

Comparative Analysis of Agent-Based and Population-Based Modelling in Epidemics and Economics¹

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Abstract.

This paper addresses comparative evaluation of population-based simulation in comparison to agent-based simulation for different numbers of agents. Population-based simulation, such as for example in the classical approaches to predator-prey modelling and modelling of epidemics, has computational advantages over agent-based modelling with large numbers of agents. Therefore the latter approaches can be considered useful only when the results are expected to deviate from the results of population-based simulation, and are considered more realistic. However, there is sometimes also a silent assumption that for larger numbers of agents, agent-based simulations approximate population-based simulations, which would indicate that agent-based simulation just can be replaced by population-based simulation. The paper evaluates such assumptions by two detailed comparative case studies: one in epidemics, and one in economical context. The former case study addresses the spread of an infectious disease over a population. The latter case study addresses the interplay between individual greed as a psychological concept and global economical concepts. It is shown that under certain conditions agent-based and population-based simulations may show similar results, but not always.

Keywords: agent-based and population-based modelling, simulation, epidemics, economics, greed.

¹ Parts of this paper have been presented at the conferences ECMS'08 [20] and IEA/AIE'10 [7]. The current paper extends these conference papers by providing additional simulation experiments, simulation results relating to empirical data, more detailed analyses of simulation results, and a more extensive discussion of related work and of the differences between agent-based and population-based modelling.

1 Introduction

The classical approaches to simulation of processes in which groups of larger numbers of individuals are involved are based on the notion of *population*: in these approaches, a number of groups are distinguished (populations) and each of these populations is represented by a numerical variable indicating their number or density (within a given area) at a certain time point. The simulation model takes the form of a system of difference or differential equations expressing temporal relationships for the dynamics of these variables. Well known classical examples of such population-based models are systems of difference or differential equations for predator-prey dynamics (e.g., [9], [25], [26], [35], [36]) and the dynamics of epidemics (e.g., [1], [9], [16], [19], [22], [30]). Such models can be studied by simulation and by using analysis techniques from mathematics and dynamical systems theory.

From the more recently developed agent modelling perspective it is often taken as a presupposition that simulations based on individual agents (in the literature called agent-based or individual-based) are a more natural or faithful way of modelling, and thus will provide better results (e.g., [2], [13], [14], [15], [28], [31]). Also in specific disciplines, for example, in human-directed areas such as economics, epidemics or ecology such claims are made; (e.g., [5], [8], [17], [18], [27], [29], [37], [38]). Although for larger numbers of agents such agent-based modelling approaches are more expensive computationally than population-based modelling approaches, such a presupposition may provide a justification of preferring their use over population-based modelling approaches, in spite of the computational disadvantages. In other words, agent-based approaches with larger numbers of agents are justified because the results are expected to deviate from the results of population-based simulation, and are considered more realistic.

However, in contrast there is another silent assumption sometimes made, namely that for larger numbers of agents (in the limit), the global results produced by agent-based simulations approximate the results of population-based simulations (e.g., [39], [40]). This would indicate that agent-based simulation just can be replaced by population-based simulation, which would weaken the justification for agent-based simulation discussed above. A contrasting hypothesis, sometimes made in the complex systems area, is that the global patterns emerging from local interactions made in the complex systems area, is that the global patterns emerging from local interactions between agents can only be studied adequately by agent-based simulation (e.g., [18], [27]).

In principle such assumptions can never be evaluated in an exhaustive and decisive manner. It is only possible to evaluate them in certain specific case studies where population-based models and agent-based models for the same phenomenon are compared. Moreover, it can also be argued

that these assumptions by themselves are not so relevant because the more important issue is the issue of empirical validation for the two types of models: to which extent do the models describe empirical data accurately. Although it can be agreed that the issue of validation indeed is important, the perspective in this paper is that it is still worth while to know to which extent the two types of models differ in some given context. This gives information on whether a choice between the two types matters or not. If by simulation experiments and formal analysis only it is already shown that the differences are only marginal, any of the types can be chosen for an application. In contrast, if the differences are substantial, further empirical exploration is needed to make a justified choice between them.

Keeping in mind the deliberations in the previous paragraph, in this paper, by two case studies, one in epidemics and one in economics, the above assumptions and considerations are explored in more detail. Comparative simulation experiments have been conducted based on different simulation models, both agent-based (for different numbers of agents), and population-based. The results are analysed and related to the presupposition and assumption discussed above.

In the epidemics area an important question is whether for a contagious disease by measures the number of infected persons in a population can be kept limited. Traditionally such questions have been addressed by population-based models (with populations of susceptible, infectives and recovered agents, respectively). See, for example, [22], [30]; more recent presentations can be found in [1] and [16], Ch. 6, pp. 183-215. However, recently also the agent-based perspective has been advocated (e.g., [10], [23], [29]).

In the economics area, a traditional distinction exists between macroeconomics and microeconomics. Macroeconomics traditionally addresses the behaviour of a world-wide, national or regional economy as a whole [4], whereas microeconomics investigates the economic behaviour and decision making of individual agents, for example, consumers, households or firms [24]. Since the latter aims to understand why and how agents make certain economic decisions, various social, cognitive, and emotional factors of human behaviour are studied. This has resulted in the emergence of the field of behavioural economics [32]. Although this may be very useful when one wants to analyse the behaviour of individual agents, there is some debate about the extent to which it is useful to incorporate these aspects when studying global processes in economics, e.g., [8]. Do personal factors such as risk avoidance, greed, and personal circumstances provide more insight in the global patterns, or can they simply be ignored or treated in a more abstract, aggregated manner? This paper provides some answers to these questions from a computational perspective. In recent years, various authors have studied processes in economics by building computational models of them, and analysing the dynamics of these models using agent-based simulation techniques [34].

As shown by these examples, in different areas of agent-based modelling, a debate exists about the pros and cons of agent-based and population-based modelling. Agent-based models are often assumed to produce more detailed, faithful behaviour, whereas population-based models abstract from such details to focus on global patterns (e.g., [2], [13], and [20]). The goal of the current paper is to explore the differences and commonalities between population-based and agent-based modelling in the two case studies addressed. One of them addresses the analysis of epidemics, and the other one the interplay between individual greed and the global economy.

This paper is structured as follows. In Section 2, both an agent-based and a population-based model are introduced for the example domain of epidemics, which is one of the two cases addressed in this paper. Section 3 introduces the second case addressed: an agent-based and a population-based model for greed dynamics in economical context. In Section 4 a mathematical analysis for agent-based and population-based models is discussed and illustrated in both domains. In Section 5 the agent-based and population-based models for both domains are evaluated by simulation experiments and by an empirical analysis. Section 6 concludes the paper with a discussion.

2 A Population-Based and Agent-Based Model for the Epidemics Case

Microbes such as viruses, bacteria, fungi and parasites, may have disturbing effects when they enter the human body. Not seldom humans suffer from such infections and in the mean time propagate them to each other. Examples of types of infectious diseases are influenza, Chlamydia, HIV, hepatitis, tuberculosis, and many others. The battle against such infections takes place both at the biological level in the body, and at the behavioural and social level. At the behavioural and social level, humans sometimes try to adapt their interaction behaviour to prevent propagation of infections from one human to another one. This paper focuses on the propagation of infections in populations, in relation to the interaction behaviour, in particular the frequency and intensity of contacts that individuals have in the population.

Agents within a population can be in different states: susceptible (not infected yet), infective, or recovered (immune and not infectious). When an agent who is infective, has contact with another, susceptible agent then there is a chance that the other agent will also be infected due to this contact. This chance depends on the intensity of the contact. The overall chance that a susceptible agent is infected also depends on the number of contacts with infective agents. A possible pattern, for example, for an easy transmittable infection such as influenza, is that the propagation goes so fast that only in a few weeks time almost the whole population is infected. In such a case the term epidemic is used to indicate the spreading of the infection over the population.

For other types of infections, for example HIV or Chlamydia, more intensive contacts (which usually occur less frequently) are needed for transmission, and therefore propagation may proceed slower.

An important question, especially for the more harmful infections, in a society is whether by measures at the behavioural and social level, it is possible to keep the number of infected persons in a population limited. And if so, how far should such measures go? It is clear that by avoiding any contact between agents, propagation can be stopped, but that is often not a realistic option. On the other hand, if there are still some contacts between agents, will at the end the infection not be spread (perhaps by very slow propagation) over the whole population? Such questions are addressed in this paper by two types of models: population-based models (with populations of susceptible, infectives and recovered agents, respectively) and agent-based models. Note that the modelling choices made for these models closely relate to what is found in application-oriented literature on population-based and agent-based epidemics modelling.

2.1 A Population-Based Model for Epidemics

This section describes the population-based model, sometimes called the SIR-model (for Susceptible, Infected, Recovered). The analysis of epidemics via this type of model has a long history, going back, for example, to [22], [30], or more recent presentations in [1] and [16], Ch. 6, pp. 183-215. First of all, a distinction is made between the population of *susceptibles* vs. the population of *infectives*, the latter of which are infectious for the former. A third population consists of those that already were infected, but have *recovered* and therefore are immune and not infectious anymore, based on a *recovery rate* indicating the fraction of infectives that recovers per day. Furthermore the *frequency of contacts* (per day, the time unit chosen) plays a main role; the chance that in a contact *infection transmission* occurs depends on the *contact intensity*. The populations can be described by their sizes, but often they are characterised by their densities: size divided by area. As the area is considered fixed, the sizes (numbers) will be used to characterize the populations. In summary, the following concepts are used in the model:

- susceptibles: non-infected individuals
- infective individuals
- recovered individuals: immune and non-infective (also dead individuals can be considered here)
- infection transmissions (per day)
- relevant contacts (per day)
- recovery rate
- contact intensity

- contact frequency

The dynamic relationships between these concepts are depicted in Figure 1.

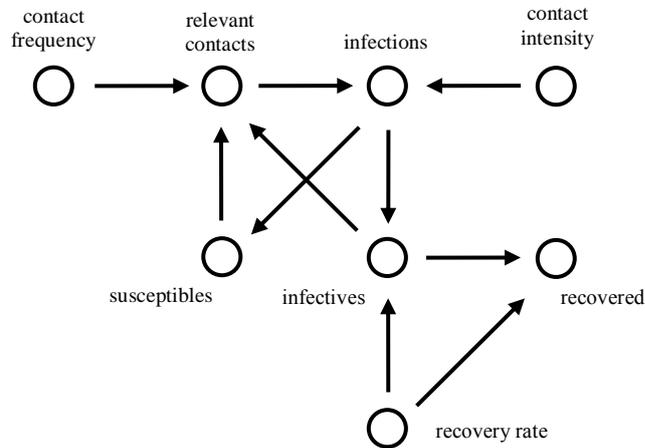


Fig. 1. Dynamic Relationships in the Model

For a mathematical formalisation usually the contact frequency times the contact intensity divided by the overall size of the populations together is combined in one parameter, called the *contact rate*. Thus the following variables and parameters are used.

S	size of the population of susceptible individuals
I	size of the population of infective individuals
R	size of the population of recovered individuals
N	size of all populations together
β	contact rate
γ	recovery rate

Here $\beta = \text{ContactFrequency} * \text{ContactIntensity} / N$. Note that, for given values of contact frequency and contact intensity, this parameter β depends on the overall population size. The dynamics of these concepts involve temporal relationships, which are analysed in more detail below. Each susceptible person has (per day) a number of contacts indicated by *ContactFrequency*. From these contacts a fraction $I(t)/N$ is with infective individuals, where N is the size of the three populations together (assumed fixed). Therefore the number of relevant contacts per day is:

$$\text{RelevantContacts}(t) = \text{ContactFrequency} * S(t) * I(t) / N$$

Moreover, in a fraction of the contacts the infection is transmitted. This fraction is indicated by *ContactIntensity*; therefore the number of new infections per day is:

$$\begin{aligned}
 & \text{Infections}(t) \\
 &= \text{ContactIntensity} * \text{RelevantContacts}(t) \\
 &= \text{ContactIntensity} * \text{ContactFrequency} * S(t) * I(t) / N = \beta * S(t) * I(t).
 \end{aligned}$$

Given the number of infections *Infections(t)* per time unit, in a time interval between *t* and *t+Δt* the number of (new) infections is *Infections(t)*Δt*. This is subtracted from the susceptible population, and added to the infective population. Furthermore, *γ* indicates the fraction of the infective population per day that becomes recovered (and not infective anymore): over the interval between *t* and *t+Δt* a number of *γ*I(t)*Δt* is taken from the infective population and added to the recovered population. Therefore the following temporal relationships are used.

$$\begin{aligned}
 S(t+\Delta t) &= S(t) - \text{Infections}(t) * \Delta t \\
 I(t+\Delta t) &= I(t) + (\text{Infections}(t) - \gamma * I(t)) * \Delta t \\
 R(t+\Delta t) &= R(t) + \gamma * I(t) * \Delta t
 \end{aligned}$$

Note that, by these relationships, the sum of the three populations always remains the same: what adds to the recovered population subtracts from the infective population, and what subtracts from the susceptible population adds to the infective population. In the more usual notation, by replacing *Infections(t)* the equations can be written as:

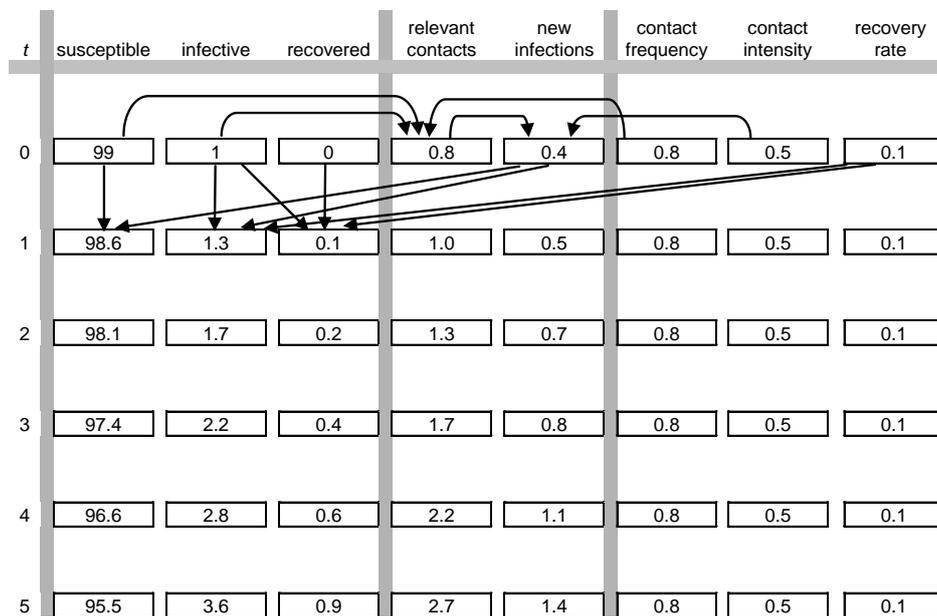
$$\begin{aligned}
 S(t+\Delta t) &= S(t) - \beta * S(t) * I(t) * \Delta t \\
 I(t+\Delta t) &= I(t) + (\beta * S(t) * I(t) - \gamma * I(t)) * \Delta t \\
 R(t+\Delta t) &= R(t) + \gamma * I(t) * \Delta t
 \end{aligned}$$

In differential equation form they are represented in the following manner; for example, see also in [1], [16], [22], [30]:

$$\begin{aligned}
 \frac{dS(t)}{dt} &= - \beta * S(t) * I(t) \\
 \frac{dI(t)}{dt} &= \beta * S(t) * I(t) - \gamma * I(t) \\
 \frac{dR(t)}{dt} &= \gamma * I(t)
 \end{aligned}$$

Note again, that the parameter β in principle depends on the overall population size. This means that to do experiments with different overall population sizes, different values for β may have to be used.

