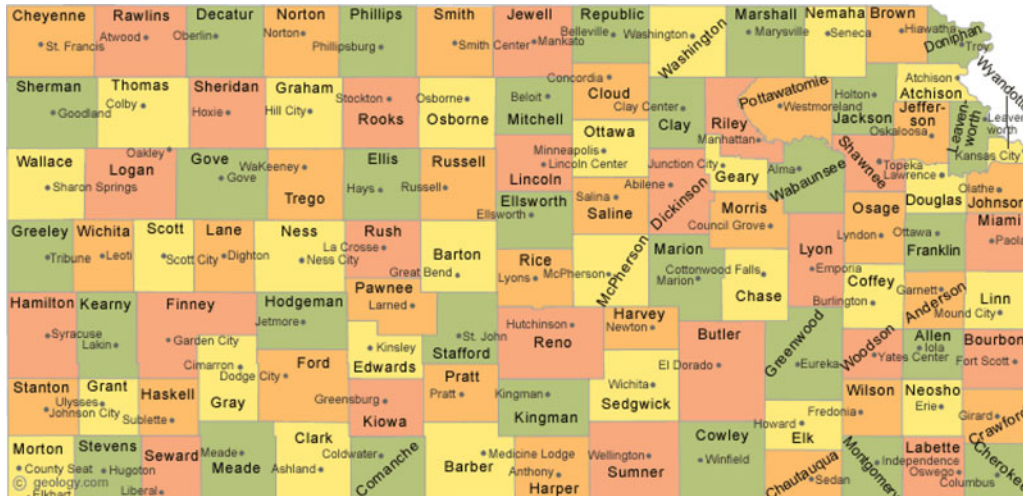
## 4. Numerical study

### 4.1. Model comparison

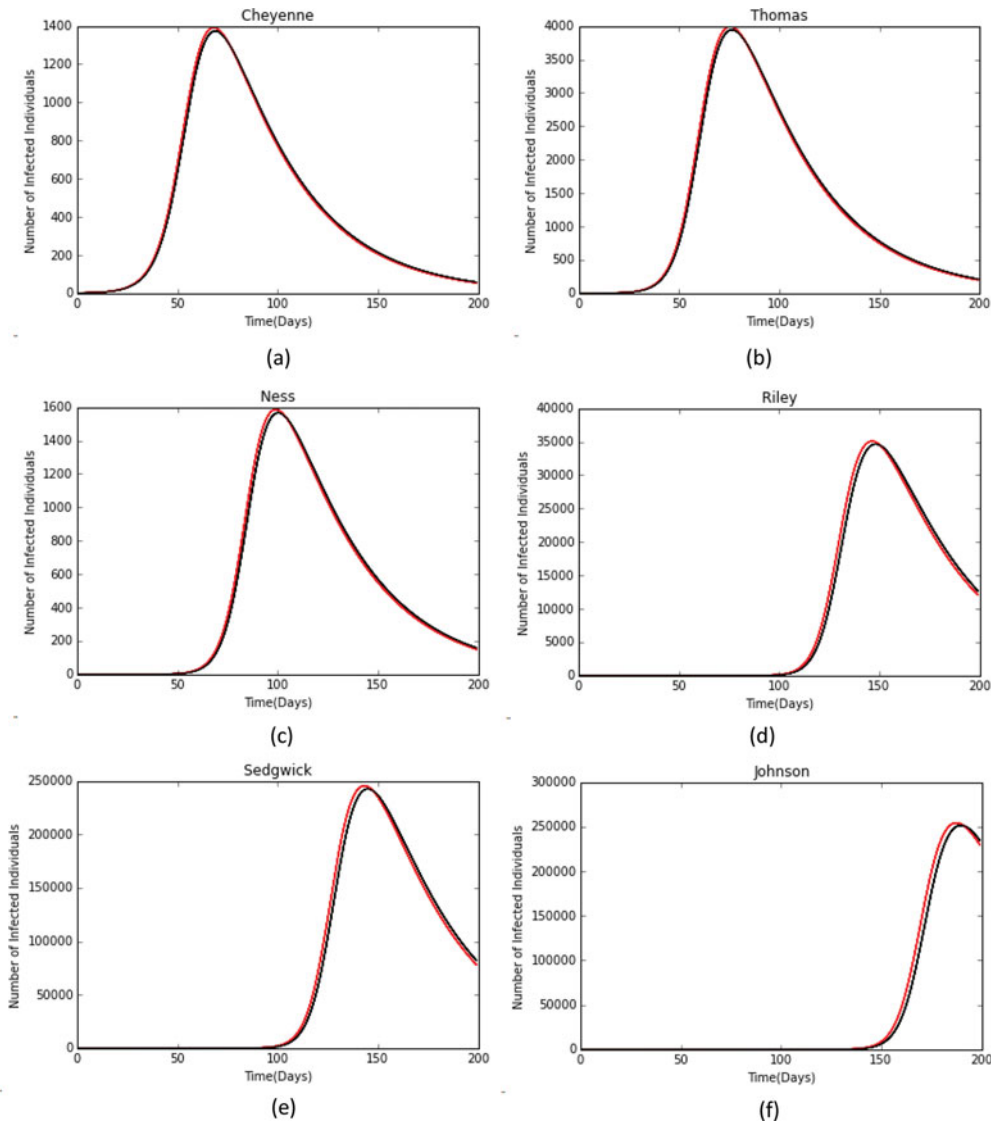
This section includes numerical simulations for the SEGM model in Zhao, Wu, and Ben-Arieh (2015) and the MDM model using a county map of the state of Kansas with county-level population in order to compare the SEGM model to the MDM model. The map is shown in Fig. 3.

The SEGM model and MDM model were compared using the following three settings: deterministic commuting contacts, stochastic commuting contacts, and long-distance travel. Although the contact pattern significantly affected dynamics of an epidemic, most researchers relied on a presumed contact pattern with little or no empirical basis. Theoretically, any type of contact pattern could be applied to the model. Only local contacts were allowed in the first contact patterns, meaning that individuals could only contact others in the same county or in a neighboring county. In the second contact pattern, we assumed that individuals would travel to cities which are not their neighborhood for business or recreation. Testing the two contact patterns confirmed that results from the MDM model are consistent with results in the SEGM model.

