

SimZombie: A Case-Study in Agent-Based Simulation Construction

Matthew Crossley and Martyn Amos

School of Computing, Mathematics and Digital Technology,
Manchester Metropolitan University, Manchester M15GD, UK.

Abstract. In this paper we describe a general method for the conversion of an equation-based model to an agent-based simulation. We illustrate the process by converting a well-known recent case-study in epidemiology (zombie infection), and show how we may obtain qualitatively similar results, whilst gaining access to the many benefits of an agent-based implementation.

To appear in the Proceedings of the 5th International KES Conference on Agents and Multi-agent Systems - Technologies and Applications (KES-AMSTA), Manchester, UK, 29 June-1 July 2011.

1 Introduction

Modelling is a fundamental technique for the study of a wide range of problems [5, 6, 12]. Example application domains include disease epidemics [2], crowd behaviour [24] and traffic management [20]. Many models are based on systems of *differential equations*, and examples include elastic deformation [30] and socio-economic phenomena [8]). However, such models are often difficult to *extend*, do not easily capture the notion of *space*, and fail to handle “*mixed*” *populations* of entities [17, 19, 27, 31]. An alternative approach, which has gained popularity in recent-years, is the *agent-based method* [18], where *individual entities* (and their interactions) within a system are explicitly *simulated* computationally [15, 21, 28]. There are many benefits to this approach, including *extendibility*, *ease of understanding* for the non-specialist, consideration of *spatial factors* and *population heterogeneity* [3, 7, 22, 31].

Although the continued rapid growth in computer power has made the agent-based approach increasingly attractive, one common barrier to its adoption has been the lack of a *coherent process* by which *existing* “traditional” models may be expressed within this *new* framework. This is the main problem that we address here. By describing in detail how an existing differential equation-based model may be *converted* into an equivalent agent-based solution, and by comparing the results obtained by each, we offer a convincing roadmap for the agent-based implementation of mathematical models. We emphasise that the problem chosen is simply used as a vehicle for illustrating the conversion process; we offer no additional insights into the fundamental nature of epidemics.

The rest of the paper is organized as follows: We briefly motivate the work, before presenting an existing epidemiological model based on “Zombie” infection, which has been successfully used as an exemplar of the equation-based approach. We then show how the components of this model may be mapped onto an agent-based simulation framework, and compare the results obtained by each. In doing so, we describe a generic “workflow” for the conversion of such models, which is the main contribution of the paper. We conclude with a discussion of outstanding issues, and suggest future lines of enquiry.

2 Background and Motivation

Mathematical models are used to describe many different systems of interest, and facilitate analysis, prediction and optimisation [13]. Several different techniques exist for this, including statistical models [11] and game theory [25]. Another well-established modelling technique is the process of determining and subsequently evaluating a series of *ordinary differential equations* (ODEs). ODEs are used to accurately describe changes in the value of a variable, or a number of variables, with respect to time. These variables represent quantities which may change over time, such as the size of bacterial populations [4], monetary amounts [29] or plant mass [1], and there exist many numerical methods for approximating solutions to systems of ODEs [10].

Unlike ODEs, which attempt to model using a “top-down” approach (the behaviour of the system *as a whole* is described at the outset by a set of equations), an *agent-based model* (ABM) is populated with a number of autonomous *agents*, that are each assigned a set of (often very simple) rules which govern their behaviour. The microscopic actions and interactions of agents *give rise* to macroscopic, “emergent” system-level behaviour (the “bottom-up” approach) [7].

Many real world scenarios have been modelled using both the ODE approach and the agent-based approach. In these cases it is common to compare the results to determine the quantitative *and* qualitative differences between methods. This is common in fields such as ecology, using, for example, a standard predator-prey model [32]). In the molecular biology domain, a model for intracellular chemical interactions is presented by Pogson *et al.* [26] with specific reference to the *advantages* that ABM can offer. The impact of different *network structures* on both types of method is considered by Rahmandad and Sterman [27], using a common infectivity model, the Susceptible-Exposed-Infected-Removed (SIR) model.