To illustrate the working of the model, below the dependencies between the different values are shown for an example scenario. Here the column on the left indicates different time steps, and the other columns indicate the values of the different variables and parameters. The arrows indicate which values influence each other:



2.2 An Agent-Based Model for Epidemics

To obtain a model at the level of individual agents, N distinct agents and L distinct locations are introduced. At every time point each agent is at some location, at random. Contacts between agents are modelled as being at the same location. By taking the number L of locations (numbered by $1, 2, \dots, L$) lower or higher, a specific contact frequency is modelled. Each agent is in precisely one of three infection states (susceptible, infective, recovered).

The number of locations has a relationship with the contact frequency in the following manner. If L is the number of locations, and N the number of agents, then the average number of agents at one location is N/L , so the average number of contacts of one agent at such a location is $N/L - 1$. This is equal to the contact frequency. Therefore

$$\text{ContactFrequency} = N/L - 1$$

gives the relation between number of locations and contact frequency. To be able to compare this model at the agent level to the model at the population level, it is convenient to have contact frequency as a basic parameter. To this end, the relation between the number of locations and contact frequency shown above is used in an inverse manner to determine the number of locations for a given value of the contact frequency:

$$L = N/(\text{ContactFrequency} + 1).$$

For a given contact frequency, this L is taken as a bound for the number of locations: they are indexed by the natural numbers k with $1 \leq k \leq L$. At each time point locations of the agents are determined at random, using this bound L by taking at random one of the natural numbers between 1 and L .

When a susceptible agent A is at a certain location, the probability that infection takes place depends on the contact intensity, but also on the number k of infective agents present at that location. Although in an agent-based model, contact intensity may be taken as depending on the agent or even on the pair of agents involved in a contact, for reasons of comparability with the population-based model the contact intensities are taken uniform: in any contact between any susceptible agent A and any infective agent B , the probability that A will be infected is ContactIntensity . Given this assumption, the probability that agent A will not be infected by a specific infective agent at the same location is $1 - \text{ContactIntensity}$. Assuming independence of these probabilities, the probability that A will not be infected by any of the infective agents present at that location is $(1 - \text{ContactIntensity})^k$. Therefore the probability that A will be infected at that location (at that time point) is

$$1 - (1 - \text{ContactIntensity})^k.$$

The following relationships describe the changes of the infection state of an agent A . Here $r1$ and $r2$ are two independent random numbers between 0 and 1 : fixed per time point but refreshed at new time points where $\Delta t = 1$. When a susceptible agent is at a location where one or more infective agents are present, the transmission of the infection at that time point has a probability given by the contact intensity. Moreover, for someone who is infective there is a probability of recovery given by the recovery rate. This is modelled by the following relationships:

$$\text{if } \text{InfectionState}(A, t) = \text{susceptible} \text{ and}$$

there are k infective agents at the same location as A and $r1 < 1 - (1 - ContactIntensity)^k$
 or $InfectionState(A, t) = infective$ and
 $r2 \geq RecoveryRate$
 then $InfectionState(A, t+1) = infective$
 else if $InfectionState(A, t) = infective$ and
 $r2 < RecoveryRate$
 or $InfectionState(A, t) = recovered$
 then $InfectionState(A, t+1) = recovered$
 else $InfectionState(A, t+1) = susceptible$

3 An Agent-Based and Population-Based Model for the Economics Case

In this section, the two simulation models are introduced addressing greed dynamics in economical context. First, an agent-based perspective is taken.

3.1 An agent-based model for greed dynamics

The main idea behind this model is that the state of the global (world) economy influences the level of greed of the individual agents in the population, which is supposed to relate to the risk level of their investment decisions: in case the economic situation is positive, then people are tempted to take more risk. Moreover, the investment decisions of the individual agents in turn influence the global economy: in case agents become too greedy [21], this is assumed to have a negative impact on the economic situation, for example, due to higher numbers of bankruptcy. In addition, the state of the economy is assumed to be influenced by technological development which is driven by innovation. Inspired by these ideas, the interplay between agents' greed and the global economy is modelled as a dynamical system, in a way that has some similarity to predator-prey models in two variations: agent-based, where each agent has its own greed level, and population-based, where only an average greed level of the whole population is considered.

The agent-based model assumes n heterogeneous agents, which all interact within a certain economy. For each agent k , the individual greed is represented using a variable y_k , and the global economic situation is represented using a variable x . The complete set of variables and parameters used for the agent-based model is shown in Table 1, and for the population-based model in Table 2.

Table 1. Variables and parameters used for the agent-based model

Variables	x	World economy
	$y^{(1)}, \dots, y^{(n)}$	Greed of individual agents
	z	Average greed of the agents (i.e., arithmetic mean of all $y^{(k)}$)
	TD	Technological development level
Parameters	a	Growth rate of the economy
	b	Decrease rate of the economy due to average greed
	c_1, \dots, c_n	Growth rate of an agent's greed based on the economy
	e_1, \dots, e_n	Decrease rate of an agent's greed
	inn	Innovation rate

Based on these concepts, a system of difference equations was designed that consists of $n+3$ formulae; here (2) specifies a collection of n equations for each of the n agents, where each agent has its individual values for $y^{(k)}$, c_k and e_k :

(1) Updating the world economy

$$x_{new} = x_{old} + (a * x_{old} - b * x_{old} * z_{old}) * \Delta t$$

(2) Updating the greed of the agents

$$y^{(k)}_{new} = y^{(k)}_{old} + (c_k * b * x_{old} * y^{(k)}_{old} * (2 - y^{(k)}_{old}) / TD_{old} - e_k * y^{(k)}_{old}) * \Delta t \quad (\text{for all agents } k)$$

(3) Updating the technological development

$$TD_{new} = TD_{old} + inn * TD_{old} * \Delta t$$

(4) Aggregating greed

$$z_{old} = (\sum_k y^{(k)}_{old}) / n$$

Table 2. Variables and parameters used for the population-based model

Variables	x	World economy
	y	Average greed of the population
	TD	Technological development level
Parameters	a	Growth rate of the economy
	b	Decrease rate of the economy due to population greed
	c	Growth rate of the population greed based on the economy
	e	Decrease rate of the population greed
	inn	Innovation rate

3.2 A population-based model for greed dynamics

The population-based dynamical model is similar to the agent-based model, but the difference is that it abstracts from the differences of the individual agents. This is done by replacing the average greed z over all $y^{(k)}$ in formula (1) by one single variable y indicating the greed of the population as a whole, and using a single formula (2'), which is only applied at the population level, in contrast to the collection of formulae (2) in the agent-based model, which are applied for all agents separately. The resulting population-based model is shown in Table 2 and in the formulae below.

(1') Updating world economy

$$x_{new} = x_{old} + (a * x_{old} - b * x_{old} * y_{old}) * \Delta t$$

(2') Updating the greed of the population

$$y_{new} = y_{old} + (c * b * x_{old} * y_{old} * (2 - y_{old}) / TD_{old} - e * y_{old}) * \Delta t$$

(3') Updating the technological development

$$TD_{new} = TD_{old} + inn * TD_{old} * \Delta t$$

Note that, in differential equation format, the agent-based and population-based dynamical model can be expressed by $n+2$, respectively 3 differential equations as shown in Table 3. Moreover, as the innovation rate inn is assumed constant over time, for both cases the differential equation for TD can be solved analytically with solution $TD(t) = TD(0) e^{inn t}$.

Table 3. The two models expressed by $n+2$, respectively 3 differential equations

Agent-based model

$$dx/dt = ax - bxz$$

$$d y^{(k)} / dt = (c_k b x y^{(k)} (2 - y^{(k)}) / TD) - e_k y^{(k)}$$

$$dTD/dt = inn TD$$

$$z = (\sum_k y^{(k)}) / n$$

Population-based model

$$dx/dt = ax - bxy$$

$$dy/dt = (cb xy(2-y) / TD) - ey$$

$$dTD/dt = inn TD$$

4 Mathematical Analysis of the Agent-Based and Population-Based Models

Mathematical analysis of the behaviour of models has a long tradition for population-based models. For example, equilibria of the model can be determined, as well as other properties such

as monotonicity or limit behaviour. Since the number of equations is usually much lower for the population-based case, such a mathematical analysis is easier to undertake than for the agent-based case.

4.1 Mathematical Analysis for the Epidemics Case

In differential equation form the population-based model is represented by

$$\begin{aligned}\frac{dS(t)}{dt} &= -\beta S(t)I(t) \\ \frac{dI(t)}{dt} &= \beta S(t)I(t) - \gamma I(t) \\ \frac{dR(t)}{dt} &= \gamma I(t)\end{aligned}$$

Based on these equations the following analysis has been made:

4.1.1 Threshold for increase/decrease of infective population

Increase and decrease of the size of the population of infectives are characterised by

$$\begin{aligned}\frac{dI(t)}{dt} \geq 0 &\Leftrightarrow \beta S(t)I(t) - \gamma I(t) \geq 0 \\ \frac{dI(t)}{dt} \leq 0 &\Leftrightarrow \beta S(t)I(t) - \gamma I(t) \leq 0\end{aligned}$$

This can be characterised by the size of the population of susceptibles as follows (where the *threshold* $\rho = \gamma/\beta$):

$$\begin{aligned}I(t) \text{ increasing} &\Leftrightarrow S(t) \geq \rho \\ I(t) \text{ decreasing} &\Leftrightarrow S(t) \leq \rho\end{aligned}$$

This shows that the usual pattern is that the size of the population of infectives will increase until the size of the population of susceptibles has become lower than the threshold ρ , after which it will decrease. In particular, when the initial size $S(0)$ is already less than this threshold ρ , then the number of infectives will decrease right from the start. This is called the *epidemic threshold law* with *threshold* ρ .

4.1.2 Equilibria

An equilibrium occurs if and only if

$$\frac{dS(t)}{dt} = \frac{dI(t)}{dt} = \frac{dR(t)}{dt} = 0$$

which is characterised by

$$\beta^* S(t) * I(t) = \beta^* S(t) * I(t) - \gamma^* I(t) = \gamma^* I(t) = 0$$

This is equivalent to $I(t) = 0$. Notice that by itself this does not put any constraint on $S(t)$ or $R(t)$. Equilibria may depend on initial values as well. However, taken together with a) in the usual pattern in an equilibrium state $S(t)$ will have become below ρ . So, when ρ is rather small (e.g., individuals remain infective for a long time, or contact intensity is high), the number of individuals that never become infected will also be small, or even zero. These observations are illustrated by simulations in the next section.

4.1.3 Relation between equilibria and initial values

From the set of differential equations, in particular the first and third one, it can be derived that

$$\begin{aligned} \frac{dS(t)}{dt} &= -\beta^* S(t) * I(t) = -\frac{1}{\rho} S(t) \frac{dR(t)}{dt} \quad \text{or} \\ \frac{dR(t)}{dt} &= -\frac{\rho}{S(t)} \frac{dS(t)}{dt} \end{aligned}$$

By integration, using the natural logarithm \log , it follows for all t it holds

$$R(t) = C - \rho \log(S(t))$$

with C a constant. Assuming $R(0) = 0$, it holds $C = \rho \log(S(0))$. Therefore

$$R(t) = \rho \log(S(0)) - \rho \log(S(t)) = \rho \log(S(0)/S(t)).$$

Equivalent forms are:

$$e^{R(t)/\rho} = S(0)/S(t)$$

$$S(t) = S(0) e^{-R(t)/\rho}$$

$$S(0) = S(t) e^{R(t)/\rho}$$

Now, according to Section 4.1.2, an equilibrium occurs if and only if $I(t) = 0$, which is equivalent to $S(t) + R(t) = N$. Filled in the above formula this obtains:

$$S(0) = (N - R(t)) e^{R(t)/\rho} \text{ or}$$

$$S(0) = S(t) e^{(N-S(t))/\rho}$$

This shows a relation between the population sizes in an equilibrium state and the initial values; note that $S(0) = N - I(0)$. Note that, conversely, each of these relations also implies that $S(t) + R(t) = N$, hence $I(t) = 0$ and an equilibrium state occurs. So, these relations provide if and only if criteria for an equilibrium to occur.

4.2 Mathematical Analysis for the Economics Case

In this section a mathematical analysis is presented concerning the conditions under which partial or full equilibria occur for the economic case. For this case we will show that both for an agent-based model and a population-based such an analysis is possible. For this analysis, the parameters a , b , c and e are assumed to be nonzero. For an overview of the equilibria results, see Table 4.