For all of the simulation runs, the first infected individual was located in the northwest corner county of Cheyenne. Results in six counties were tested for comparison, including Cheyenne (source), Thomas (neighbor of Cheyenne, subgraph a), Ness (two counties away from Cheyenne, subgraphs b and c), Riley (far away from source in the north, subgraph d), Sedgwick (county with second largest population in Kansas, subgraph e), and Johnson (county with the largest population in Kansas, subgraph f) in Figs. 4, 5, 6, 8, 12, and 13. Parameters



**Figure 3.** County map of Kansas. (Source: <http://geology.com/county-map/kansas.shtml>). Population distribution was collected from the U.S. Census Bureau (Census 2010 Redistricting Data (Public Law 94–171) Summary File).



**Figure 4.** Simulated number of infected individuals in Cheyenne, Thomas, Ness, Riley, Sedgwick, and Johnson Counties in Kansas over time for model comparison under deterministic contacts (red line is the plot of the SEGM model; black line is the plot of the MDM model).

were initialized as follows:  $\alpha = 0.5$ ,  $k_c = 1$ ,  $\theta = 1$ ,  $\gamma = 0.294$ ,  $m_1 = 100$ ,  $m_2 = 10$ ,  $n_1 = 100$ ,  $n_2 = 10$ . The following subsections present spatial-temporal comparisons to confirm the consistency of simulation results for the two models.

#### 4.1.1. Deterministic commuting contacts

In this section, we assume that individuals contact a fixed number of people each day, denoted as  $n_2$ . The number of contacts for risk-neutral individuals and risk-averse individuals differs, and parameter  $\gamma_2$  denotes the discount rate of contacts for risk-averse individuals. Similarly, protective behaviors could reduce the infection rate for risk-averse individuals; parameter  $\gamma_1$  denotes the corresponding discount rate.  $\beta$  represents the infection rate per contact between infected individuals and susceptible individuals. All parameters used in models should be consistent in order to compare two models. The parameter relationships between the two models are

$$\beta_n = -n_2 \ln(1 - \beta) \quad (21)$$

$$\beta_a = -\gamma_2 n_2 \ln(1 - \gamma_1 \beta) \quad (22)$$

where  $n_2$ ,  $\beta$ ,  $\gamma_1$ , and  $\gamma_2$  are parameters also used in Zhao, Wu, and Ben-Arieh (2015). All other parameters are identical for the two models.

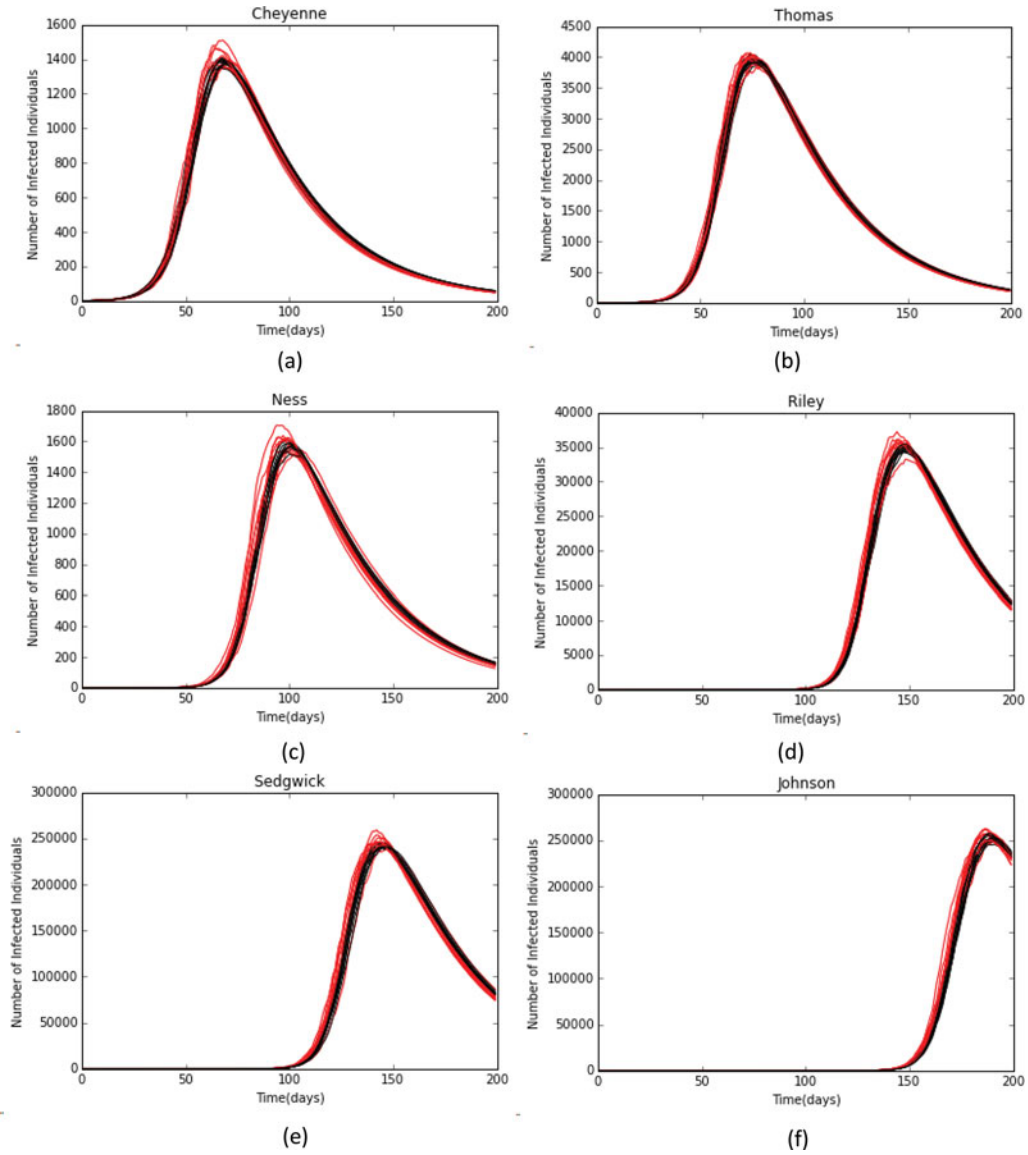
According to comparison results in Fig. 4, the number of infected individuals in each county was consistent in the two models, spatially and temporally, and wherever the county is located does not impact the consistency of results from the two models for all tested six counties. In addition, the further from the source of the infectious disease, the later the infection occurred.