The obvious conclusion to be drawn from this short survey is that *both* approaches to modelling have their strengths and weaknesses. This, in itself, is not a particularly helpful observation, so it is useful to then consider the *particular aspects* of each where benefits may accrue. Several papers highlight the benefits and limitations of each [19, 31, 17], which we now summarise. ODEs are often very difficult to *extend* – equations can very rapidly become intractable [26]. They do not handle *heterogenous populations* very well. They are often difficult

for the *non-specialist* to understand (and thus construct), but are, however, often *quick* to compute. These disadvantages easily translate to the advantages of ABM; *additional model complexity* is relatively trivial to incorporate within ABM, fully *heterogeneous* populations are possible, and both the model design and its results may be presented in a form that is easily understood by experts in fields other than computation or mathematics [3]. ABM is not without drawbacks, as obtaining results from such a model can often require a significant amount of computational resource. While this problem is becoming less of an issue as computational power increases and parallel architectures such as the GPU become increasingly widespread, it is important to note that ABM can take considerably longer (in terms of run time) to obtain results than a system of ODE.

The process of creating and developing an ABM has been well-documented [16], but there exists no clear guidance on how to exploit the wealth of ODE models *already available* as a potential starting point for *new*, agent-based studies. That is, it is not immediately clear how “legacy” ODE models might be converted into a more “useful”, agent-based form (in terms of being rendered extendable, implementable on parallel computers, and so on). In the following Section we describe a *general approach* for such conversions, and illustrate its application by converting a well-known epidemiological model into an ABM.

3 Methodology

In this Section we consider the model of Munz *et al.* [23], and discuss the process of converting this specific series of differential equations into an ABM. This model uses the outbreak of a zombie infection as a case-study example of an epidemic. Within the model there exist three basic classes of individual: *susceptible*, *removed* and *zombified*. These classes map closely to those of the Susceptible-Infected-Removed model; indeed, the “zombie” model is presented as an accessible introduction to the SIR approach. *Zombified* individuals attack nearby susceptible individuals in order to transmit the zombie infection. A *susceptible* individual might successfully defeat a zombified individual with some probability. In these instances, the zombie infection is fought off, and the susceptible remains unaffected, while the zombie moves to the *removed* class. Susceptible individuals may die of natural, non-zombie-related causes, entering the removed class *without* become zombified. Finally, there is a chance that members of the removed population may be “resurrected” as zombies, reflecting a natural influx of zombies from the deceased [14]. The model is described, as a series of ODE:

$$S' = \Pi - \beta SZ - \delta S \tag{1}$$

$$Z' = \beta SZ + \zeta R - \alpha SZ \tag{2}$$

$$R' = \delta S + \alpha SZ - \zeta R \tag{3}$$

where Π represents some birth rate, α represents the rate at which zombies are defeated by susceptibles, β represents the rate at which a zombie successfully

transmits the “zombification” infection, δ represents the natural death rate of susceptible individuals, and ζ represents the rate at which removed individuals resurrect as zombies.

The four cornerstones of our approach are Agents, Behaviours, Parameters and Space. These components form the basis of any successful agent-based model, and we now describe in detail how each is “extracted” from the set of ODEs.

3.1 Agents

ABMs use different classes of agent to represent heterogenous populations. Class-set extraction from an ODE system is achieved by defining each class as a *population* within the ODE model. In our example, analysis of the ODE reveals three classifications: S, R and Z (susceptible, removed and zombified, respectively).

3.2 Behaviours

These are derived from the equations themselves, unlike agents which are usually derived from the *subject* of the equations. Any transaction within an equation indicates a behaviour that must be considered. Behaviours often occur in *pairs* – in our model, for example, as the number of susceptibles shrinks due to natural deaths, the number of removed individuals grows. It is possible to identify all behaviours that affect populations from examining the ODE alone. There are two types of behaviour to note – those that occur *spontaneously* in a population, and those that occur only when a population member *interacts* with a member of either the same population or another population.