4.2.1 Dynamics of the economy

The economy grows when $dx/dt > 0$ and shrinks when $dx/dt < 0$; it is in equilibrium when $dx/dt = 0$. Assuming x nonzero, according to equation (1') for the population-based model, this can be related to the value of the greed as follows

economy grows	$dx/dt > 0 \Leftrightarrow ax - bxy > 0 \Leftrightarrow a - by > 0 \Leftrightarrow y < a/b$
economy shrinks	$dx/dt < 0 \Leftrightarrow ax - bxy < 0 \Leftrightarrow a - by < 0 \Leftrightarrow y > a/b$
economy in equilibrium	$dx/dt = 0 \Leftrightarrow ax - bxy = 0 \Leftrightarrow a - by = 0 \Leftrightarrow y = a/b$

So, as soon as the greed exceeds a/b the economy will shrink (for example, due to too many bankruptcies), until the greed has gone below this value. This indeed can be observed in the simulation traces. For the agent-based model similar criteria can be derived, but then relating to the average greed z instead of y .

4.2.2 Full equilibria for the population-based greed model

The first issue to be analysed is whether (nonzero) equilibria exist for the whole population-based model, and if so, under which conditions. This can be analysed by considering that x , y and TD are constant and nonzero. For x constant above it was derived from (1') that the criterion is $y = a/b$. For TD constant the criterion is $inn = 0$ as immediately follows from (3'). The criterion for $dy/dt = 0$ can be derived from (2') as follows

$$\begin{aligned} dy/dt = (cbxy(2-y)/TD - ey) = 0 &\Rightarrow \\ cbx(2-y)/TD = e &\Rightarrow \\ x = (e / ((2b-a) c)) TD & \end{aligned}$$

This provides the conditions for a full equilibrium

- (1) $y = a/b$
- (2) $x = (e / ((2b-a) c)) TD$
- (3) $inn = 0$

It turns out that for any nonzero setting for the parameters a , b , c and e and for setting $inn = 0$ for the innovation parameter and for any value of TD a nontrivial equilibrium is (only) possible with values as indicated above. Note that this shows that for inn nonzero a nontrivial full equilibrium is not possible, as TD will change over time. However, partial equilibria for greed still may be possible. This will be analysed next

4.2.3 Equilibria for greed in the population-based model

Suppose that the innovation inn is nonzero. In this case it cannot be expected that technological development TD and economy x stay at constant nonzero values. However, still for the greed variable y , an equilibrium may exist. From the second equation (2') by putting $dy/dt = 0$ it follows

$$\begin{aligned} cbx(2-y)/TD = e &\Rightarrow \\ x = \alpha TD & \quad \text{with } \alpha = e / cb(2-y) \end{aligned}$$

By filling this in differential equation (1') it follows

$$\begin{aligned} d \alpha TD / dt = a \alpha TD - b \alpha TD y &\Rightarrow \\ d TD / dt = (a - by) TD & \end{aligned}$$

By differential equation (3') it can be derived

$$\begin{aligned} dTD/dt &= (a - by)TD = innTD \Rightarrow \\ (a - by) &= inn \Rightarrow y = (a - inn)/b \end{aligned}$$

Note that, for $inn = 0$, this also includes the result for the full equilibrium obtained earlier. Moreover, as the equation for TD can be solved analytically, and $x = \alpha TD$, also an explicit solution for x can be obtained:

$$\begin{aligned} TD(t) &= TD(0) e^{inn t} \\ x(t) &= \alpha TD(t) = \alpha TD(0) e^{inn t} = x(0) e^{inn t} \end{aligned}$$

Here α can be expressed in the parameters as follows:

$$\begin{aligned} \alpha &= e / cb (2-y) \\ &= e / cb (2-(a - inn)/b) \\ &= (e / c) / (2b - a + inn) \end{aligned}$$

This shows that according to the model greed can be in an equilibrium $y = (a - inn)/b$, in which case the economy shows a monotonic exponential growth.

4.2.4 Full Equilibria for the agent-based greed model

Similar to the approach followed above:

$$\begin{aligned} (1) \quad dx/dt &= (ax - bxz) = 0 \\ (2) \quad d y^{(k)}/dt &= (c_k bx y^{(k)} (2 - y^{(k)}) / TD - e_k y^{(k)}) = 0 \quad (\text{for all agents } k) \\ (3) \quad dTD/dt &= inn TD = 0 \\ (4) \quad z &= (\sum_k y^{(k)}) / n \end{aligned}$$

A full equilibrium can be expressed by the following equilibria equations:

$$\begin{aligned} (1) \quad ax &= bxz \\ (2) \quad c_k bx y^{(k)} (2 - y^{(k)}) / TD &= e_k y^{(k)} \\ (3) \quad inn TD &= 0 \\ (4) \quad z &= (\sum_k y^{(k)}) / n \end{aligned}$$

It is assumed that a , b , c_k and e_k are nonzero. One trivial solution is $x = y^{(k)} = 0$. Assuming that x , $y^{(k)}$ and TD all are nonzero, the equations (1) to (3) are simplified:

$$\begin{aligned} (1) \quad a &= bz \\ (2) \quad c_k bx (2 - y^{(k)}) / TD &= e_k \end{aligned}$$

$$(3) \text{ inn} = 0$$

$$(4) z = (\sum_k y^{(k)})/n$$

This provides

$$(1) z = a/b$$

$$(2) y_k^{(j)} = 2 \cdot e_k TD / (c_k b x)$$

$$(3) \text{ inn} = 0$$

$$(4) z = (\sum_k y^{(k)})/n$$

From the second, first and last equation it follows that

$$\begin{aligned} a/b &= (\sum_k y^{(k)})/n \\ &= (\sum_k (2 \cdot e_k TD / (c_k b x))) / n \\ &= 2 \cdot \sum_k (e_k TD / (c_k b x)) / n \\ &= 2 - (TD/bx) (\sum_k (e_k / c_k)) / n \Rightarrow \\ x &= TD \sum_k (e_k / c_k) / (2b - a)n \end{aligned}$$

From this the values for the $y^{(j)}$ can be determined:

$$\begin{aligned} y^{(j)} &= 2 \cdot e_j TD / (c_j b x) \\ &= 2 \cdot e_j TD / (c_j b TD \sum_k (e_k / c_k) / (2b - a)n) \\ &= 2 \cdot e_j / (c_j b \sum_k (e_k / c_k) / (2b - a)n) \\ &= 2 \cdot e_j (2b - a)n / (c_j b \sum_k (e_k / c_k)) \\ &= 2 \cdot e_j (2 - (a/b))n / (c_j \sum_k (e_k / c_k)) \\ &= 2 \cdot (2 - (a/b))n / (\sum_k (e_k / e_j) (c_j / c_k)) \end{aligned}$$

It turns out that for any nonzero setting for the parameters a , b , c_k and e_k and for setting $\text{inn} = 0$ for the innovation parameter, and for any value of TD a nontrivial equilibrium is (only) possible with values as indicated above.

4.2.5 Equilibria for greed for the agent-based model

From the second equation

$$c_k b x (2 - y^{(k)}) / TD = e_k$$

with $y^{(k)}$ constant it follows that

$$x = \alpha_k TD$$

with α_k the constant

$$\alpha_k = e_k / c_k b (2 - y^{(k)})$$

which apparently does not depend on k , as both x and TD do not depend on k , so the subscript in α_k can be left out. Filling this in (1) provides:

$$\begin{aligned} d \alpha TD/dt &= (a \alpha TD - b \alpha TD z) \Rightarrow \\ d TD/dt &= (a - bz) TD \end{aligned}$$

By differential equation (3) it can be derived

$$\begin{aligned} dTD/dt &= (a - bz) TD = inn TD \Rightarrow \\ (a - bz) &= inn \Rightarrow \\ z &= (a - inn)/b \end{aligned}$$

Now the equilibrium values for $y^{(j)}$ can be determined as follows.

$$\begin{aligned} \alpha &= e_k / c_k b (2 - y^{(k)}) \Rightarrow \\ 2 - y^{(k)} &= e_k / \alpha c_k b \Rightarrow \\ y^{(k)} &= 2 - e_k / c_k \alpha b \end{aligned}$$

Next the value of α is determined $z = (\sum_k y^{(k)})/n = \sum_k (2 - e_k / c_k \alpha b)/n = 2 - (1/\alpha b n) \sum_k e_k / c_k$. Since $z = (a - inn)/b$ it follows

$$\begin{aligned} (a - inn)/b &= 2 - (1/\alpha b n) \sum_k e_k / c_k \Rightarrow \\ (1/n \alpha) \sum_k e_k / c_k &= 2b - (a - inn) \Rightarrow \\ \sum_k e_k / c_k &= (2b - (a - inn)) n \alpha \Rightarrow \\ \alpha &= \sum_k (e_k / c_k) / (2b - (a - inn)) n \end{aligned}$$

Given this value for α the equilibrium values for the greed $y^{(j)}$ are

$$\begin{aligned} y^{(j)} &= 2 - e_j / c_j \alpha b \\ &= 2 - e_j / b c_j \sum_k (e_k / c_k) / (2b - (a - inn)) n \\ &= 2 - (2 - (a/b)) n / \sum_k (e_k c_j / e_j c_k) \end{aligned}$$

Table 4. Overview of the equilibria of the two models

	Agent-based model	Population-based model
Full equilibrium	$inn = 0$ $x = (1/(2b - a)) (\sum_k (e_k / c_k) / n) TD$ $z = a/b$ $y^{(j)} = 2 - (2 - (a/b)) n / \sum_k (e_k / e_j) (c_j / c_k)$	$inn = 0$ $x = (1/(2b - a)) (e/c) TD$ $y = a/b$

Partial equilibrium for greed	$TD(t) = TD(0) e^{inn t}$	$TD(t) = TD(0) e^{inn t}$
	$x(t) = (1 / (2b - a + inn)) (\sum_k (e_k / c_k) / n) TD(0) e^{inn t}$ $z = (a - inn) / b$ $y^{(j)} = 2 - ((a - inn) / b) n / \sum_k (e_k / e_j) (c_j / c_k)$	$x(t) = (1 / (2b - a + inn)) (e / c) TD(0) e^{inn t}$ $y = (a - inn) / b$

Note that, for the case that all e_k are equal to one value e , and the same for c_k , then from the formulae for the equilibria it is easy to see that the equilibria for the agent-based model and the population-based model become the same.

5 Evaluation of the Agent-Based and Population-Based Models

In Section 5.1 and 5.2, respectively, both for the epidemics case and for the economics case the presented models are evaluated by presenting and discussing a number of simulation results for different parameter settings. Moreover, in Section 5.3 the epidemics models are evaluated by having them reproduce empirical data.

5.1 Evaluation by Simulations for the Epidemics Case

In this section, simulation results are discussed for both models in epidemics. More simulation results can be found in Appendix A and Appendix B.

5.1.1 Population-based simulations for the epidemics case

A number of population-based simulation experiments have been performed using a Spread Sheet (Microsoft® Office Excel® 2007). In Figures 2 and 3 results are shown of one of them, with time scale in days. In the first simulation shown in Figure 2 the whole population gets infected; it used the following parameter settings:

$$\begin{aligned}
 N &= 100 \\
 ContactFrequency &= 0.8 \\
 ContactIntensity &= 0.5 \\
 \beta &= 0.004 \\
 \gamma &= 0.05 \\
 \rho &= 12.5
 \end{aligned}$$

Initially the size of the infective population is 1. Given the analysis above, in this case it may be expected that the size of the population of susceptibles will become below 12.5. Note that, in this and next figures, the scales on the vertical axis differ.

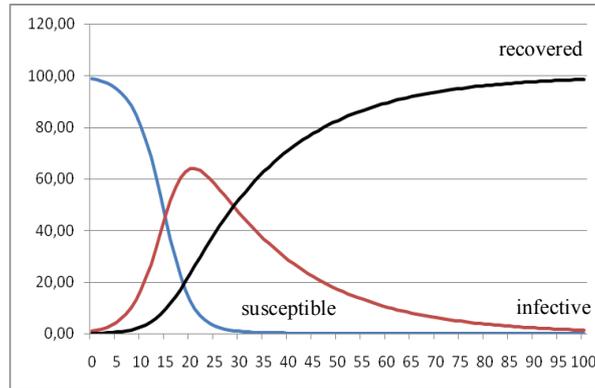


Fig. 2. Pattern in which the Whole Population gets Infected

The size of the susceptibles decreases to zero, while the size of the infective population increases until day 20 and decreases after this day. The size of the recovered population shows a logistic growth pattern with the whole population of 100 as limit. Notice that the maximal size of the population of infectives is taken at the time point that the size of the susceptibles population is around 12.5, which is the value of the threshold ρ (see Section 4.1.1). In the second simulation, (see Figure 3), only a part gets infected; parameter settings were:

N	100
$ContactFrequency$	0.6
$ContactIntensity$	0.2
$\beta = 0.0012$	
$\gamma = 0.1$	
$\rho = 83.3$	

Here initially the size of the infective population is 10. Apparently here the contact frequency and intensity were low enough to let the infection die out: around 50% of the population is never infected. The logistic growth pattern of the (infected and) recovered population has its limit around 50. Nevertheless, the individuals still did not bring their contacts down to zero, or even close to zero.

These settings correspond to the ones for the traces shown in Figure 2 and 3, respectively. As can be seen in Figure 4, in this simulation initially one agent is infective (this is agent A2, although this cannot be seen from the figure). This was simply initialised by hand. Already from the second day on, three other agents (A4, A7 and A10) get infected. Apparently, these agents were (by chance) at the same location as A2, and had an infectious contact with that agent. After that, more agents follow (again, based on encounters with other agents that were already infected), until eventually the whole population has been infected, and (later) recovered.