#### 4.1.2. Stochastic commuting contacts

All assumptions in this subsection are identical to assumptions in Section 4.1.1, with the exception of the number of contacts on each day. Instead of using a fixed number of contacts, we let the number of contacts  $N_c$  on each day follow the Poisson distribution.

$$P(N_c = k) = \frac{e^{-\gamma_1 n_2} (\gamma_1 n_2)^k}{k!} \quad (23)$$





**Figure 5.** Simulated number of infected individuals in Cheyenne, Thomas, Ness, Riley, Sedgwick, and Johnson Counties in Kansas over time for model comparison under stochastic contacts (red line is the plot of the SEGM model; black line is the plot of the MDM model).

Parameters  $\beta_n$  and  $\beta_a$  in the MDM model were consequently changed to be

$$\beta_n = -N_c \ln(1 - \beta) \quad (24)$$

$$\beta_a = -\gamma_2 N_c \ln(1 - \gamma_1 \beta) \quad (25)$$

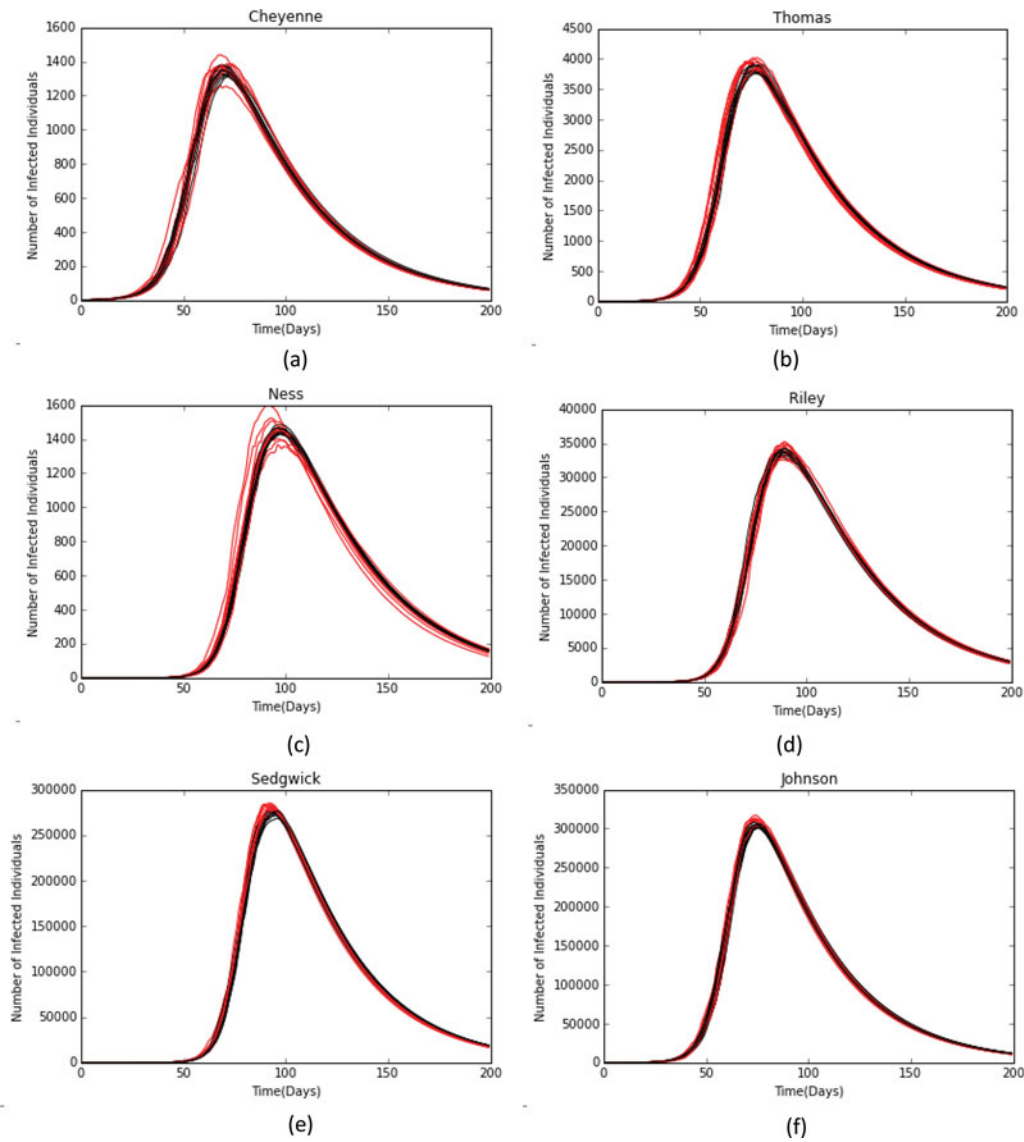
Ten replications were run for each model, and the results are presented in Fig. 5. The red curve represents results for the SEGM model; the black curve represents results for the MDM model. Results from both models were consistent, as evidenced by overlapping areas of the curves.

#### 4.1.3. Long-distance travel

Sedgwick and Johnson Counties, the top two counties by population in Kansas, were selected as network centers in our long-distance contact model. People in all other counties were assumed to travel to these counties for shopping or business.

