A Comparison of Agent-Based Models and Equation Based Models for Infectious Disease Epidemiology *

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Abstract. There are two main methods that are used to model the spread of an infectious disease: agent-based modelling and equation based modelling. In this paper, we compare the results from an example implementation of each method, and show that although the agent-based model takes longer to setup and run, it provides additional information that is not available when using an equation based model. Specifically, the ability of the agent-based model to capture heterogeneous mixing and agent interactions enables it to give a better overall view of an outbreak. We compare the performance of both models by simulating a measles outbreak in 33 different Irish towns and measuring the outcomes of this outbreak.

Keywords: Agent-based model · Equation-based model · Infectious Disease

1 Introduction

2018 marks the 100 year anniversary of the deadliest event in recent human history, the Spanish flu outbreak that killed approximately 50 million people, 10 million more than those killed in World War 1 [27]. It is commonly believed that the question concerning the next deadly pandemic is not if it will occur but when it will occur. The World Health Organization (WHO) prepares an annual review on priority diseases that they feel could be involved in a future public health emergency [29] and the UK's National Security Capability Review (NSCR) has added the threat from infectious diseases to the list of challenges that are expected to drive future security priorities [1].

One way to prepare for a pandemic is to evaluate preventative measures and responses before a pandemic occurs. As it is impossible to test such measures

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in the real world prior to a disease outbreak, one way to evaluate how well prevention measures or responses to an outbreak will work is through modelling. A model is a simplified description of a system or process that can be used to better understand that system or process, allowing one to run experiments without having to test scenarios in the real world. An important part of modelling a disease outbreak is choosing an appropriate and realistic model. While all models will make assumptions, it is important to determine which assumptions make a difference to the results. It is also essential to consider the different types of models available and the advantages and disadvantages of such models. Typically epidemic models are either created using an equation based model or with a simulation model, such as an agent-based model. Both types of models have advantages and disadvantages that may lead to the decision to choose one over the other.

Equation based models tend to be less computationally intensive than simulation models and are faster to run. However, equation based models are designed for a homogeneous population and each additional characteristic added to the population, such as age, vaccination status or socioeconomic status requires additional equations to be added into the model, making the model more complicated and harder to solve and analyse. In addition, equation based models assume homogeneous mixing, each agent has an equal probability of coming into contact with every other agent. There can be adjustments added into equation based models that allow for different contact rates across groups, for example age groups, however, within each group the mixing patterns are the same.

Alternatively, agent-based models are computationally intensive and may take a long time to run to completion. However, one of the main advantages of modelling at the agent level is the ability to create heterogeneous agents. Each agent can have a list of their own characteristics such as age, gender or vaccination status and theoretically each agent could be unique with a different combination of characteristics. These characteristics can affect the agents' likelihood to contract a disease directly or by influencing the agents' decisions and thus who they come into contact with. Because agent-based models allow the agents to make decisions and move throughout the environment the agents in an agent-based model have realistic heterogeneous contact patterns.

When deciding which model is appropriate it is important to look into these advantages and disadvantage but also to look at the ability of each model type to successfully model a disease outbreak. We have created both an agent-based model and an equation based model to better explore the differences between the types of models when applied to the Irish context. Section 2 provides an overview of agent-based models for epidemiology and equation based models for epidemiology. Section 3 discusses the agent-based model and equation based model we have created for Irish towns. Finally, Section 4 discusses and compares the results obtained from both models.

2 Background

In the following sections we describe both agent-based models and equation based models for infectious disease epidemiology.

2.1 Agent-Based Models

Agent-based models (ABMs) are a type of computer simulation composed of agents that can interact with each other and with an environment. The actions of agents are governed by a set of coded rules [18]. Because agents can make their own decisions in the model based on the rules given to them, ABMs can capture unexpected aggregate phenomena that result from combined individual behaviours in a model [5]. ABMs can be particularly useful in infectious disease epidemiology as they have the ability to capture the dynamics of the disease spread combined with the heterogeneous mixing and social networks of the agents [3]. ABMs have been run on a wide range of infectious diseases such as various strains of influenza, including H1N1[10] and H5N1[7], Ebola [21], measles [25], and HPV [23]. The results from ABMs can be used to influence public policy, for example the EpiSimdemics model looked at responses to an outbreak in a military population and determined that counterintuitively sequestration of military populations during an outbreak may lead to more infection [2]. Similarly, FRED (A Framework for Reconstructing Epidemiological Dynamics) is an agent based modelling system that is used to support research on the dynamics of infectious diseases particularly for US state and county public health officials to evaluate the effects of interventions [12]. FRED has been used by researchers to look into different aspects of outbreaks such as shutting schools down and self isolation [4].