Behaviours that occur spontaneously are easily recognisable as terms which observe the form αN , where α is some parameter, and N is a population. These terms introduce a global population change; assuming the variables are positive, a negative term indicates a population decrease, and a positive term indicates a population increase. We observe such terms in two places within our example system; the terms for removing susceptible agents due to natural death (δS), and resurrecting zombified agents from removed agents due to natural infection (ζR). The δS term is identified in the removed differential and is negated in the susceptible differential, indicating the behaviour here can be phrased as “susceptible agents become removed agents at a given rate (δ).” The ζR term is positive in the zombified differential and is negated in the removed differential, indicating the behaviour can be phrased as “removed agents become zombified agents at a given rate (ζ).” In this way, we *slowly convert a set of equations into “pseudo-code”*. The second type of behaviour occurs when agents *interact*. This is, of course, a common occurrence in studies of disease, and is modelled using mass-action incidence [9]. The term for the number of susceptible agents is defined as SZ . The only remaining terms are concerned with mixing: βSZ (infection transmission) and αSZ (zombies defeated by susceptibles). The infection transmission term (βSZ) term is negated for the susceptible differential, and is positive for the zombified differential – the behaviour may therefore be

phrased as “when a susceptible individual encounters a zombified individual, there is a chance (β) the susceptible becomes zombified.” The second term, for zombies defeating susceptibles (αSZ), is negated for the zombified differential and positive for the removed differential; that is, “when a susceptible individual encounters a zombified individual there is a chance (α) the zombified individual becomes removed.”

At this point, we observe that within traditional ODE systems, behaviours which do not affect population sizes are often not considered at all. This is discussed further in Section 3.4.

3.3 Parameters

Determining parameters is a case of examining the ODE system and extracting the variables. Each variable should map to a parameter that is a potential control point for the ABM. This process is often quite straightforward, particularly when performed after behaviour identification. Analysis of our differential equations yields five clear variables: birth rate (Π), zombie defeat rate (α), infection transmission rate (β), rate of death by natural causes, (δ), and the resurrection rate (ζ).

Parameters in the ODE operate slightly differently to their counterpart parameters in an ABM. Whereas rates in differential equations represent a *proportion* of the population, they apply on a per-agent basis within an ABM. We illustrate this subtle difference by taking the term δS as an example – rather than taking the population of S and multiplying it by δ to calculate the number of susceptibles that die to natural causes, we calculate this every “time step” for *each agent* in a population. For each member of the susceptible population there is a chance (δ) that the susceptible becomes removed. The net result is the same, within some acceptable stochastic variation, in that roughly the same proportion of susceptibles are removed each time step. Behaviours that occur when two agents interact are calculated in exactly the same way, although these are calculated on a collision-by-collision basis, rather than for a whole population. There also often exist some parameters that must be considered, but are not *explicitly* described within the differential equations. These parameters usually describe the initial state of the model (in this case, the initial number of susceptible, zombified and removed individuals).

3.4 Spatiality

ODEs are spatially implicit; the zombie epidemic model uses mass-action incidence to assume an evenly mixed population. ABM offer a much broader spectrum of possibilities for spatiality, and there are potentially many options for a *spatially explicit* design that may not have been previously considered. Some ABM may disregard the notion of spatiality, particularly when it is not relevant to the problem scope, but our problem relies heavily on spatial factors. The zombie infection is spread by *proximity*, and as such the locations of agents are important, as is their ability to be considered mobile. In order to accurately

reflect the notion of mass-action incidence, we consider our environment to be an open expanse in which agents are free to move about as desired. Several additional parameters are required for spatial explicitness. Agents are now capable of movement, so we must now consider their *speed*. It may be appropriate, depending on the model, to assign different speeds to different populations of agents. In our example we set a speed at which susceptible agents move, and a speed at which zombified agents move. This makes it possible to set the speed of zombified agents below that of susceptible agents, in order to reflect the “shambling” gait of the “traditional” zombie, or to the same value, in order to depict faster, more contemporary zombies. Additional parameters are also required to describe the *environment* (dimensions, internal structure, and so on).

3.5 Agent-Based Design

The conversion process, as we have seen, gives rise to a natural design. ABMs are often depicted in flowchart form, so we give our final design in Figure 1.