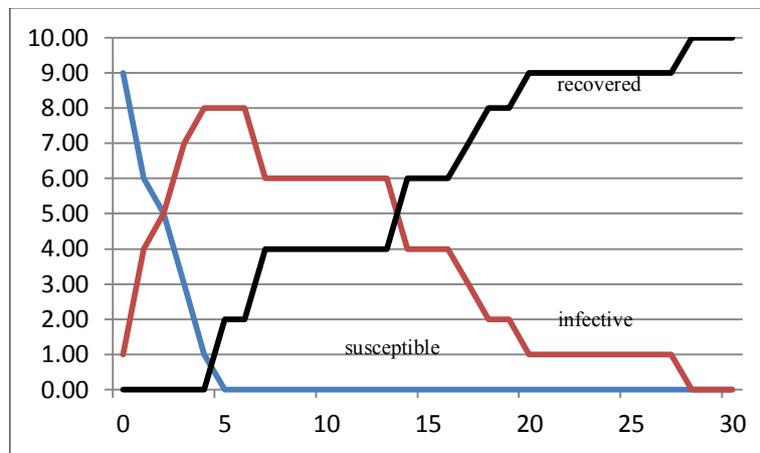


Fig. 4. Pattern in which the Whole Population gets Infected

Although the numbers are smaller, this pattern is similar to the pattern shown in Figure 2. Note that, also here, the maximal number of infectives is reached at the time point that the number of susceptibles drops under ρ (i.e., under 1.25).

In the simulation shown in Figure 5, also 1 agent (A2) is initially infective. Soon another agent (A6) gets infected, but this agent recovers already in two days. Since A2 takes longer to recover, a third agent (A8) is infected on day 5. After 6 days A8 recovers, and in the meantime also A2 recovered. No further infections took place.

The pattern in Figure 5 is similar to the pattern shown in Figure 3. Note that, also here, the maximal number of infectives coincides with the number of susceptibles dropping below the threshold ρ (i.e., under 8.3).

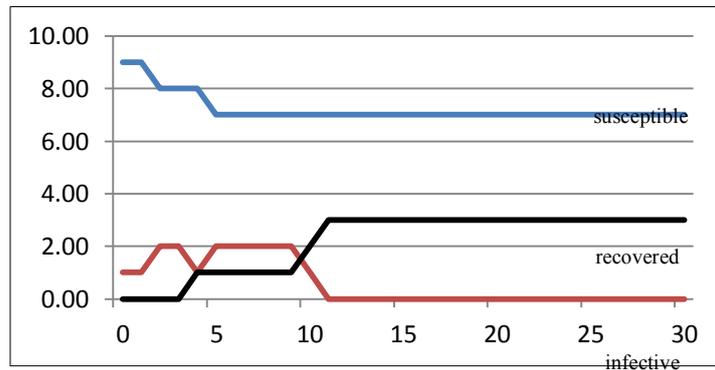


Fig. 5. Pattern in which Part of the Population gets Infected

From other simulations it was found out that this example trace is a bit exceptional for this setting. More example simulation traces for this setting are shown in Appendix A. Most traces of the individual model show either only one or two infectives, after which the epidemic dies out, or (almost) all individuals become infected. See Figure 6 for an overview of 100, resp. 1000 experiments with the model for 10 agents. The average number of recovered agents for this sample is 5.71. Note that this means that the model at the collective level shows a kind of average pattern that for the model at the individual level for 10 agents almost never occurs.

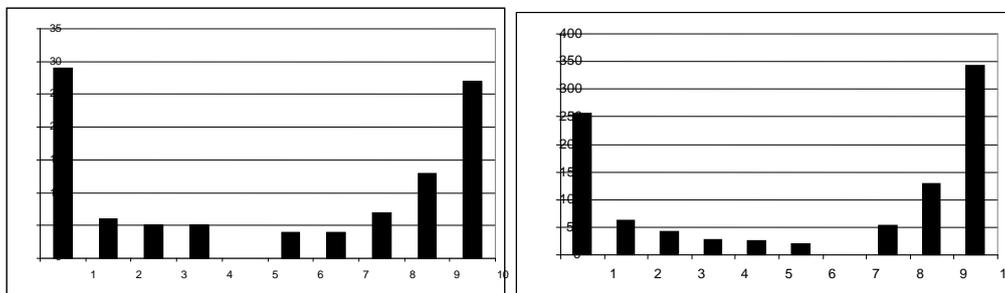


Fig. 6. Average Numbers Recovered for 100 resp. 1000 runs for 10 agents with 10% initially infected

Under similar experimental configurations simulations for larger population has been conducted through simulation software developed in the language C++. Considering the simplicity of the model, a procedural approach without multithreading was used in the software design. Figure 7 shows the results of 1000 simulations conducted for both populations of 100 and 1000 agents carrying 10 percent initially infected. These simulations have taken 0.02105 and 0.90953 seconds per simulation for 100 and 1000 agents respectively on a standard desktop computer. In these simulations the agent-based model shows a different pattern. Rather than an average pattern as for the case of 10 agents; see Figure 6, it shows single peak towards the higher number of

recovered agents with an average of (approximately) 93 percent recovered agents in both cases. Variation in number of recovered agents for 1000 samples in case of population count 100 and 1000 was 31 and 9 percent respectively, which is much lower than 90 percent variation in all samples observed in population count 10. Moreover, the average on all simulations were also close to the peak that differs a lot from both the outcome of agent based model at low population as 10 agents; see Table 5, and the population-based model.

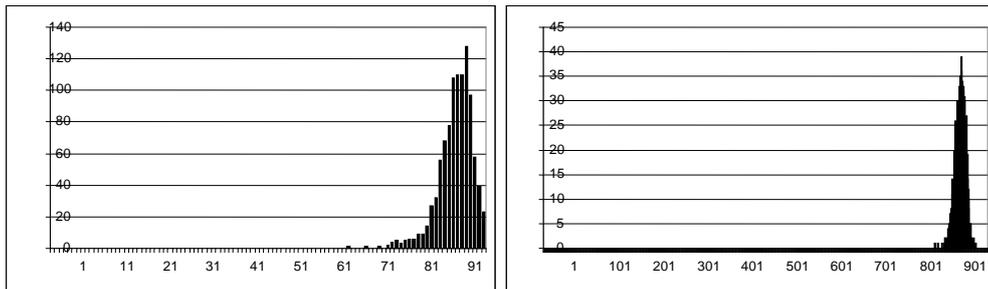


Fig. 7. Average Numbers Recovered for 1000 runs for 100 resp. 1000 agents with 10% initially infected

Table 5. Percentage of Min, Max and Average Recovered in the Sample of 1000 Simulations for 10, 100 and 1000 Agents resp. with 10% Initially Infected

Total Population	10	100	1000
Initial Susceptible	9	90	900
Initial Infected	1	10	100
Average Recovered	61.62	93.50	93.83
Min Recovered	10.00	69.00	88.20
Max Recovered	100.00	100.00	97.30
Variation in Samples	90.00	31.00	9.10

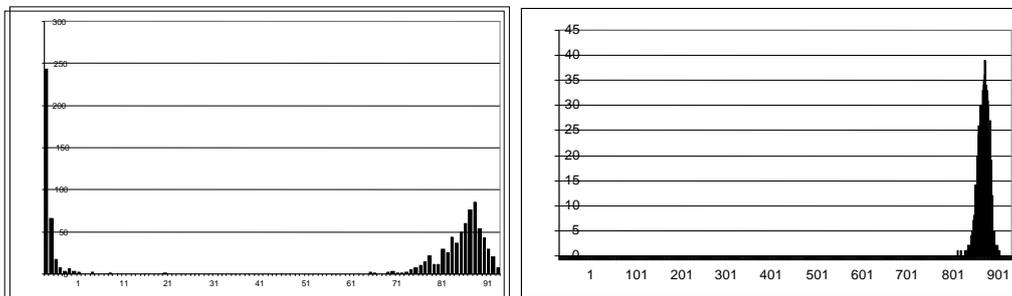


Fig. 8. Average Numbers of Recovered Agents for a Sample of 1000 Simulations for 100 and 1000 Agents resp. with 1% Initially Infected

In Figure 8 the results for similar populations have been shown with 1% initially infected. In these simulations, for a population of overall size 100, an average of 60.5% recovered and 99% variation in all samples was observed which is somewhat similar in behaviour as of population count 10; see Fig. 6 that also shows two peaks with nearly average pattern. But the population of overall size 1000 has shown a graph almost similar to an average of 92.98% and 8.40% variation in all samples as that has been seen for 10% initially infected for the same population count; see Figure 7. To further investigate this behaviour change as seen in a population of overall size 100 with a change of percentage of initially infected, simulations were performed for 0.1% initially infected for a population count of 1000. These simulations have confirmed the graph change pattern observed in case of population count 100; see Figure 9.

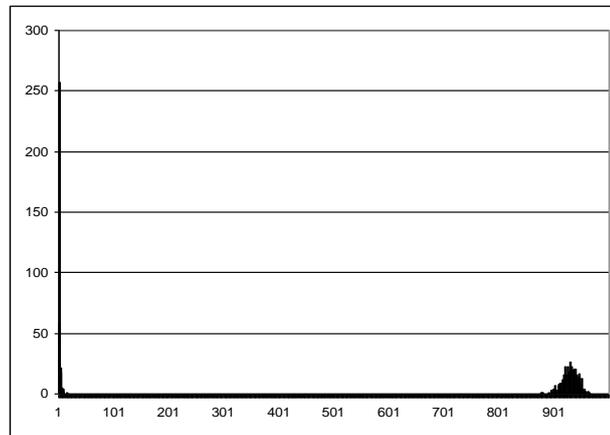


Fig. 9. Numbers of Recovered Agents for a Sample of 1000 Simulations for 1000 Agents resp. with 0.1 Percent [1 Agent] Initially Infected

From the above simulations it is evident that in agent-based simulations for epidemics the percentage of the initially infected population is not the factor to be taken the same for similar experimental configuration for different population sizes but it is the number of initially infected agents that should be taken the same; see also Table 6.

Table 6. Average Percentage of Min, Max and Average Recovered in the Sample of 1000 Simulations for 10, 100 and 1000 Agents with 1 Agent Initially Infected

Total Population	10	100	1000
Initial Susceptible	9	99	999

Initial Infected	<i>1</i>	<i>1</i>	<i>1</i>
Average Recovered	<i>61.62</i>	<i>60.4</i>	<i>58.5</i>
Min Recovered	<i>10.00</i>	<i>1.00</i>	<i>0.10</i>
Max Recovered	<i>100.00</i>	<i>100.00</i>	<i>96.40</i>
Variation in Samples	<i>90.00</i>	<i>99.00</i>	<i>96.30</i>

From above it is found that in population-based modelling of epidemics a similar percentage of initially infected population yields in a similar percentage of recovered population for all total population sizes; see Table 7. But in case of agent-based modelling the initial count of the infected population the (approximately) yields a similar percentage of recovered population for all total population sizes; see Table 8.

Table 7. Percentage of Recovered Population in Total Population Count [N] 10, 100 and 1000 Agents resp. with 10, 1 and 0.1 Percent Initially Infected [I(0)] in Population Based Simulation.

N/I(0)	10	100	1000
10%	<i>55.620</i>	<i>55.620</i>	<i>55.620</i>
1%	<i>34.910</i>	<i>34.910</i>	<i>34.910</i>
0.10%	<i>27.070</i>	<i>27.070</i>	<i>27.070</i>

Table 8. Average Percentage of Recovered in the Sample of 1000 Simulations for Total Population Count [N] 10, 100 and 1000 Agents resp. with 1, 10 and 100 Initially Infected Agents [I(0)] in Agent Based Simulation.

N/I(0)	10	100	1000
1	<i>61.620</i>	<i>60.485</i>	<i>58.502</i>
10	<i>100.00</i>	<i>93.506</i>	<i>92.982</i>
100	<i>-----</i>	<i>100.00</i>	<i>93.830</i>

Taking this number of initially infected agents rather than percentage of initially infected population as a parameter for similar experimental configuration is yet another subtle difference between population-based and agent-based simulation results of epidemics; see Table 7 and Table 8.

5.2 Evaluation by Simulations for the Economics Case

Based on the models introduced above, a number of simulation experiments have been performed under different parameter settings (with population size varying from 2 to 400 agents), both for the agent-based and for the population-based case. Below, a number of them are described.

5.2.1 Agent-based simulations for the economics case

First an agent-based simulation experiment is described. In this first experiment, 25 agents were involved. The initial settings used for the variables and parameters involved in the experiment are shown in Table 9.

Table 9. Initial settings for variables and parameters

Parameter	Value	Variable	Initial value
<i>a</i> (growth rate of economy)	1.5	<i>x</i> (world economy)	5
<i>b</i> (decrease rate of economy due to population greed)	5.8	<i>y</i> (average greed of population)	random in [0.2, 0.3]
<i>c</i> (growth rate of population greed based on economy)	random in [0.0260, 0.0274]	<i>TD</i> (technological development level)	1
<i>e</i> (decrease rate of population greed)	random in [0.85, 0.89]		
<i>inn</i> (innovation rate)	0.01	Δt (step size)	0.1

The results of the simulations are shown in Figure 10a and 10b. In Figure 10a, time is on the horizontal axis and the value of the world economy is represented on the vertical axis. It is evident from the graph that the economy grows as time increases (but fluctuating continuously). Figure 10b shows the individual greed values of all 25 agents. As can be seen they fluctuate within a bandwidth of about 25% with lowest points between about 0.1 and 0.25, and highest points between about 0.25 and 0.45. This pattern is similar to the well-known pattern often shown by predator-prey models, where the role of the predators and the prey are played, respectively, by the population greed and the world economy, which mutually influence each other. Specifically, an

increase in the world economy (or the number of prey) leads to an increase in the population greed (or the number of predators). In turn, this will result in a decrease of the world economy, which leads to a decrease in the population greed, and so on. The pattern of the average greed over all 25 agents (which is calculated simply by taking the arithmetic mean of the 25 individual greed values as displayed in Figure 10b) is shown in Figure 10c.