2.2 Equation-Based Models

Historically equation based models have been used to model the spread of infectious diseases. The most common type of equation based model used for infectious disease modelling is the compartmental model, which is made up of a set of differential equations [13]. The population in a compartmental model is assumed to be homogeneous, well mixed, and split into compartments based off of health status. Each compartment is defined with its own differential equation [9]. The simplest compartmental model is the SIR model where the population is split into three compartments: susceptible individuals (S), infected individuals (I), and recovered individuals (R). The following equations define the system:

$$\frac{dS}{dt} = \frac{-\beta SI}{N} \tag{1}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I \tag{2}$$

$$\frac{dR}{dt} = \gamma I \tag{3}$$

where N is the population size, β is the rate of transmission per contact, γ is the recovery rate, and $S(t) + I(t) + R(t) = N$ [13].

Typical variations of the SIR model include the SEIR model (susceptible, exposed, infected and recovered), the SIS model (susceptible, infected and susceptible) and the SIRS model (susceptible, exposed, infected, recovered and susceptible). The models can be made more complicated and realistic by adding additional compartments for various characteristics of agents including age groups or vaccination status. These models can be used to better understand the dynamics of a disease. Hogan et al. [14] create an age structured model for Respiratory Syncytial Virus, a common childhood infection, where each age group has its own compartments. The model can be useful when simulating age-dependent interventions such as vaccination. The effects that vaccination rates have on measles outbreaks are studied using the Pang et al. model [24].

There are many examples of equation based models beings used to analyse a specific outbreak or epidemic after the fact. These models are often used to determine lessons learned from the outbreak. For example, Vaidya et al. [28] model the spread of H1N1 in a rural university town and determine that a portion of the susceptible population was protected from infection through self-isolation, social distancing or other preventative measures and this protected population played a substantial role in the dynamics of the epidemic. Mamo and Rao [19] show that to best capture the dynamics of Ebola spreading in West Africa an additional compartment, isolated, is needed since isolation is commonly used in Ebola cases. Equation based models have also been used to help shape policy during an outbreak. A series of models were used to help inform policy decisions to control the 2001 foot-and-mouth disease epidemic in the UK [17].

Although equation based models have proven to capture the macro level dynamics of an infectious disease outbreak and have been used in the development of control policies and responses to outbreaks, there are some disadvantages to using an equation based model. Equation based models can not provide detailed information on the spread of the disease. In addition, the small set of variables that are used in an equation based model may not be enough to define an outbreak. Assuming that the population is homogeneous within a compartment can also be a problem in not capturing the individual variations and actions that can have a major impact on the course of an outbreak [9].

3 Experimental Setup

The following sections discuss the models we use in our comparison.

3.1 Agent-Based Model

The ABM we use in this paper is the same as the infectious disease model described in Hunter et al. [16][3]. We use the computer software Netlogo [30] to

[3] The model described in Hunter et al. uses a burn-in model as a step in setup to capture socioeconomic segregation. This paper does not use the burn-in model during setup

implement our model. Netlogo is an easy to use and popular environment for creating ABMs [11]. We chose to use Netlogo due to the increasing popularity of the platform with agent-based modellers and its ability as a medium to large scale modelling platform.

Our model is a data driven ABM for human airborne infectious diseases such as the flu or measles. We have created a simulation with a more general disease model so that it can adjusted for various airborne diseases. It follows an SEIR (susceptible, exposed, infected, and recovered) type compartmental model with the agents moving between the four states relating to infectiousness [13]. Parameters for infectivity, exposed time and recovery time can be adjusted based on the disease being modeled. Our society model is created using openly available data mostly from the Irish Central Statistics Offices to create a realistic synthetic population for a town in Ireland. We also use data from the HPSC to get age specific vaccination rates for the population. The data sources used to create the population and a description of how the society is set up can be found in the paper [15]. The model includes transportation with agents moving between their current location and desired destination in a straight line in steps allowing them to interact with other agents along their route. The model environment includes maps of the towns being modelled. The small area boundary files[4] from the CSO were used to determine the layout of the towns and zoning data is used to determine where residential, community and industrial areas should be placed. School location data from the Irish Department of Education is used to place primary and secondary schools in appropriate locations within towns. Figure 1 shows an example of a town in the agent-base model. The white lines are the outlines of the small areas and the yellow figures represent people in the town. The model runs on time steps of two hours and runs until no agents are exposed or infected.