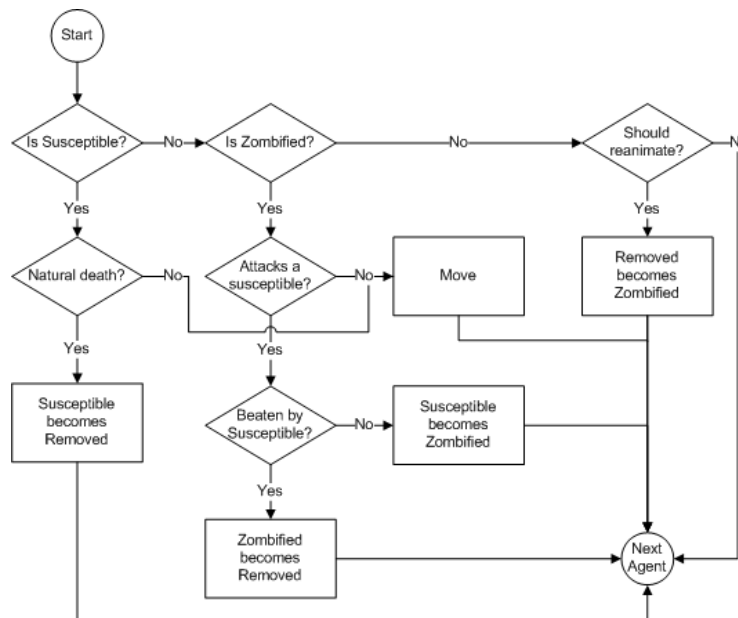


Fig. 1. Design of the agent-based model

4 Implementation and Testing

In order to test the quality of our conversion, we implemented both our ABM design and the original model [23] in a single Java application. We depict the

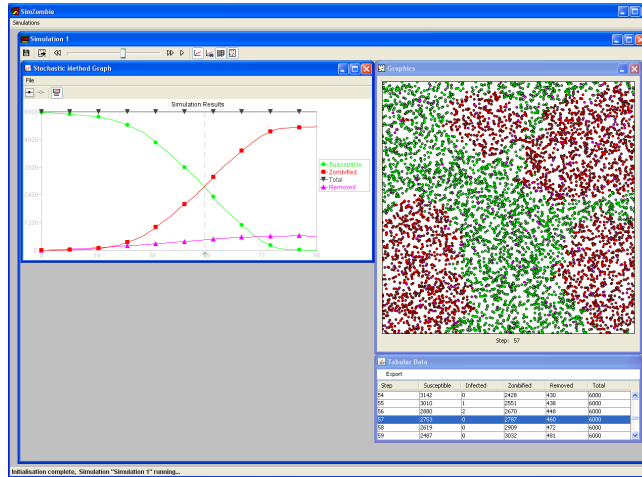


Fig. 2. Screenshot of the running application

running application in Figure 2, and the source code is available by request from the authors¹. The ABM results were averaged over 100 runs. In Table 1 we supply the parameter values used in *both* implementations (those below the bar are used only by the ABM).

Parameter	Value
Population size	6000
Birth rate, Π	0.1%
Natural death rate, δ	0.1%
Resurrection rate, ζ	0.1%
Zombie defeat chance, α	5%
Infection transmission rate, β	100%
Environment size	500x500px
Infection range	10px
Initially infected	0
Initially zombified	1
Susceptible speed	1-3px/step
Zombie speed	1-2px/step

Table 1. System parameters

We select the parameter values as follows (note that the values are the same for our implementations of both the ABM and the original model). Birth rate

¹ Email: M.Amos@mmu.ac.uk

(II), natural death rate (δ) and natural infection (resurrection) rate (ζ) were all set to small values (0.1%). Death rate and birth rate are described as being equal in the original model, the underlying assumption being that the “outbreak” occurs over a short period of time. These three factors are not the key focus of the model. Similarly, a high value for natural infection would model a scenario in which “zombification” occurs “naturally” rather than through transmission. We also selected a small value for “zombie defeat chance” (α) (5%), representing a population unprepared for a zombie attack. Altering this parameter would allow us to explore a scenario in which a population has some form of “resistance”. Finally, transmission rate (β) was set to 100%. This gives a scenario in which the zombie infection is always successfully transmitted. Since we are examining the spread of zombie infection, this creates a simulation with a maximum possible number of zombies due to transmission. Altering this parameter would allow us to investigate the *virulence* of infection, perhaps more closely mirroring a *realistic* scenario.