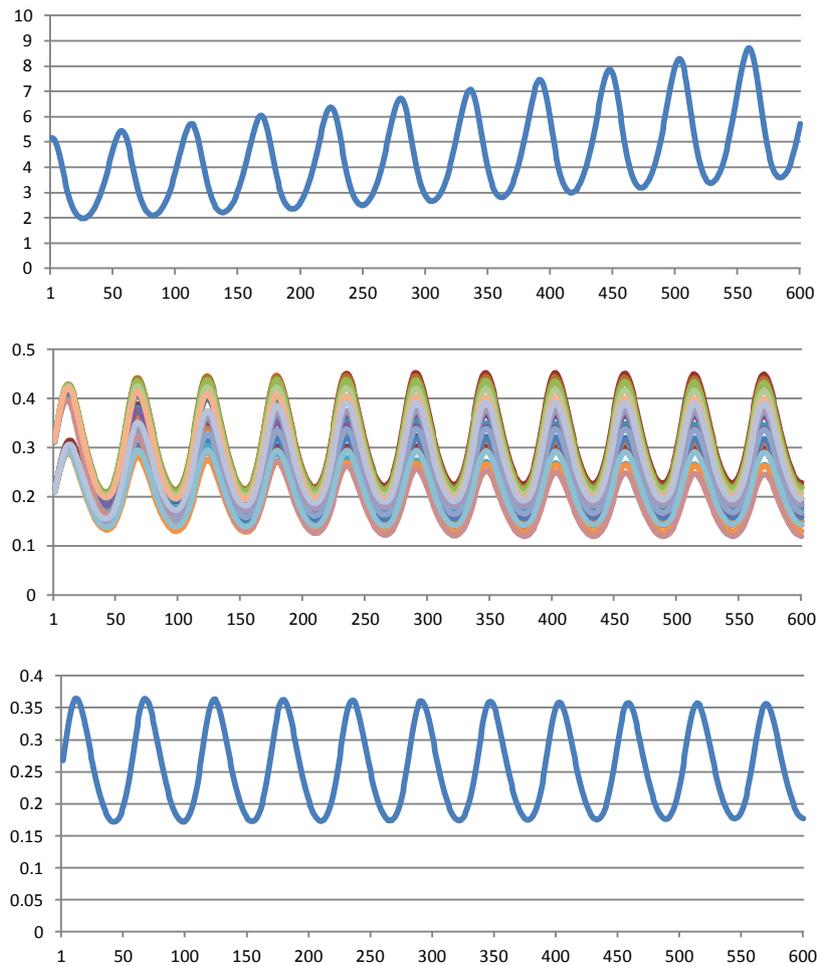


Fig. 10. Agent-based simulation results:

a) world economy, b) individual greed of 25 agents, and c) average greed (over 25 agents)

5.2.2 Population-based simulations for the economics case

For the population-based simulation, all the parameter settings are the same as in Table 9, except parameters y , c and e . The values for parameters y , c and e used in the population-based simulation

were determined on the basis of the settings for the agent-based simulations by taking the average y , c and e for all fifty agents:

$$y = (\sum_k y_k)/n$$

$$c = (\sum_k c_k)/n$$

$$e = (\sum_k e_k)/n$$

The results of the population-based simulations are shown in Figure 11a (economy) and 11b (greed). As can be seen from these figures, the results approximate the results for the averages for the agent-based simulation. The difference of the world economy for the population-based and agent-based simulation (averaged over all time points) turns out to be 0.112 , and the difference between the average greed of the 25 agents in the agent-based simulation and the greed for the population-based simulation is 0.005 .

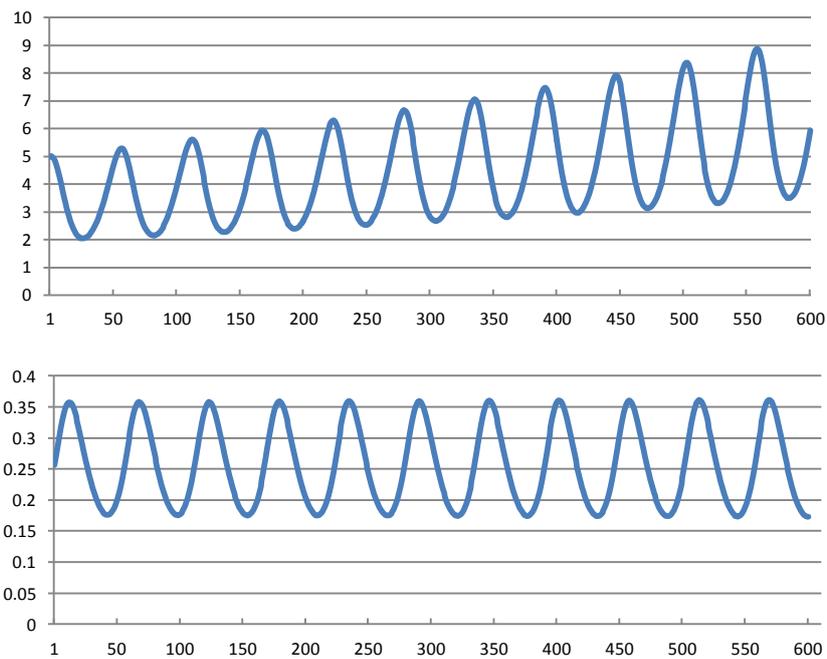


Fig. 11. Population-based simulation results: a) world economy, and b) greed

In addition, a number of simulation runs have been performed for other population sizes. Figure 12a displays the (maximum and average) absolute difference between the world economy in the agent-based model and the world economy in the population-based model for various

population sizes. Note that, as the economy has initial values above 2 and it substantially grows over time, the relative difference will approximate 0.

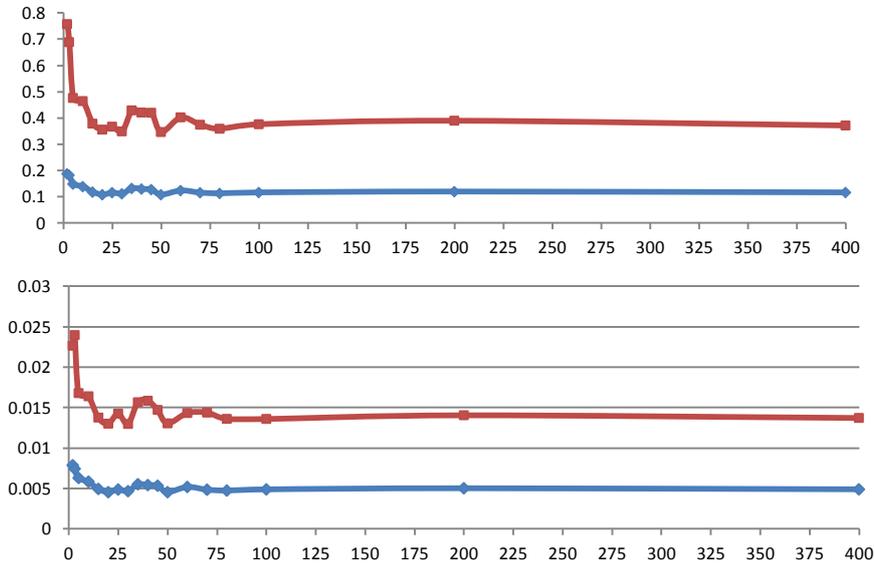


Fig. 12. Difference between both models for various population sizes:
a) world economy, and b) greed

Similarly, Figure 12b displays the absolute difference between the average greed in the agent-based model and the greed in the population-based model for various population sizes. The red line indicates the maximum value and the blue line the average value over all time points. As the figures indicate, all differences approximate a value that is close to 0 as the population size increases. Although the results of these particular simulation experiments should not be over-generalised, this is at least an indication that for higher numbers of agents, the results of the agent-based model can be approximated by those of the population-based model.

5.3 Evaluation Using Empirical Data for the Epidemics Case

For empirical validation of the models of the epidemics case presented in the previous section, empirical data of epidemic spread was taken from [43], in particular from Table 3.1 presented on page 44. From there, data for four cities (namely Birmingham, Richmond, Boston and Chicago) was taken, as only these cities have data available for a time span of seven weeks. To reproduce the empirical data, the following methodology was applied. First the parameters of both models (agent-based and population-based) are learned against the epidemic pattern of the first four weeks

and then these learned parameters are used to predict the epidemic pattern for the remaining weeks. Here it should be noted that the population size of these cities is very large as compared to the actual number of infected cases, hence a lower count of maximum population is considered for practical reasons. The experimental configurations used for learning of the known data (first four weeks) and validation of the learned models against unknown data (last three weeks) are given in Table 10.

Table 10. Experimental configuration for parameter learning and model validation

Parameter	Value
<i>Learned parameters</i>	3 (<i>CF, CI and RR or γ in PBS case</i>)
<i>Granularity of parameters during learning process</i>	0.1 for ABS and 0.01 for PBS
<i>Number of samples used to reduce random effect in ABS during leaning and validation</i>	2
<i>Time granularity for PBS difference equations</i>	0.1
<i>Maximum population count</i>	2500

Figure 13 shows the empirical data used for the spread of the epidemic in the four cities.

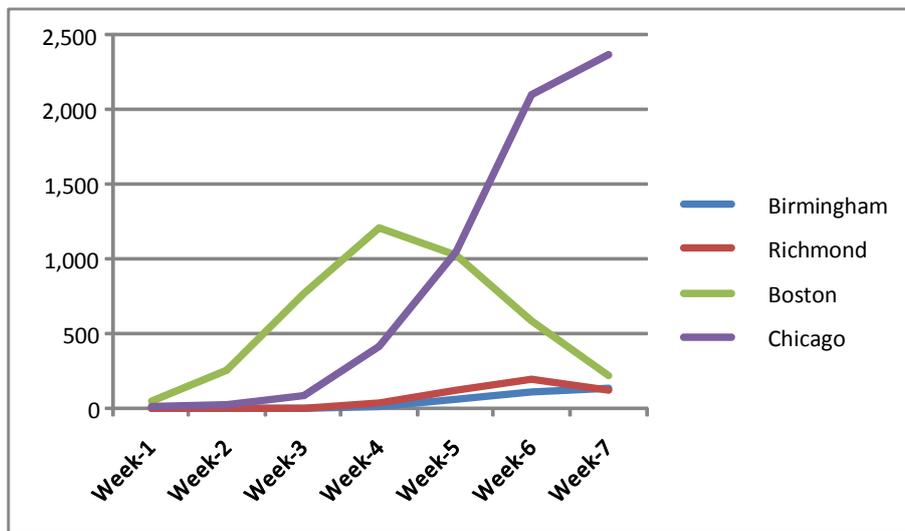


Fig. 13. Empirical spread of influenza in four cities

As stated earlier, first parameter learning is performed for both models. As the number of parameters used in these models is low, an exhaustive search technique is used for this purpose [42]. Figure 14 shows the results of parameter tuning of both models for the four cities. Here it should be noted that the bars presented are the normalized root mean squared errors for learned

parameters. From Figure 14 it can be observed that on average the Agent-Based Simulation (ABS) has a low learning error as compared to the Population-Based Simulation (PBS) for known data.

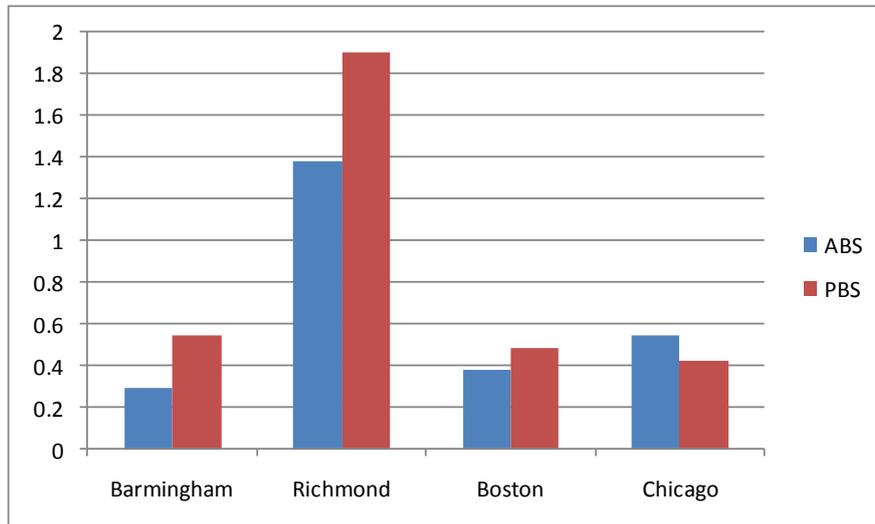


Fig. 14. Parameter learning error of agent-based and population-based models for four cities

After the parameter learning of the models, the learned models are used to predict the trend of the epidemic spread for the coming weeks. Figure 15 shows the normalized root mean squared errors for the validation process of both models. Here it can be observed that the PBS outperforms the ABS in the validation process.

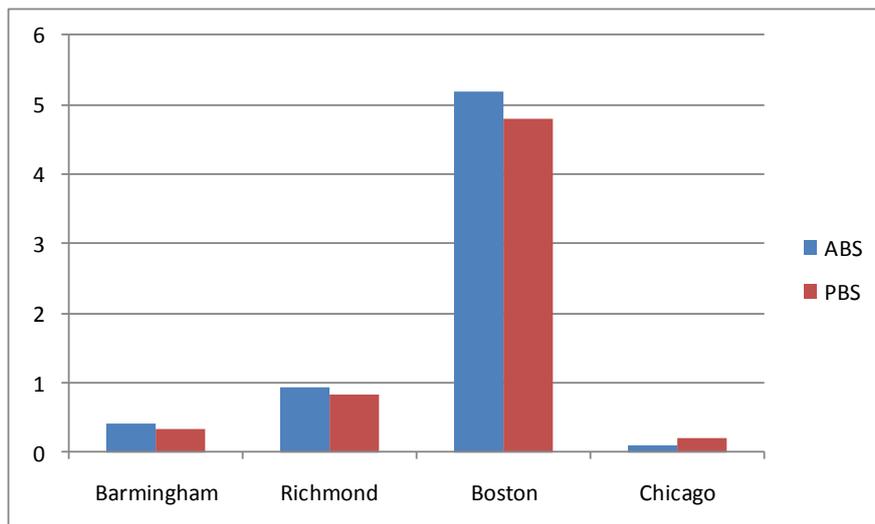


Fig. 15. Validation error of agent-based and population-based models for four cities

In Figure 16, numbers of infected individuals of empirical data, ABS and PBS are shown over time. Here it can be noted that these curves are very tight together for the first few weeks and then trends shown by ABS and PBS start to deviate from the empirical data. This is due to fact that these models are learned on the basis of the first four weeks, and then the curves for next three weeks are predicted based on this initial learning.