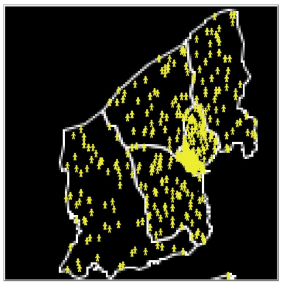

Fig. 1. An example setup of the Agent-Based Model. The town modelled here is Schull, Ireland.

[4] Small areas are the smallest area over which census data is aggregated. Each small area is made up of 50 to 200 households.

3.2 Equation-Based Model

We created an equation based model to compare to the ABM. The equation base model is a compartmental model with age groups that determine vaccination status. There are 61 equations in the model and 29 age groups. There is one age group for each age between 0 and 27 and then another group for all other adults. These match with the vaccination data that we have and with our ABM. For each age group there are two equations: susceptible but not vaccinated, and susceptible and vaccinated. We consider homogeneous mixing within the model so the exposed, infected and recovered groups contain individuals from all 29 age groups. The model is represented with the following equations:

$$\frac{dS_i}{dt} = \frac{-\beta S_i I}{N} \tag{4}$$

$$\frac{dS_{vi}}{dt} = -(1-\alpha)\frac{\beta S_{vi} I}{N} \tag{5}$$

$$\frac{dE}{dt} = \Sigma(\frac{\beta S_i I}{N} + (1-\alpha)\frac{\beta S_{vi} I}{N}) - \sigma E \tag{6}$$

$$\frac{dI}{dt} = \sigma E - \gamma I \tag{7}$$

$$\frac{dR}{dt} = \gamma I \tag{8}$$

Where S_i is the susceptible, unvaccinated population for age group i, S_{vi} is the susceptible, vaccinated population for age group i, E is the exposed but not infectious population, I is the infectious population, R is the recovered population, N is the total population, β is the rate of transmission per contact, α is the vaccination success rate, $\frac{1}{\sigma}$ is the duration of the exposed period and $\frac{1}{\gamma}$ is the duration of the infectious period. We take the duration of the exposed period to be 10 days and the duration of the infectious period to be 8 days. We then determine β using the formula $\beta = R_0\gamma$ [8]

The model is solved using Matlab ODE solver [20]. The initial conditions for each town were adjusted to match the 2011 census data and the vaccination statistics. Both datasets are also used in the creation of the ABM.

4 Results

To compare the two models we simulate a measles outbreak in 33 different towns. The towns are small to medium size towns in Ireland with populations between 390 and 9,548. The areas of the towns range from 5.26 km^2 to 63.96 km^2. The towns included were selected to have a range of diverse towns to test the models. Data for each town is used to setup the ABM and we use the population statistics from the town as initial conditions in the equation based model. We keep age-based vaccination rates constant across all towns using all Ireland vaccination

levels. The models run until no agents are exposed or infected, which means that the length of a simulation varies between towns and between runs for the same town. For example, across 100 runs for the town of Schull, the average length of a simulation was 8 weeks but the simulation ended in some runs after one week and in some runs after 15 weeks.

For the purpose of comparison we take as the outcome of an outbreak[5] the final recovered number from the equation based model, this is the number of individuals in the model who started as susceptible, became exposed, moved to infected and then recovered and represents the magnitude of the outbreak. For the ABM we use the average number of infected agents across 200 runs, as ABMs have stochasticity in the model each run can have different results. For each model run there is a total number of immune agents, these are the agents who have been infected and recovered. We take the average across the 200 runs for each town and find an average magnitude of the outbreak for the town. The ABM provides us with a range of outbreaks that might occur in the current system. The average does not need to be calculated for the equation based model because there is no stochasticity in the system. The lack of stochasticity in the model means that the same result is found each time. Table 1 presents the results for the equation based model for each town, the average number of immune agents from the ABM and the maximum number of infected agents across all runs of the ABM. Looking at the results it can be noted that in some towns such as Arainn, Kilkee and Schull the results are similar between the ABM and the equation-based model. However, many of the towns have different results between the two models, showing that the results can vary and that a comparison is necessary. It is important to note that there are only two towns, Blarney and Kilcock, where the number of infected people in the equation based model is greater than the maximum number infected in the ABM. This means that for all other towns the outbreak produced in the equation-based could be in the range of outbreaks produced in the ABM.