By comparing the plots obtained from both implementations (Figure 3), we observe a qualitative similarity in terms of their outputs. We therefore assert that the conversion process, from ODE to ABM, has preserved the inherent fidelity of the original model.

5 Conclusion

In this paper we describe the process of converting an ordinary differential equation model into an agent-based model with no apparent loss of accuracy. This framework unlocks a large library of models that have already been well researched and carefully verified and validated. Crucially, agent-based versions of these models will be more easily extended, and amenable to implementation on parallel architectures. Future work will use this approach to investigate a range of such models, which will, in turn, inform future refinements of the conversion process itself.

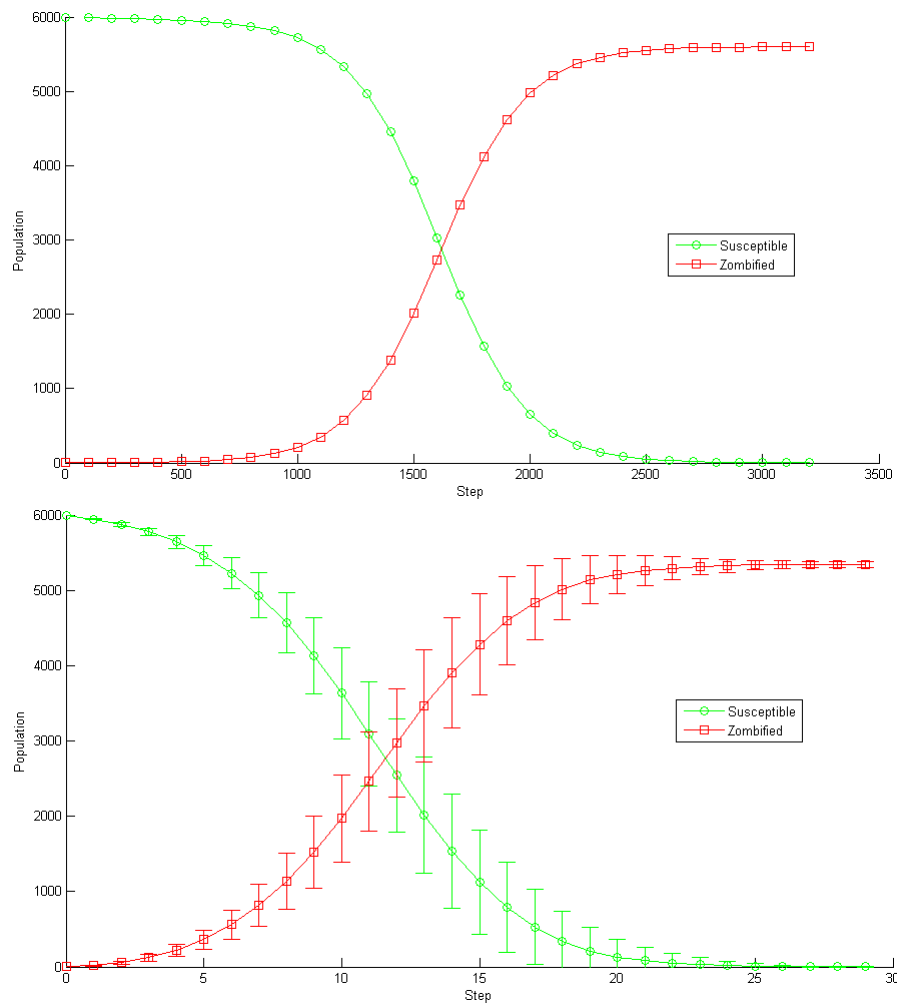


Fig. 3. Model comparison. (Top) ODE implementation; (Bottom) Agent-based implementation.

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