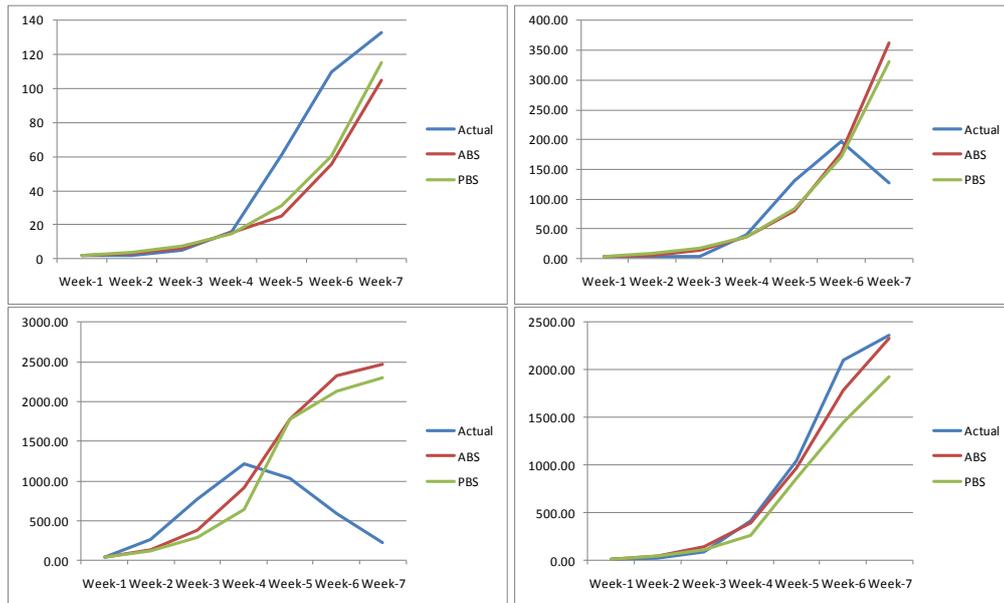


Fig. 16. Learning and validation trends of agent-based and population-based models over time
a) Birmingham b) Richmond c) Boston d) Chicago

Finally, in Figure 17, the computational time taken by both models for the learning and validation process is depicted. Here the y-axis shows the total time taken in minutes for the parameter learning and validation process for different cities. From Figure 17 it can be observed that ABS is much more computationally expensive than PBS. In these experiments, the ABS has taken almost 73.5 times more computational time than the PBS.

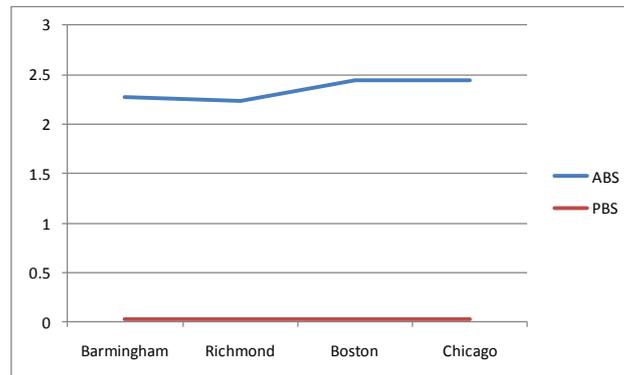


Fig. 17. Time consumed for learning and validation of models

6 Discussion

The comparative exploration of population-based simulation and agent-based simulation reported in this paper shows different phenomena that were not directly easy to predict. This has been addressed for two case studies.

For the epidemics case study, a large number of agent-based simulations based on only 10 agents provided an average of infected and recovered persons around 5 that is not far from the results of the population-based model with the same settings. Also the well-known threshold law shows in both the agent-based and population-based simulations. However, the variation was very wide. It was very rare that the simulation came up with a result that is close to the average. On the contrary, almost half of them ended up in 1 recovered person, and almost the other half in the maximal number of 10 recovered persons. For higher numbers of agents (100 and 1000) the outcome is completely different. For these cases the outcomes concentrate on the maximal number of infected and recovered persons; the variation is very low for these cases. Furthermore, the averages are also close to the maximal number of persons and therefore deviate a lot (around 100%) from the outcome of the population-based model with the same settings with average around 5.

In this paper, the epidemics model was kept relatively simple on purpose, to facilitate the comparison between population-based and agent-based modelling. Nevertheless, various extensions are possible to make the model more realistic. Such extensions include making the population size dynamic, adding locality of contact behaviour, including cognitive decision processes for contact behaviour, allowing the possibility that recovered individuals become infected again, and including the notion of external influences (like vaccination programmes).

The second case study focuses on behavioural economics, inspired by variants of predator prey models (e.g., [9], [18], [25], [26], [27], [35]). For this second case study also a large number of

simulation experiments for different population sizes were performed for both an agent-based and a population-based model. For both cases the results show that for a nonzero innovation rate the world economy grows in a fluctuating manner over time, and the average greed of the agents fluctuates between 0.1 and 0.45 . It turned out that, in particular for large population sizes, the (relative) differences in the economy and average greed between agent-based and population based simulations are close to zero.

Also for the economics model, various extensions are possible to make it more realistic. Such extensions include the introduction of different personality aspects concerning risk profile and emotions (e.g. feeling insecure) that influence the agents' investment decisions, and adding local (e.g., cultural) aspects of the world economy.

Based on the obtained results, in summary the following can be noted about two of the main issues in the comparison:

- *To what extent do averages for agent-based simulations match population-based simulations?*

The assumption that a population-based model shows the same results as the average of agent-based models has been shown not to hold in general. The remarkable outcome was that for the epidemics case study it only holds for small numbers of agents, but clearly not for larger numbers, whereas the economics case study shows the opposite: it holds for larger numbers but less for smaller numbers of agents. This may raise the question whether in such cases a more differentiated point of view on this issue can be considered, namely that for numbers of n agents population-based models have an extent of approximation of averages of agent-based models, which is a function $a(n)$ of n . It can be an interesting challenge for a given application to find this function $a(n)$; the graphs in Figure 12 give an indication of such a function, which for the economics case does not even seem to be monotonic in n , but shows a fluctuating pattern instead. Even when different experiments were performed, the fluctuating pattern always came up.

- *Variation for the agent-based simulations*

Within the epidemics case, for large numbers of agents, the variations are relatively low, for example, as shown in Figure 7. However, for small numbers of agents the variation is very high so that the average number gets less meaning. For example, as shown in Figure 6, sometimes practically all agents get infected, whereas in other cases almost no agents get infected. In the former case the fraction of recovered agents is almost 100%, and in the latter case around 10%. This phenomenon was also reported as a disturbing factor in [12]. Within the economics case study variations between agents are substantial, as is visible in Figure 10b. However, the averages over all agents do not vary too much, even for smaller numbers of agents.

A question that may arise is whether agent-based simulations are more faithful than population-based simulations: the issue of validity. In literature on agent-based simulation such as in (e.g., [2], [13], [14], [15], [28], [31]), it is argued that although agent-based modelling approaches are more expensive computationally than population-based modelling approaches, they are preferable due to more accuracy. The current paper was not aiming at answering this question. Nevertheless some steps in this direction were made as well. The main question addressed in the current paper is to explore by simulation and formal analysis to which extent the two types of models differ. Answers in the latter question can be useful input for application-directed empirical studies: when there is known to be no substantial difference between the two types of models, any of them can be chosen for an application. In contrast, when it is known that there are substantial differences, the choice is to be explored in more depth. In such cases one may decide to choose for an agent-based model (in spite of its higher computational complexity) as this might be expected to describe reality in a more adequate manner.

The results in the current paper indicate that under certain conditions agent-based approaches can be closely approximated by population-based simulations. For cases when a real difference is shown, the agent-based model may be closer to reality, although this may not be clear at forehand. To verify this, detailed empirical data have to be analysed. In the current paper, this has been done for the epidemics case, where the agent-based model did not show to have a substantial advantage over the population-based model with respect to faithfulness. This is an indication that the added value of agent-based modelling over population-based modelling cannot be concluded in general, but depends very much on the domain and research goal. Other cases where the results of population-based models are (in some conditions) comparable to those of agent-based models are reported in [39] (for the case of cellular receptor dynamics) and [40] (for the case of freeway traffic).

Sometimes it is taken as a distinction that in agent-based models each agent only has a local view and local interactions (see, e.g., [6]). Indeed, population-based models may exist where only global information and global interaction occurs. However, it may well be possible to incorporate, for example, locality of interaction in a population-based model. As an example, this happens in the population-based epidemics model by assuming only a limited contact rate.

Note that the agent-based models for social simulation used as illustration here are uniform or homogeneous, in the sense that all of them have the same model structure with the same parameters, and differences between individual agents are expressed (only) in values of these parameters. Investigating agent-based simulations with heterogeneous agent models (for example, resulting from evolutionary processes) and comparing them to population-based models would be another challenge.

Papers addressing agent-based simulation of epidemics usually do not make a comparison between population-based models and agent-based models; for some exceptions, however, see, [3], [12], [33]. Although in [3], a number of different types of models are briefly discussed, these models have not been compared by applying them to certain scenarios. Moreover, the relationship between equilibria and the initial values for susceptibles and infectives can be explored further in the context of empirical data. Recently, other comparison work [12], [33] was found on models for epidemics that have much similarity with the case study in epidemics presented in the current paper, which by itself was based on our earlier work as reported in [20]. It turns out that the work described in [12], [13] show less results of experiments and less differentiated conclusions than reported above, but in what was reported globally confirms our results.

For more studies in which agent-based and population-based approaches are compared, the interested reader is referred to [28] and [41]. Like the current paper, these papers also present a number of criteria that can be used to point out similarities and differences between both approaches, and illustrate their claims by performing real case studies (in the domains of supply networks and intelligent building control systems, respectively). Besides only focusing on the question whether both approaches produce similar results, they provide a number of arguments in favour of using agent-based modelling in certain cases, such as the possibility to model heterogeneous agents, modelling flexibility, and the increasing availability of dedicated tools. The authors of [28] also claim that researchers ‘... should consider explicit case comparisons of their agent-based models with existing or potential equation-based models where relevant. Such comparisons are particularly valuable in simple systems in which one can trace the causes of divergence between the models’. We strongly agree with this encouragement, and the current paper can be seen as a next step in that direction, hopefully resulting (on the long term) in a clear overview of the conditions in which both approaches may or may not lead to similar results.

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Appendix A - Example Simulation Traces for the Epidemics Case

Below, a number of simulation traces of the agent-based model of epidemics are shown for the following settings:

$$N = 10$$

$$\text{ContactFrequency} = 0.6$$

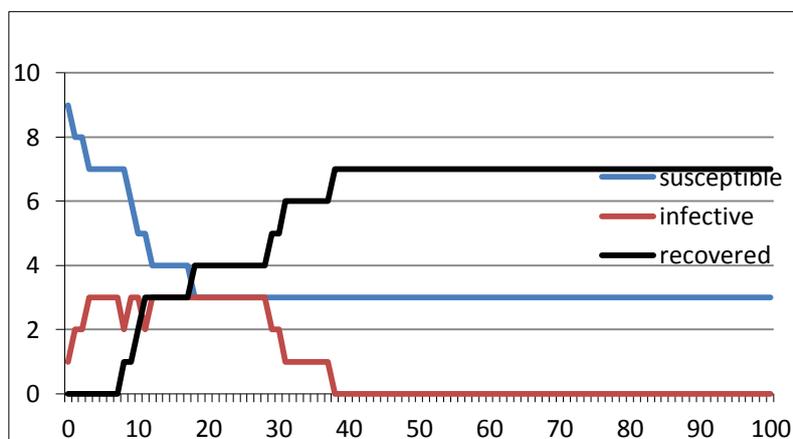
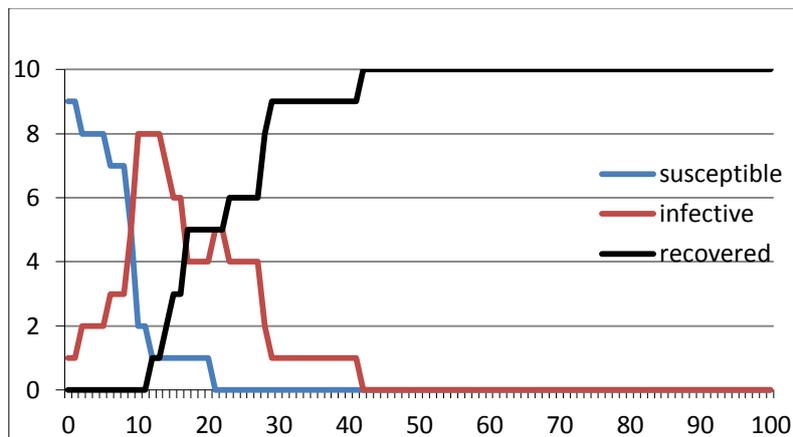
$$\text{ContactIntensity} = 0.2$$

$$\beta = 0.012$$

$$\gamma = 0.1$$

$$\rho = 8.3$$

These figures give more insight in the process underlying the results shown in Figure 18: in most cases, the small percentage of agents that are initially infective *either* infects other agents, which rapidly causes a substantial part of the population to be infected (see upper two figures), *or* they rapidly recover before they had the opportunity to infect many other agents (see lower two figures). The situation in which about half of the population gets infected (middle figure) is rare.