To determine which descriptors of the towns (e.g. population and area) are most related to the results of the model simulations we calculated Pearson correlation coefficients between simulation results and town descriptors. Table 2 shows the correlations between the results of the ABM and the equation based model and other variables including the population size, percent of unvaccinated individuals, percent students in the town and the area of the town. From the correlations it can be seen that the results for both models are correlated with the population of the town. However, the equation based model has a much higher correlation with population than the agent based model.
In fact the ABM has a higher correlation with the equation based model results than with the population. From the correlations it can also be seen that the equation based model is correlated with the percent of unvaccinated individuals and the percent of students in the town. This makes sense as these are variables that are included in the model. Area, however, has a near zero correlation with

[5] We define an outbreak as two or more cases of measles. This is based off of the WHO's definition of a measles outbreak

the equation based model as the variable is not included. The ABM has a small correlation with the percent of unvaccinated agents, the percent of students in the town and the area. The smaller correlations compared to the equation based model are believed to be because the results of the ABM are not simply determined by the variables programmed into the model but by the individual agent decisions and interactions between the variables that are not found within the equation based model. The correlations help to show that ABM captures more complex relationships and interactions between variables than the equation based model.

For a more in depth look at the output from both models we look at the results of both models for Kinsale. We picked Kinsale because it was determined, based on a detailed analysis of the Irish census data, that Kinsale was the town that statistically best represents Ireland [22]. It also has a large variation between the results in the ABM and the equation based model. As ABMs are designed to be stochastic each model run produces a different result, Table 1 presents the average number of infected agents but we can find additional statistics on the outbreaks such as the percent of runs that lead to an official outbreak (2 or more cases). The equation based model is non stochastic and thus we only get the one outbreak. It would be possible to change the initial conditions of the equation based model to get different results, however, the initial conditions are based off of the actual population. In the ABM there are 87% of runs that lead to an outbreak.

To test how both models react to a change in the initial conditions we look at how a change in the vaccination policy would influence the outbreak. For all non school age individuals we leave the vaccination levels the same, however, for any individual in the model who is in school we implement the policy that all school age children must be vaccinated for measles. This is a policy that is implemented in many states in the USA,and France and has been discussed as a potential policy for Ireland [6]. To account for children with medical exemptions we use the average percent of children in the USA that do not receive the MMR vaccination due to medical reasons, resulting in a 99.25% vaccination rate among school children in the model [26]. In the equation based model for Kinsale this results in a reduction of the size of the outbreak from an outbreak of size 23 individuals to an outbreak of size 2. The ABM for Kinsale sees a reduction in the average number of infected agents from 438 to 129, a reduction in the maximum number of infected agents from 655 to 534 and a reduction in the percent of runs that lead to an outbreak from 87% to 63%.

Both models show that a reduction in the outbreak size occurs when changing the vaccination policy, however, because we have a range of outbreaks that might occur with the ABM results we are better able to understand how the vaccination policy might influence an outbreak in the real world. It is highly unlikely that a real outbreak will match the equation based model results exactly. It is much more likely that a real outbreak will fall into the range of our ABM results. Thus we can show a vaccination policy will influence the likelihood of an