Stochastic contacts remained in this simulation, and 10 replications were run for each model. Results from the two models were consistent. In addition, the spread of infectious disease was faster than the spread shown in the local contacts pattern (around 50 and 100 days earlier for the peak in Sedgwick and Johnson counties, respectively), as shown in Figs. 6e and 6f (compared to Figs. 4e, and 4f). Infectious disease typically is more readily transmitted to large cities, (around 50 and 100 days earlier for the occurrence in Sedgwick and Johnson counties, respectively) when long-distance travel is involved in the model.

Due to the high volume of transportation and large populations within Sedgwick and Johnson counties, infectious diseases are rapidly transmitted to areas surrounding those network centers. Peak time for the number of infected individuals in Johnson County is approximately 100 days earlier compared to that in the model without long-distance travel. To further explain the long-distance travel effect, the number of infected individuals in each county is calculated for day 3. It turns out that Cheyenne County showed one infected case as the source



**Figure 6.** Simulated number of infected individuals in Cheyenne, Thomas, Ness, Riley, Sedgwick, and Johnson Counties in Kansas over time for model comparison under long-distance travel (red line is the plot of the SEGM model; black line is the plot of the MDM model).

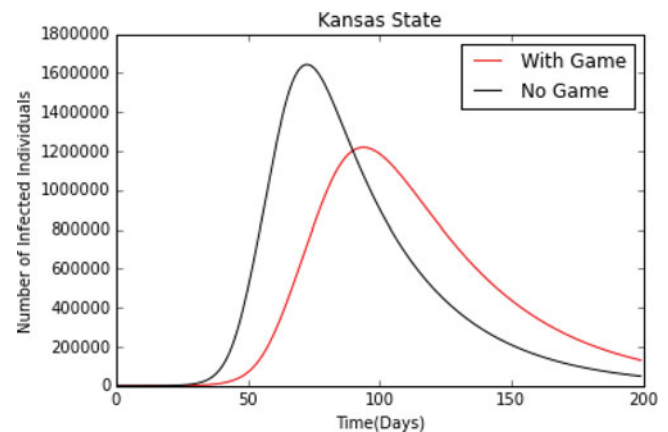
location of infectious disease, but Johnson County indicated three cases. Because the spread of infectious disease is extremely fast in Johnson County due to its large population, avoidance of long-distance travel to the network center may be a crucial strategy for decreasing the spread of infectious disease.

#### 4.2. Impacts of changes in human behaviors

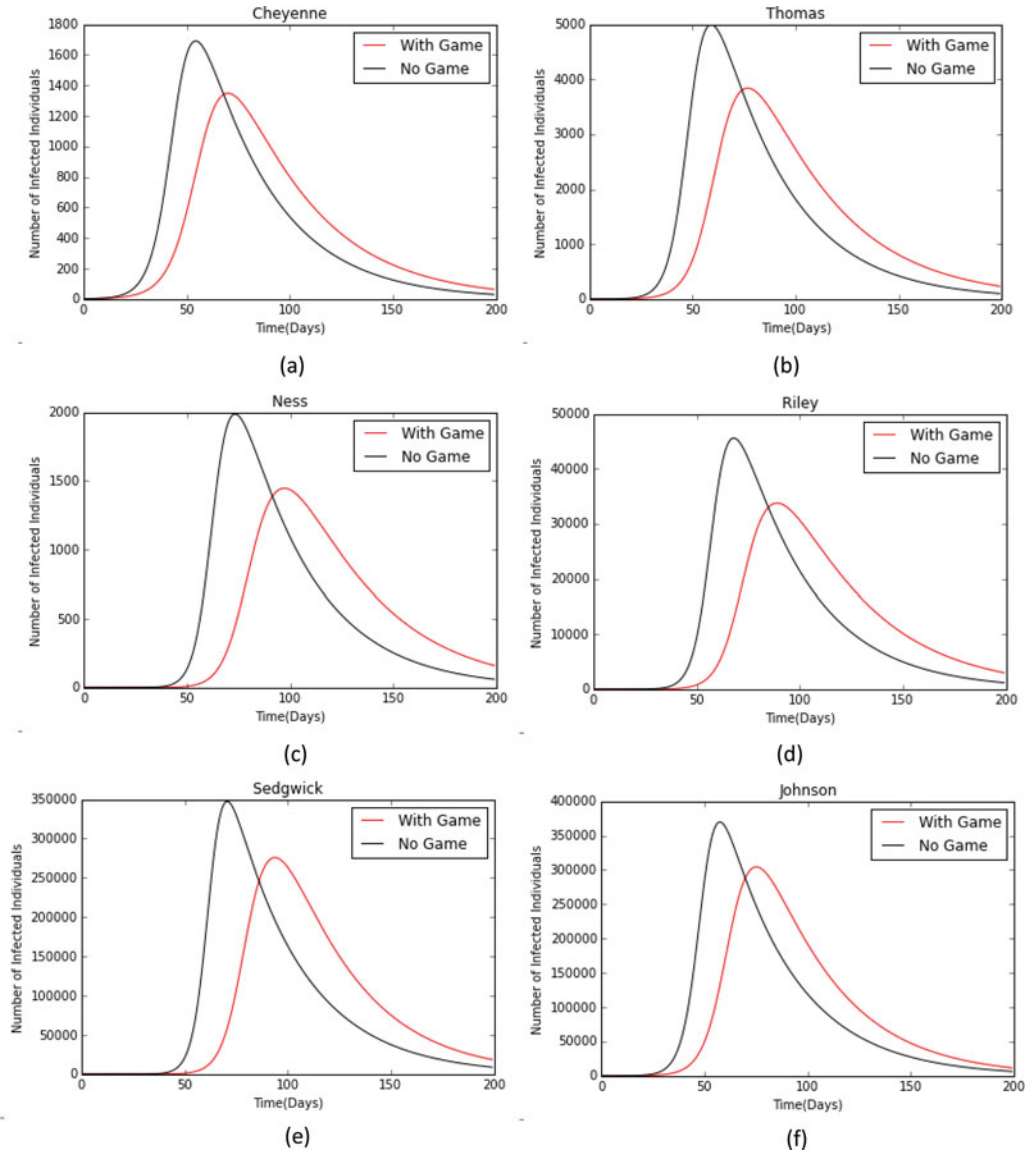
This section includes discussion of the impacts on disease transmission dynamics due to changes in human behaviors temporally and spatially on state and county scales, respectively. Long-distance travel was involved, and commute contacts are assumed to be deterministic. Comparisons of the number of total infected individuals in the entire state of Kansas and in various counties in Kansas are shown in Figs. 7 and 8, respectively.