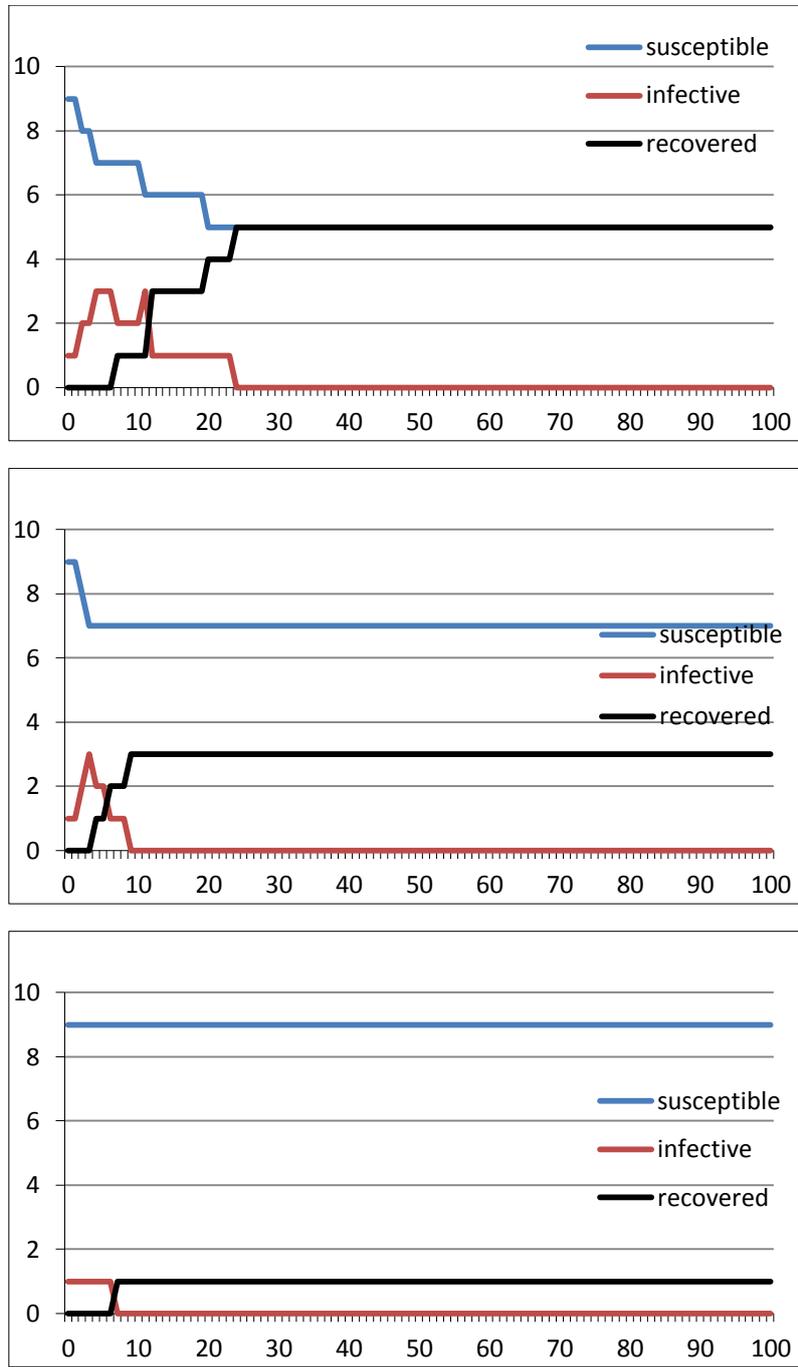


Fig. 18. Simulation traces for the epidemics case

Appendix B - Example Simulation Traces for the Economics Case

In this experiment, the initial settings used for the variables and parameters involved in the experiment are same as in the experiment-1 discussed in Section 5.2 except $a=1.6$ as shown in table 10. First the case is described when 30 agents are involved.

Table 10. Initial settings for variables and parameters

Parameter	Value	Variable	Initial value
<i>a</i> (growth rate of economy)	1.6	<i>x</i> (world economy)	5
<i>b</i> (decrease rate of economy due to population greed)	5.8	<i>y</i> (average greed of population)	random in [0.2, 0.3]
<i>c</i> (growth rate of population greed based on economy)	random in [0.0260, 0.0274]	<i>TD</i> (technological development level)	1
<i>e</i> (decrease rate of population greed)	random in [0.85, 0.89]		
<i>inn</i> (innovation rate)	0.01	Δt (step size)	0.1

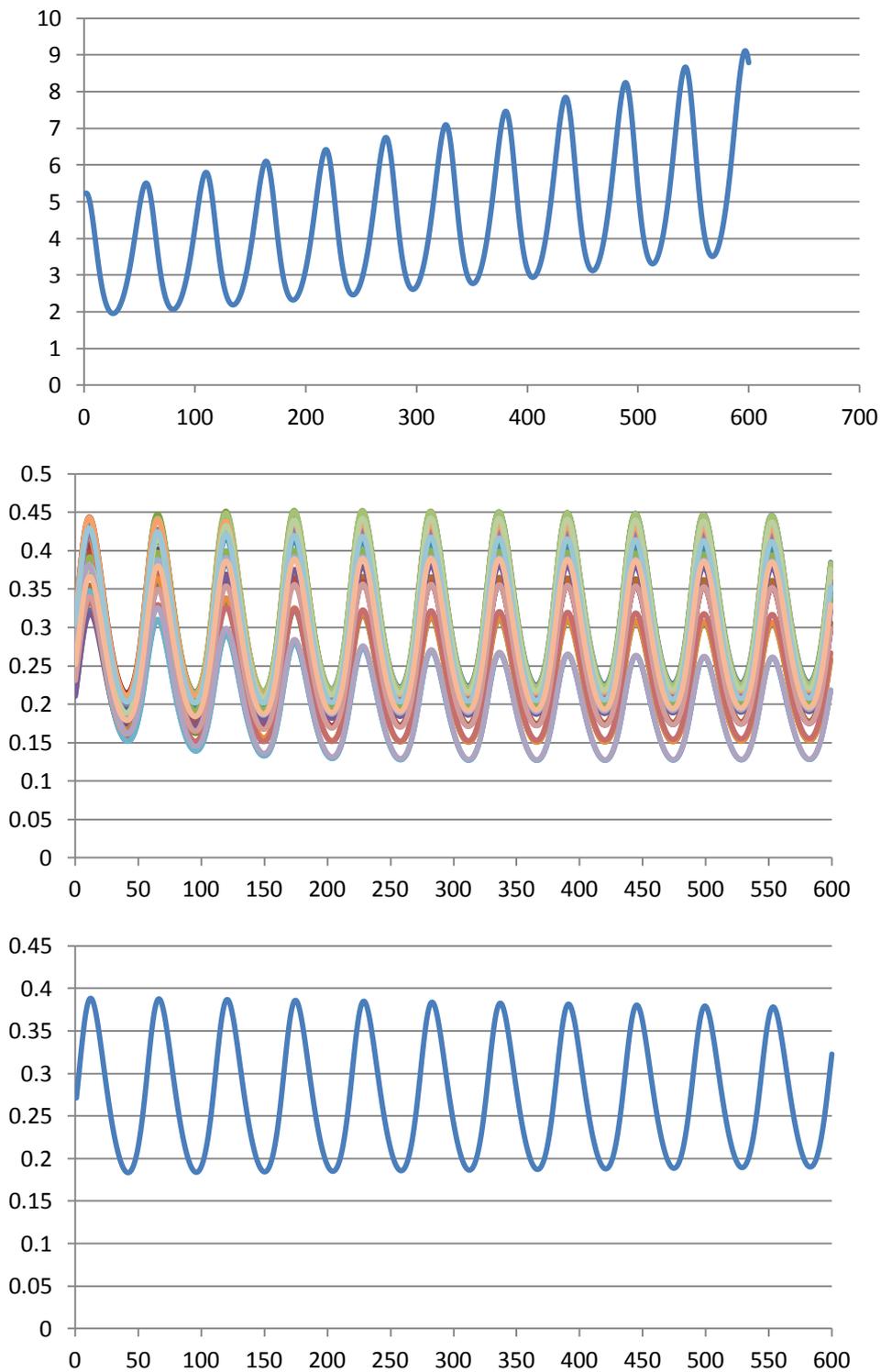


Fig. 18. Simulation traces for the economics case for $a=1.6$ (30 agents)
a) world economy, b) individual greed of the agents, and c) average greed

The results of the simulations are shown in Figure 18a and 18b. In Figure 18a, time is on the horizontal axis and the value of the world economy is represented on the vertical axis. It is evident from the graph that the economy grows as time increases (but fluctuating continuously). Figure 18b shows the individual greed values of all 30 agents. As can be seen they fluctuate within a bandwidth of about 25% with lowest points between about 0.13 and 0.3, and highest points between about 0.3 and 0.45. This pattern is similar as discussed in the experiment-1. The pattern of the average greed over all 30 agents (which is calculated simply by taking the arithmetic mean) is shown in Figure 18c.

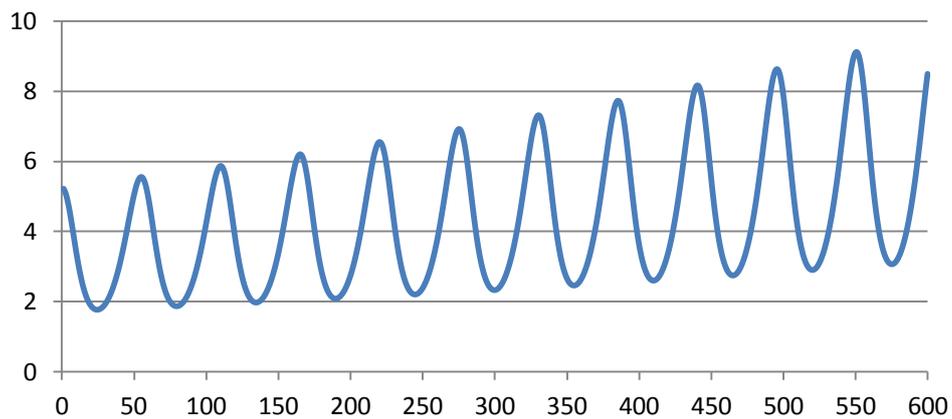
For the population-based simulation, all the parameter settings are the same as in Table 10, except parameters y , c and e . The values for parameters y , c and e used in the population-based simulation were determined on the basis of the settings for the agent-based simulations by taking the average y , c and e for all fifty agents:

$$y = (\sum_k y_k) / n$$

$$c = (\sum_k c_k) / n$$

$$e = (\sum_k e_k) / n$$

The results of the population-based simulations are shown in Figure 19a (economy) and 19b (greed). As can be seen from these figures, the results approximate the results for the averages for the agent-based simulation. The difference of the world economy for the population-based and agent-based simulation (averaged over all time points) turns out to be 0.07, and the difference between the average greed of the 30 agents in the agent-based simulation and the greed for the population-based simulation is 0.003.



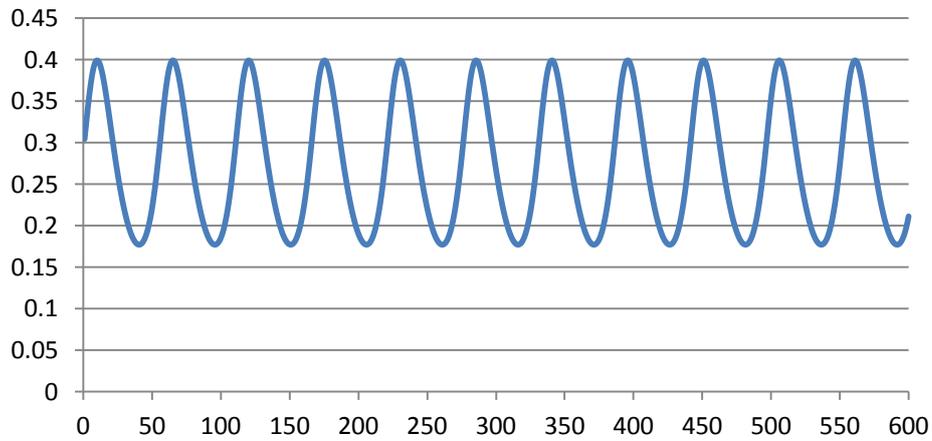
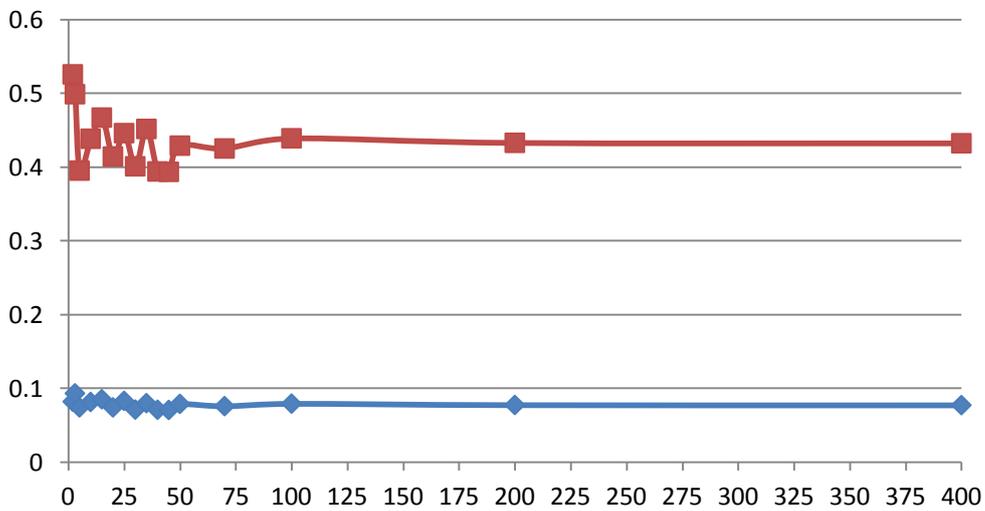


Fig. 19. Simulation traces for the epidemics case for $a=1.6$
 Population-based simulation results: a) world economy, and b) greed

In addition, a number of simulation runs have been performed for other population sizes for these parameter settings. Figure (20a) displays the (maximum and average) absolute difference between the world economy in the agent-based model and the world economy in the population-based model for various population sizes. Note that, as the economy has initial values above 1.8 and it substantially grows over time, the relative difference will approximate 0.