Town	Population	Area (km^2)	Population Density	Average Infected ABM	Max Infected ABM	Total Infected Mathematical Model
Arainn	1,251	47.48	26.35	11.64	62	10.65
Ardamine	3,293	23.33	141.15	173.96	334	44.80
Ardfert	997	7.97	125.09	7.77	47	24.60
Arranmore	514	18.08	28.43	15.95	59	5.40
Bagenalstown	3,421	18.00	190.06	10.16	59	52.80
Ballyjamesduff	3,134	21.60	145.09	219.27	406	106.33
Banagher	1,993	19.85	100.40	118.17	220	38.05
Blarney	5,310	23.30	227.90	5.08	52	82.27
Castlereagh	3,077	40.09	76.75	170.82	277	14.90
Clane	7,527	18.89	398.46	687.12	1024	219.75
Croom	1,690	18.17	93.01	5.80	88	62.33
Donegal	4,010	31.49	127.34	266.22	415	35.97
Gort	2,671	11.21	238.27	185.99	340	38.17
Kenmare	2,912	55.61	52.36	69.07	234	14.81
Kilcock	6,234	16.40	385.61	6.26	56	162.07
Kildare	9,325	37.09	251.42	871.69	1206	259.71
Kilkee	1,037	5.26	197.15	10.05	62	8.16
Killadysert	922	63.96	14.42	8.08	62	9.61
Kinsale	6,871	12.96	530.17	438.14	655	22.92
Lisdoonvarna	861	12.96	66.44	7.21	45	12.08
Louisburgh	983	23.30	42.19	8.70	51	11.50
Moate	3,046	21.34	149.75	258.04	401	55.86
Oranmore	4,325	22.38	193.25	8.92	114	90.72
Portmagee	390	16.77	23.26	4.67	40	6.17
Rathnew	3,294	6.90	477.39	25.28	176	85.89
Roscrea	6,318	48.45	130.40	638.40	843	146.30
Rosslare	2,057	17.90	114.91	3.60	40	11.01
Roundstone	459	28.01	16.39	21.43	48	15.57
Schull	987	17.03	57.96	13.88	88	12.57
Shanagolden	946	17.79	53.18	4.73	42	7.26
Stamullin	4,694	37.68	124.58	173.70	516	95.05
Strokestown	1,003	18.11	55.38	16.86	63	13.14
Tramore	9,548	16.60	575.18	44.63	228	141.75

Table 1. Area, population and model results for each of the 33 selected towns

outbreak occurring along with how it will reduce the magnitude of an outbreak if it does occur.

5 Conclusion

The work in this paper presents a comparison between an ABM for a measles outbreak in Irish towns and an equation based model for the same outbreak. Through analysis of the results we show that the two models can appear to produce very different outbreaks, however, in most cases the equation based model is in the range of outbreaks that the ABM produces. Looking at the

	Mathematical Model	ABM	Population	Unvaccinated	Students	Area
Mathematical Model	1	0.700	0.844	0.596	0.543	0.005
ABM	0.700	1	0.674	0.286	0.209	0.333
Population	0.844	0.674	1	0.462	0.388	0.203
Unvaccinated	0.596	0.286	0.462	1	0.589	-0.105
Students	0.542	0.209	0.388	0.589	1	0.001
Area	0.005	0.333	0.203	-0.105	0.001	1

Table 2. Correlation table for percent outbreaks and the other town characteristics

correlations between the results of the models and factors that are coded into or included in the model we can conclude that the agent-based model captures interactions that the equation based model does not.

As the ABM follows agents through the environment it can provide us with more detailed information such as where an agent becomes infected or who infected them. This could lead to a better understanding of how the disease spreads and allow public health officials to focus on specific areas. While some exploratory work, such as looking at overall changes in vaccination rates, can be done easily in both agent-based and equation based models, something such as including push vaccinations during an outbreak or studying the effects of isolation are more complicated when done with an equation based model requiring additional equations and interaction terms, while the same could be done in an ABM with the introduction of a few extra behavioural rules. Further work could be done to expand both models to include such interventions. It should be noted, however, that one of the advantages of the ABM comes in its adaptability. In order to add push vaccinations or change contact patterns the same ABM could be used just with different parameters while a new equation based model would need to be created.

Using an ABM allows one to capture the stochasticity that exists in a real world system. Agents are allowed to make decisions similar to how individuals in the real world will. Running the ABM multiple times will capture different possible scenarios for the outbreak that are all determined by how the agents interact. For example, if the initial infected agent decides to self isolate and does not come into contact with other individuals once they know they are sick the outbreak will be much smaller than if the agent does not stay home at all. This is similar to what could happen in a real world scenario.

The equation based model does not capture these different decisions and simply presents one course of the outbreak. The equation based model, however, does have the advantage of time and computing power. Running 200 runs of the agent-based model depending on the population size and area can take days while the equation based model takes seconds. Despite the extra time it takes to run the agent-based model we feel that the results show that it has more advantages over the equation based model when trying to capture the true course of an outbreak. More work should be done to compare not only the end results of the

models but also the overall patterns of the outbreaks from each type of model and how the early stages of an outbreak differ between the two models.

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