In Figs. 7 and 8, the black line (“no game”) indicates no changes in human behaviors in epidemics; the red line (“with game”) indicates that changes in human behaviors were considered. On a statewide scale, human behaviors significantly impacted the dynamics of disease transmission, lowering the

total number of infected individuals (with game: 2,806,949; no game: 2,852,778) and delaying the peak time of epidemics. On a county scale, identical impact patterns were obtained for



**Figure 7.** Simulated number of infected individuals in Kansas over time for scenario without and with game.



**Figure 8.** Simulated number of infected individuals in Cheyenne, Thomas, Ness, Riley, Sedgwick, and Johnson Counties in Kansas over time for scenario without and with game.

all counties in Kansas, implying that the distance between the studied county and the source county for patient 0 did not affect the impacts of human behaviors on the spread of infectious diseases, reflected in the distance between small counties and network centers due to our homogeneous assumption of risk estimates for each county. Individuals' perspectives of the infectious disease based on prevalence were scaled by parameters  $m_1$  and  $m_2$  in Eq. (10), indicating local information and global information, respectively. Global information impacts were assumed to be identical for all individuals, but local information impacts potentially varied. The following section discusses the impact of local information (parameter  $m_1$ ) in detail.

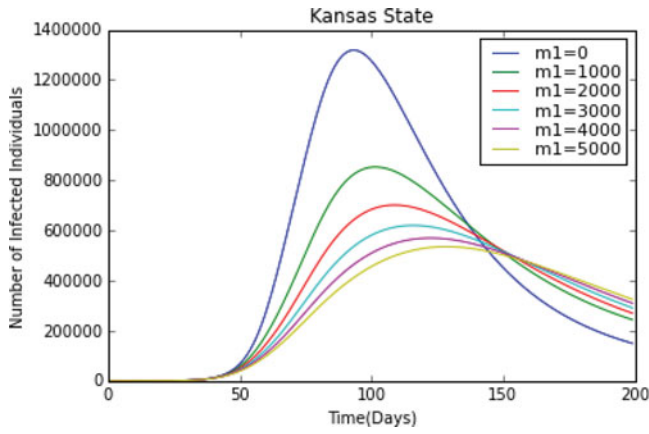
#### 4.3. Impacts of risk estimates based on local information

As mentioned in Section 4.2, individuals' perspectives of an infectious disease based on local information may differ by location. As a multiplier of local prevalence in Eq. (10), parameter  $m_1$  essentially bridges the local information and risk estimates

by individuals. Individuals' behaviors are determined by the game update rule, which is calculated by the differences of payoff values for risk-neutral and risk-averse individuals, while the payoff value is primarily impacted by the product of  $m_1$  and local prevalence, as explained in Zhao, Wu, and Ben-Arieh (2015). Therefore, local information is translated to payoff by  $m_1$  to motivate individuals to choose either risk-neutral or risk-averse behavior, thereby implicitly affecting the dynamics of the epidemic. In addition, the value of  $m_1$  could be changed due to intervention strategies. Public health education, policies of vaccination, and quarantine measures could also alter an individual's risk estimate of the infectious disease, leading to changes in  $m_1$ . Consequently, impacts of  $m_1$  must be studied further in order to understand human behaviors in epidemics. Analyses for  $m_1$  are discussed in the following subsections.

##### 4.3.1. Sensitivity analysis for $m_1$

A sensitivity analysis is conducted in this section in order to understand the impact of  $m_1$  on the dynamics of disease



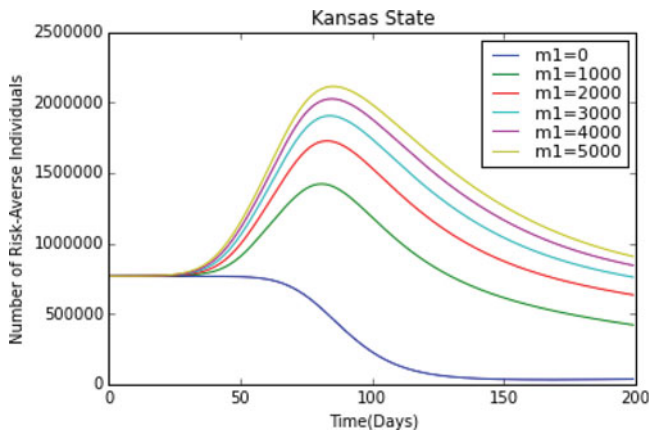
**Figure 9.** Simulated number of infected individuals in Kansas over time for different impacts of local information.

transmission. The range of  $m_1$  was set from 0 to 5000, and the step size was set at 500.

As shown in Fig. 9, the peak number of infected individuals in Kansas decreased as the value of  $m_1$  increased from 0 to 5000. The higher the value of  $m_1$  was, the more risk individuals estimated, proving that individuals were more self-protective if  $m_1$  become larger, consequently decreasing the numbers of infected individuals, as shown in Fig. 9. Similarly, as shown in Fig. 10, an increasing value of  $m_1$  led to an increasing number of risk-averse individuals throughout the state of Kansas. An identical pattern of changes also occurred in all counties.