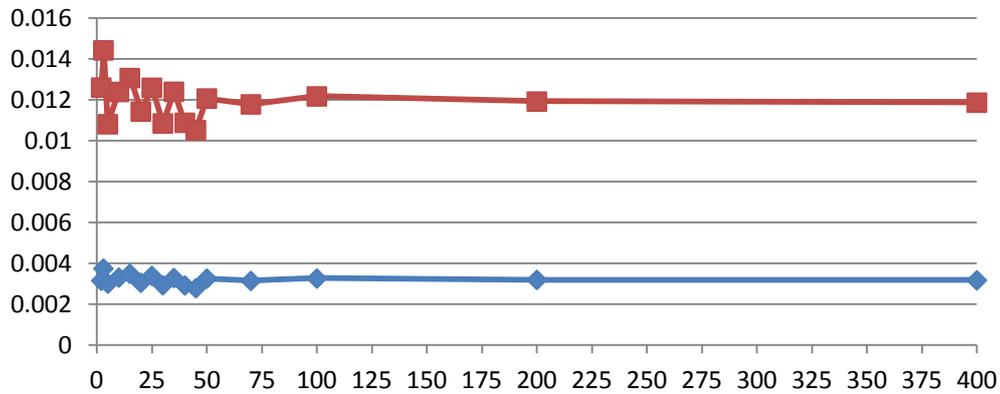


Fig. 20. Difference between both models for various population sizes for $a=1.6$:
a) world economy, and b) greed

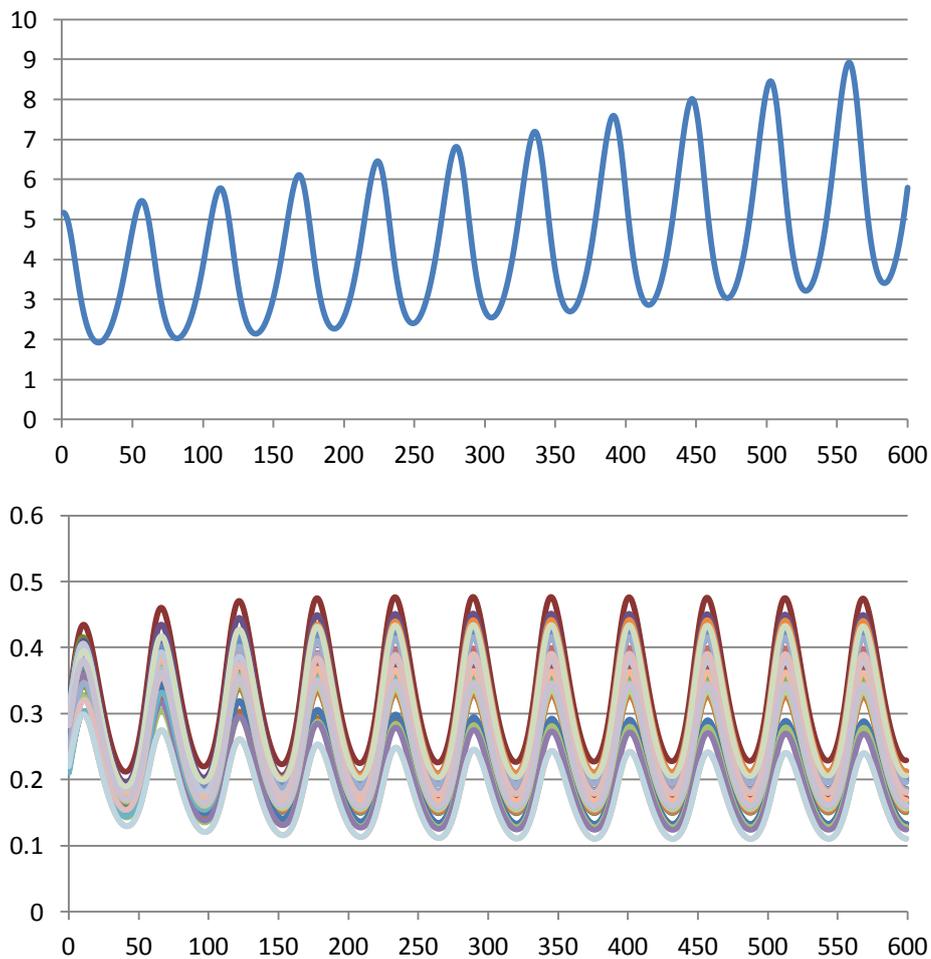
Similarly, Figure 20(b) displays the absolute difference between the average greed in the agent-based model and the greed in the population-based model for various population sizes. The red line indicates the maximum value and the blue line the average value over all time points. As the figures indicate, all differences approximate a value that is close to 0 as the population size increases.

In another experiment, the initial settings used for the variables and parameters are same as in experiment-1 described in Section 5.2 except $b=5.85$; see Table 11. First results are discussed when 35 agents are involved.

Table 11

Parameter	Value	Variable	Initial value
a (growth rate of economy)	1.5	x (world economy)	5
b (decrease rate of economy due to population greed)	5.85	y (average greed of population)	random in [0.2, 0.3]
c (growth rate of population greed based on economy)	random in [0.0260, 0.0274]	TD (technological development level)	1
e (decrease rate of population greed)	random in [0.85, 0.89]		
inn (innovation rate)	0.01	Δt (step size)	0.1

The results of the simulations of experiment 3 are shown in Figure 21a and 21b. It is evident from the graph that the economy grows as time increases (but fluctuating continuously). Figure 21b shows the individual greed values of all 35 agents. As can be seen they fluctuate within a bandwidth of about 25% with lowest points between about 0.1 and 0.28, and highest points between about 0.28 and 0.48. experiment -3 shows the same pattern as experiment-1 and experiment-2. The pattern of the average greed over all 35 agents (which is calculated simply by taking the arithmetic mean) is shown in Figure 21c.



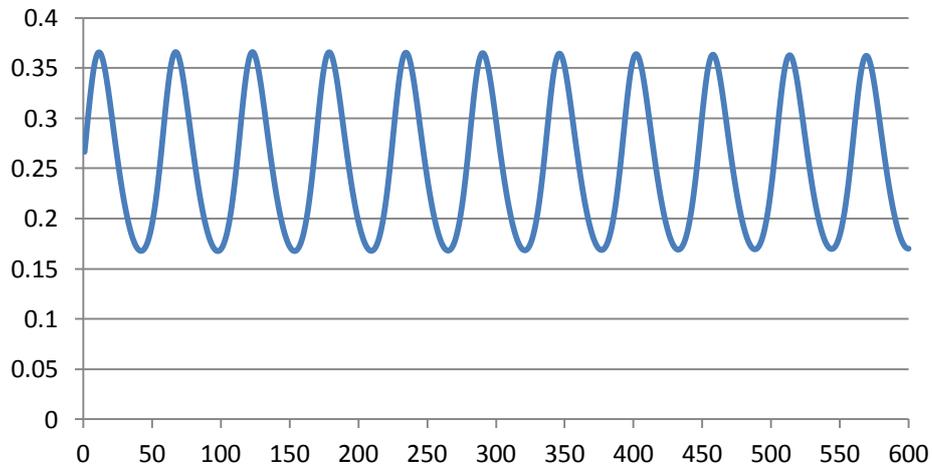
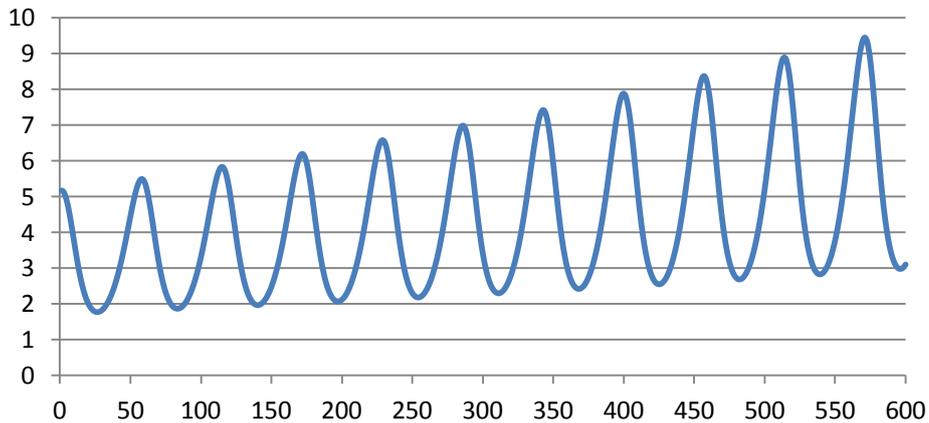


Fig. 21. Agent-based simulation results for $b=5.85$ (30 agents):
 a) world economy, b) individual greed, and c) average greed

The results of the population-based simulations are shown in Figure 22a (economy) and 22b (greed). As can be seen from these figures, the results approximate the results for the averages for the agent-based simulation. The difference of the world economy for the population-based and agent-based simulation (averaged over all time points) turns out to be 0.08 , and the difference between the average greed of the 35 agents in the agent-based simulation and the greed for the population-based simulation is 0.003 .



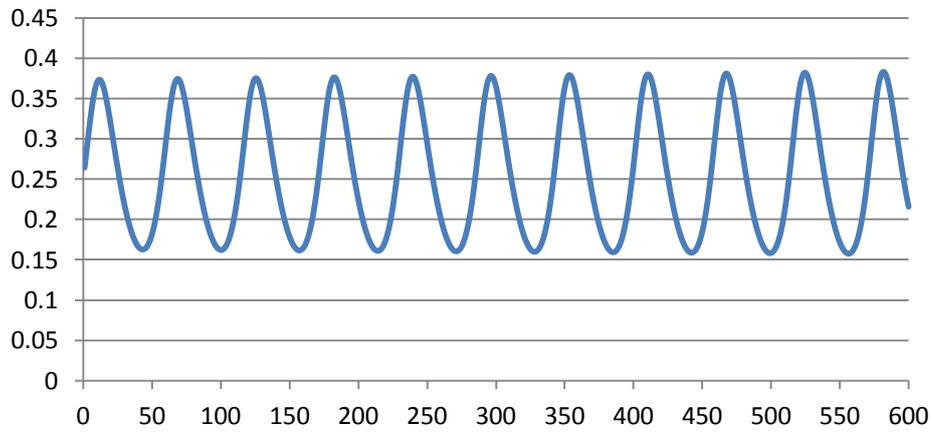
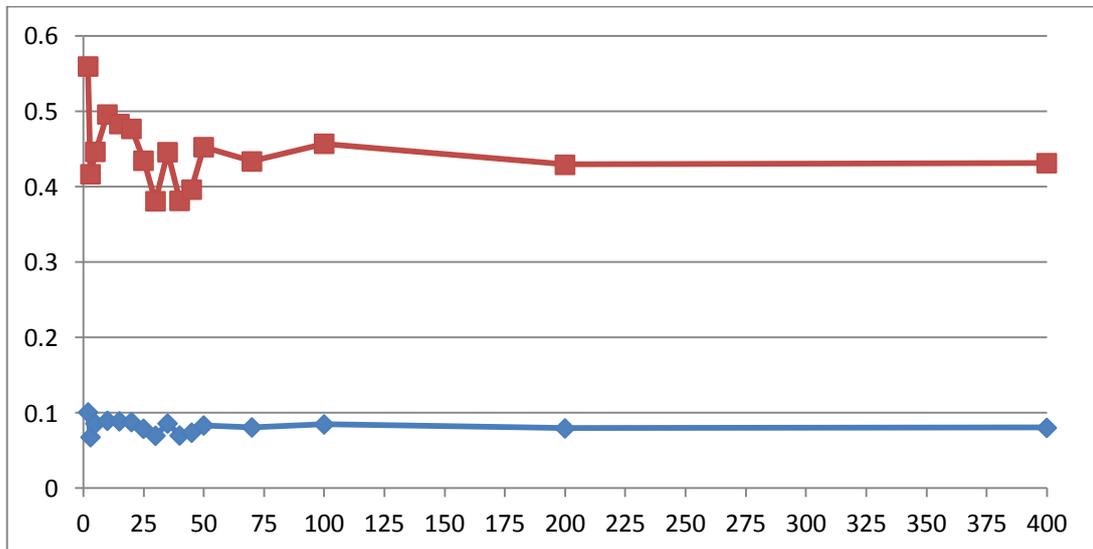


Fig. 22. Population-based simulation results for $b=5.85$: a) world economy, and b) greed

In addition, a number of simulation runs have been performed for other population sizes for these parameter settings. Figure 23a displays the (maximum and average) absolute difference between the world economy in the agent-based model and the world economy in the population-based model for various population sizes. Note that, as the economy has initial values above 1.8 and it substantially grows over time, the relative difference will approximate 0.



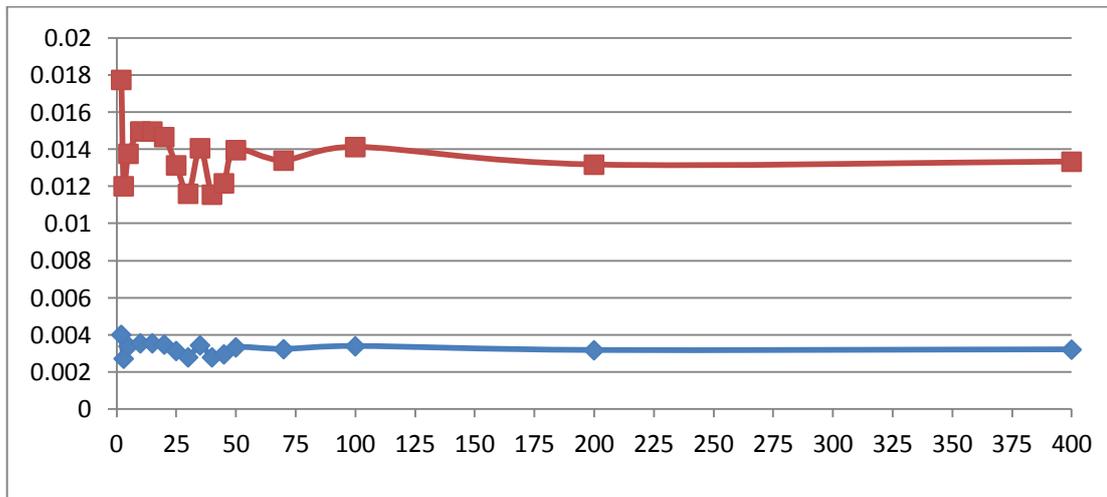


Fig. 23. Difference between both models for various population sizes for $b=5.85$:
a) world economy, and b) greed

Similarly, Figure 23b displays the absolute difference between the average greed in the agent-based model and the greed in the population-based model for various population sizes. The red line indicates the maximum value and the blue line the average value over all time points. As the figures indicate, all differences approximate a value that is close to 0 as the population size increases.