#### 4.3.2. Impacts of memory on individuals' risk estimates

Basic perception and cognition researchers have shown that “biased media coverage, misleading personal experiences, and the anxieties generated by life’s gambles cause risks to be misjudged (sometimes overestimated and sometimes underestimated), and judgments of fact to be held with unwarranted confidence” (Slovic, 2000). The perception of risk to the infectious disease does not stay the same all the time. Individuals are affected by their memories of prior information as well as the new information. For instance, after a slow exponential increase of changes in human behaviors in the beginning of the 2009 H1N1 pandemic in Italy, there was a sudden and sharp increase of growth rate which occurred in the next month due to the new



**Figure 10.** Simulated number of risk-averse individuals in Kansas over time for different impacts of local information.

cases reported (Poletti, Ajelli, and Merler, 2011). On the other hand, a quick drop in individuals' efforts to protect themselves from an infectious disease frequently occurs when the epidemic is over its peak or people are getting used to the disease prevalence reports by the media (Bagnoli, Lio, and Sguanci, 2007). Hence, it is our belief that individuals' decisions are impacted by their prior knowledge and the number of newly infected individuals. The memory mechanism was also assumed for protective behaviors in several other studies (Poletti, Ajelli, and Merler, 2011; d'Onofrio, Manfredi, and Salinelli, 2007; Ajelli et al., 2008). In this section, we attempt to model the memory mechanism via a stochastic differential equation of a Itô drift-diffusion process with a drifting factor and a random walk (Krylov, 1995). The Itô drift-diffusion process is commonly used in mathematical finance to model stock price and has value in illustrating the changes of individuals' perception to risks in epidemics. The drifting factor could represent the average change rate of individuals' perception of the risk based on prior knowledge and new information, and the random walk could represent the diversity of individuals. Hence, the dynamics of  $m_1$  is defined as a Itô drift-diffusion process with a drift factor  $\mu_t(x)$  and the uncertainty factor  $\sigma(x)$  as follows:

$$\frac{dm_1(x)}{m_1(x)} = \mu_t(x) dt + \sigma(x) dZ_t \quad (26)$$

where  $Z = \{Z_t: t \in [0, \infty)\}$  is standard Brownian motion with mean of 0 and standard deviation of 1.

Individuals were kept updated via new information and gradually forgot their prior knowledge. Hence, the information cumulating and memory fading effects must be applied to the study of average perception of risks to the infectious disease  $\mu_t(x)$  at time  $t$  and location  $x$ . The variation term  $\sigma(x)$  represents a heterogeneous risk estimate in different locales, as well as various individuals' risk perception of the underlying epidemic in a diverse population. The information cumulating process was modelled by a Hill equation, which could provide a reasonable boundary for the change rate of individuals' perception between 0 and 1. Hill equation is extensively used in biochemistry and pharmacology, and we believe that the behavior of the Hill equation can properly describe the changes of individuals' perception of the risk. The memory fading process was modelled as a negative exponential function with argument infection prevalence. As prevalence increases, the fading effects were assumed to be weaker, since large prevalence could increase individuals' risk estimates. According to the cumulating information assumption and memory fading assumption, calculation of  $\mu_t(x)$  was shown as follows:

$$\mu_t(x) = H(L_t(x), n) - \varepsilon \quad (27)$$

where

$$L_t(x) = - \sum_{y_l \in local} \left( \frac{dS_n}{dt}(y_l) + \frac{dS_a}{dt}(y_l) \right) \quad (28)$$

$$H(L_t(x), n) = \frac{(L_t(x))^n}{(K)^n + (L_t(x))^n} \quad (29)$$

where  $L_t(x)$  represents the newly infected population in location  $x$  at time  $t$ ,  $\varepsilon$  is a constant which acts as a negative exponential



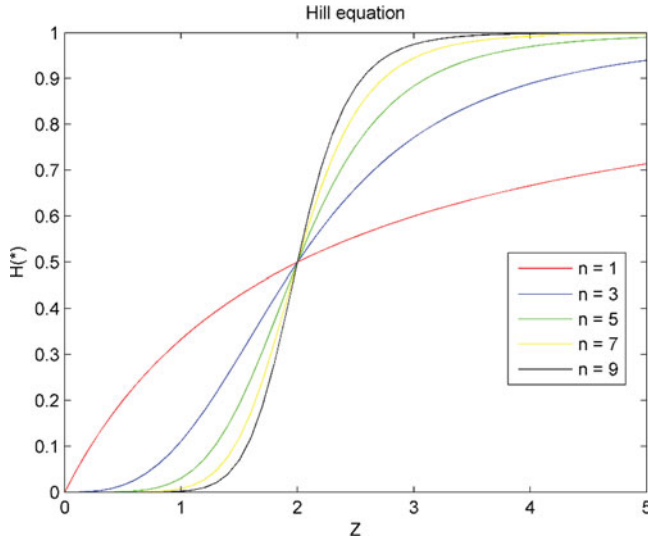


Figure 11. Illustration of the general Hill equations with different Hill coefficients.

in Eq. (26),  $K$  is the equilibrium constant, and  $n$  is the Hill coefficient in the Hill equation.

When the Hill coefficient  $n$  is greater than 1, the  $H^*$  is monotone increasing with  $L_t(x)$  and the lower bound and upper bound are 0 and 1, respectively. What's more, it increases very slowly in the beginning, which means that the first few new cases of infection have a small impact on individuals' decision, while the impacts are amplified as more individuals are infected. After a quick increasing period, the increase of impact of information slows down, since most individuals already recognize the severity of the disease transmission. An example of plots of general Hill equations with different  $n$  is shown in Fig. 11. In this example, the equilibrium constant is set to be 2.

One numerical simulation was conducted to study the impacts of  $m_1$  on the dynamics of disease transmission based on the memory mechanism. We assumed that  $\sigma^2(x) = 0.2$ , and we ran five replications. The changes of  $m_1$  are shown in Fig. 12. Overall, the value of  $m_1$  slightly decreased in the beginning and then exponentially increased due to the increasing number of infected individuals. Moreover, there is a time delay between

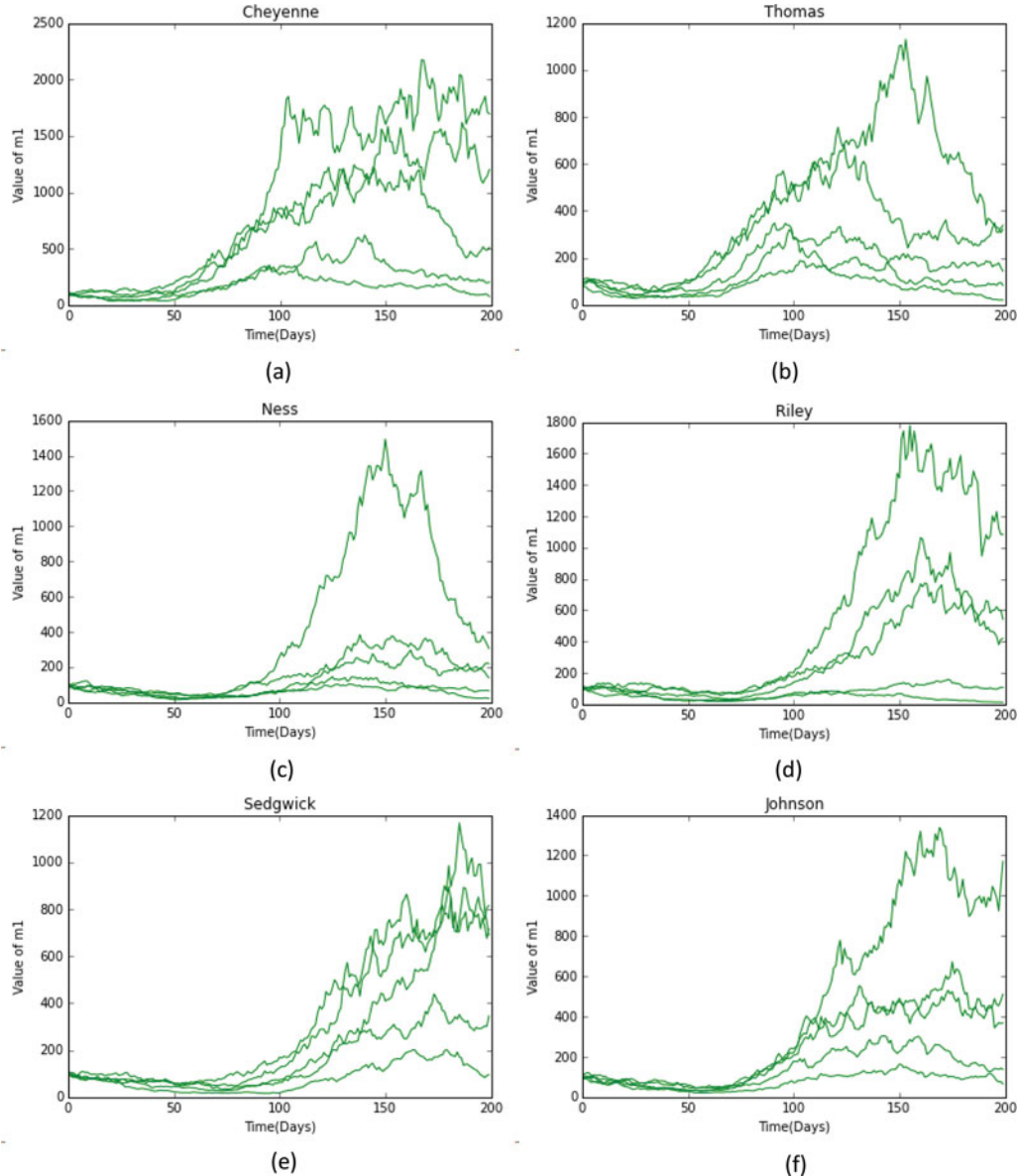
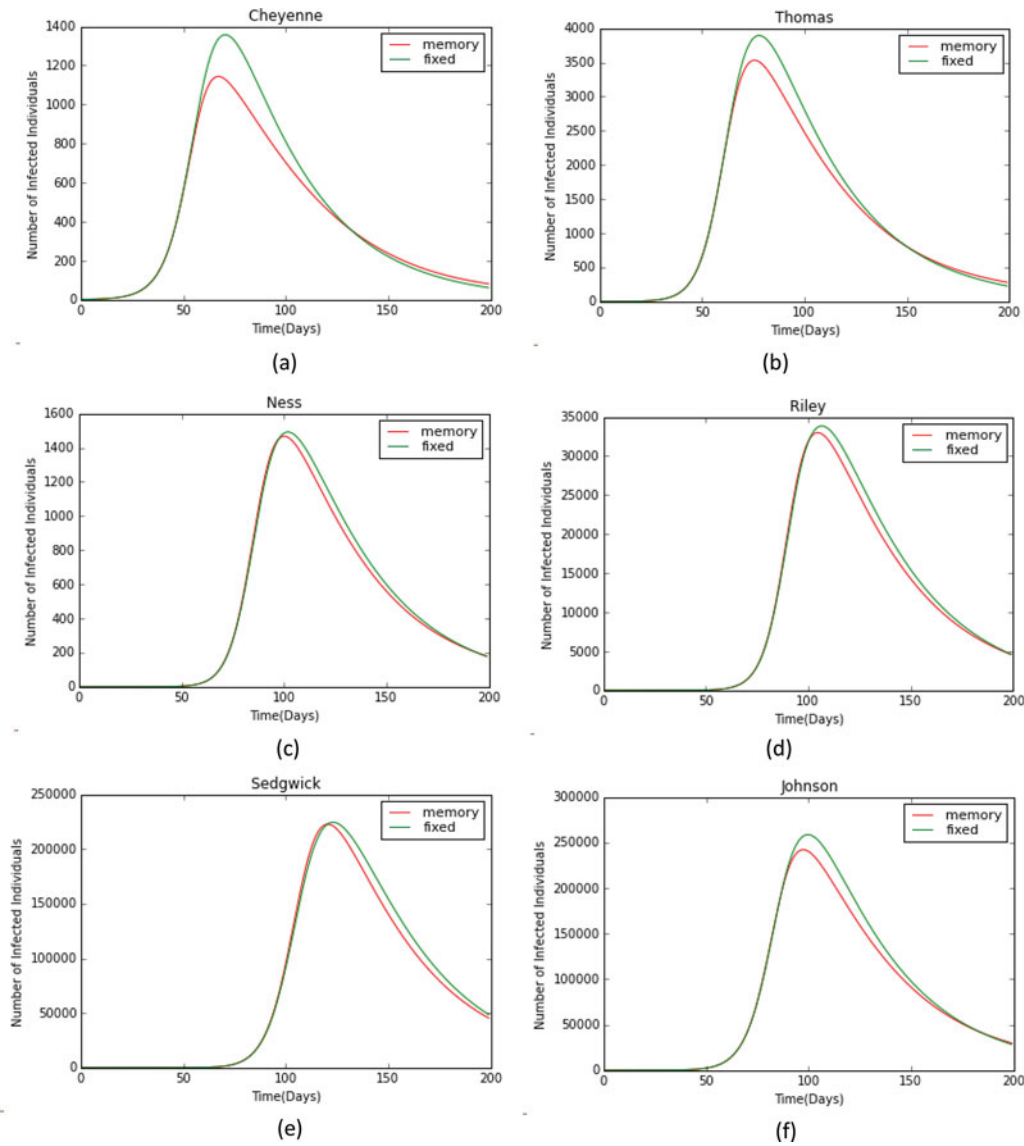


Figure 12. Simulated value of  $m_1$  in Cheyenne, Thomas, Ness, Riley, Sedgwick, and Johnson Counties in Kansas over time for scenario with memory impact.





**Figure 13.** Simulated number of infected individuals in Cheyenne, Thomas, Ness, Riley, Sedgwick, and Johnson Counties in Kansas over time for scenarios with and without memory impact.

the increase of  $m_1$  and the increase of infected individuals, since some individuals would choose to “wait and see” (Bhattacharyya and Bauch, 2011), and not all individuals changed their behaviors immediately. Susceptible individuals gradually recognized the severity of infection so that perception of the risk increased as more and more individuals were infected.

To better understand the impact of memory, a simulation was conducted to compare the number of infected individuals in each county for two scenarios: model with memory impact and model with fixed risk perception. For the simplicity of comparison, the Brownian motion effect was excluded for the memory-based model and the initial value of  $m_1$  was identical for both models. In Fig. 13, it turns out that inclusion of the memory not only makes the model more realistic, but also has a significant impact on the result.

## 5. Discussion

Spontaneous changes of human behaviors during an epidemic have recently attracted increasing research attention.

Assessment of whether benefits of protective actions outweigh the corresponding costs after estimating the payoff according to information and infectious disease risk perception significantly impacts the determination of appropriate behaviors for individuals. Game theory, a commonly used tool to study conflicts and cooperation between decision makers, provides a mathematical framework to discuss individuals’ decision-making processes. A spatial evolutionary game specifically combines spatial association between individuals’ contacts and disease information and temporal impacts of information to the dynamics of human decisions, thereby increasing understanding of the impacts of heterogeneous population and human behaviors on disease transmission dynamics.

This article applied the spatial evolutionary game used in Zhao, Wu, and Ben-Arieh (2015) to a classic dynamic system for the spread of infectious disease. The classic compartmental SIR model has been widely used for epidemic study, including changes in human behaviors due to the spread of infectious diseases. The numerical simulation first confirmed the consistency of two models, thereby validating the effectiveness of

the spatial evolutionary game. Then, the impacts of changes of human behaviors on the dynamics of disease transmission and how information impacts human behaviors were discussed using the numerical simulation. The results showed that protective behaviors decrease the numbers of infected individuals and delay the peak time of infection. Increased numbers of risk-averse individuals and preemptive actions can more effectively mitigate disease transmission; however, changes in human behavior require a high social cost (such as avoidance of crowded places leading to absences in schools, workplaces, or other public places). An appropriate response to the epidemic and wise selection of corresponding intervention strategies are our ultimate goal to prevent infectious diseases. Therefore, individuals' perceptions of risks based on available information were discussed under various assumptions. Heterogeneous responses to an epidemic showed maximum reasonableness, since individuals have unique cognitions based on personalized memories and understanding of new information. The Itô drift-diffusion process was formulated according to this assumption, and the drift factor was defined as a memory mechanism which included two parts: cumulating information and memory fading. Hill equation and negative exponential function were used to describe the cumulating information process and memory fading process, respectively.

In this article, the MDM model was only studied through numerical simulation. In order to fully understand the behavior of a dynamic system, stability analysis and bifurcation analysis should be conducted later. In addition, further studies should combine changes in human behaviors and intervention strategies to identify optimal information dissemination in order to minimize social costs and the numbers of infected individuals. Stability analysis and optimization in epidemic were studied for different infectious diseases, such as Visceral Leishmaniasis (Shi *et al.*, 2015; Zhao *et al.*, 2016). In addition, optimal control strategies for prevention of infectious disease transmission should be studied, considering changes in human behaviors coupled with intervention strategies. In order to increase understanding of the variation of individuals' responses to infectious disease, a small scale of population, including individualized behaviors, should be taken into consideration for modeling human behaviors. Correspondingly, intervention strategies should be temporally and spatially characterized. As such, an agent-based model, which was used to simulate other diseases, such as sepsis (Shi, Ben-Arieh, and Wu, 2016; Shi *et al.*, 2016), could be used as a tool to study the complex system with interactions among changes of human behaviors, disease transmission, and intervention strategies (public policy). If successful, this research should improve communication between policymakers and the public by directing educational efforts and predicting public response to infectious diseases and new risk management strategies (regulations, vaccination, quarantine, etc.).

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