Exploring Epidemiological Dynamics in a Social Dilemma

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Abstract. This paper presents a novel epidemiological extension of the El Farol Bar problem, utilizing an agent-based modeling simulation technique. The study aims to explore the complex interplay between social decision-making and epidemiological dynamics in scenarios involving contagious disease outbreaks. The model simulates individual agents making binary decisions—to visit a bar or stay home—amidst an epidemic, reflecting the impact of individual choices on disease spread within a social system. Our study shows that even basic models can reveal complex behaviors in disease spread scenarios. We found that agents with only two choices can create a repeating pattern in infection rates and social activity. This suggests real-world situations are complex and need more research for better management during epidemics.

Keywords. *Agent-based modelling; El-farol bar problem; Social dilemma; Epidemiological modelling*

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1 Introduction

The advent of Covid-19 sheds new light on the spread of epidemics in social systems, which has ascended as a research imperative (15). The pandemic has underscored the intricate interplay between disease dynamics and socio-behavioral patterns (14). Consequently, understanding and strategizing against the spread of epidemics in interconnected social systems have become paramount to safeguarding global health and socio-economic stability.

Mathematical models (2), and subsequently, simulation models (1), have long been pivotal tools in the realm of epidemic management, offering the capacity to predict (3), analyze (4), and strategize (5) against the spread of infectious diseases. The computational implementation of an epidemiological model enables the analysis of disease transmission dynamics (7) through the systematic examination of epidemiological variables, even when they are not analytically tractable (6). In this perspective, simulations can serve two main interrelated goals, although a more precise taxonomy can be defined (8; 9). First, by incorporating real-world data and multifaceted parameters, simulations provide a computational platform to assess possible outcomes and interventions in real-world systems (12; 13). Second, simulations can be employed to assess the reliability of hypotheses and to refine the objectives of empirical studies and treatments (10; 11; 27).

The El Farol Bar problem (17), a seminal example in complexity science (16), exemplifies the use of toy models to study the unpredictability of the dynamics of seemingly simple social systems (24). In the original form of the problem, multiple agents all face the same binary decision, that each of them has to make without the possibility to agree or to share information with the others: either to visit a bar with limited capacity or to stay home, where a threshold is set and known to all agents above which they no longer find it enjoyable to visit the bar. The binary outcome – either the visit was enjoyable if the bar was not too crowded or viceversa – is known to each attending agent after the event, and the time series of the outcomes of repeated events is the basis for predicting the next outcome and a decision of each accordingly. This dilemma can be coupled with the challenges posed by epidemiological scenarios, where individuals must decide whether or not to engage in social activities amidst a contagious disease outbreak, as the Covid-19 pandemic showed (18). The interactions between the underlying mechanisms of social decision-making and the epidemiological dynamics in such scenarios are largely unexplored (19).

This paper presents an epidemiological extension of the El Farol Bar problem and aims to contribute to the understanding of the intertwined nature of the social and epidemiological facets of some systems. The model is implemented using the agent-based modeling (ABM) simulation technique, a computational approach that simulates individual agents and their interactions within a defined environment (20). This methodology embodies a bottom-up approach, allowing for the representation of heterogeneous behaviors and leading to the emergence of complex system-wide phenomena (21). This methodology is widely employed across multiple fields, including ecology (25), economics (23), social sciences (26), and epidemiology (15).

The model behavior suggests that even a seemingly simplistic model can exhibit profoundly intricate dynamics. Specifically, our analysis demonstrates that a simple setting, where each agent has only two states, is sufficient for a limit cycle, and therefore a dynamic attractor, to emerge within the state space of infection rate and event attendance. This observation underscores the potential for considerable complexity in real-world scenarios, emphasizing the need for more extensive investigations to improve how social systems should be managed during the spread of a disease.

This paper is structured as follows: The agent-based model is first introduced and a detailed description of its components provided. The model exploration process is then outlined, emphasizing the methodology employed to generate the results. Finally, we present and discuss the outcomes and draw conclusions from our research.

2 Related works

Social dilemma exists with the purposes of improve the understanding regarding how people interact in a resource-bounded environment (28), especially were there is a conflict between bounded rational entities which are metabolically dependent from a shared environment (39). At the best of our knowledge, (29) was the first to introduce the concept of social dilemma, describing it as a scenario where individual decision-makers possess a dominant strategy that leads to non-cooperation and, if everyone adopt this dominant strategy, the outcome would be universally poorer, leading to a suboptimal equilibrium. The final rate of cooperation usually depends on the payoff structure (30); even then, it is an approximation and usually requires a certain number of iterations to be reached (31).

Social dilemma are present in many fields. The literature on the use of social dilemmas in economics encompasses a range of perspectives and findings, such as investigating the difference between rational behaviour and social norm (40; 41). Also, social norms have been employed for addressing environmental policies (42), conflict management strategies (43), social learning (44), and knowledge sharing (45). Ecology has a long tradition of using social dilemmas (34; 35), especially in light of the pervasive presence of cooperation in natural species (33). Social dilemmas help in understanding the origin of sociality (36) or group foraging strategies (38). Also, social dilemmas have been employed as the border between ecology and social sciences, to study how success in species conservation depends as much on individuals can collaborate to a common purpose (32) and to use classic economic concepts such as signaling and contract theory to interpret evolutionary biology (37).

Although the fields of epidemiology and social dilemmas have not traditionally intersected extensively, recent years have seen a burgeoning interest in the interplay between these disciplines, particularly highlighted by global health crises such as the COVID-19 pandemic (48). The application of social dilemma frameworks has proven insightful for examining the relationship between individual behaviors and collective outcomes, notably in the context of vaccination rates within populations (49). These analyses utilize various models to illuminate the impact of factors such as replicator dynamics (50), social efficiency (50; 52), and diffusion structures (51) on vaccination uptake. Furthermore, empirical studies highlight how pro-social behaviors may be amplified by the accelerated transmission of disease (47). Additionally, the exploration of oscillatory behaviors within social dilemmas reveals how perceived infection risks can drive a collective shift towards more cautious approaches to social interaction, such as increased adherence to social distancing measures (46).

3 Methodology

In this section an agent-based model of an epidemiological version of the El Farol Bar problem is described and the method employed to explore the model is presented.

3.1 Agent-based model

In this section an agent-based model of an epidemiological version of the El Farol Bar problem is described and the method employed to explore the model is presented.

In addressing how epidemics affects the social dynamics in the El Farol Bar problem, agent-based modeling serves for two compelling reasons: as an approach traditionally employed to address social dilemmas, it is an effective means of communication within the scientific community; and it is particularly well-suited for capturing individual behaviors and their effects on an overall epidemic spread. This enables to get insights from the global co-effect of individual (i.e., agent-related) epidemic and social variables.

At each time step t, the model orchestrates a sequence of actions, as depicted in the flowchart (see Figure 1). These actions are divided into two sets. The first is about the decision-making process on bar attendance: evaluating agents' memory of past attendance, estimating the expected crowd level, and making a decision accordingly. The second is about the dynamics of infection as induced by the interactions among

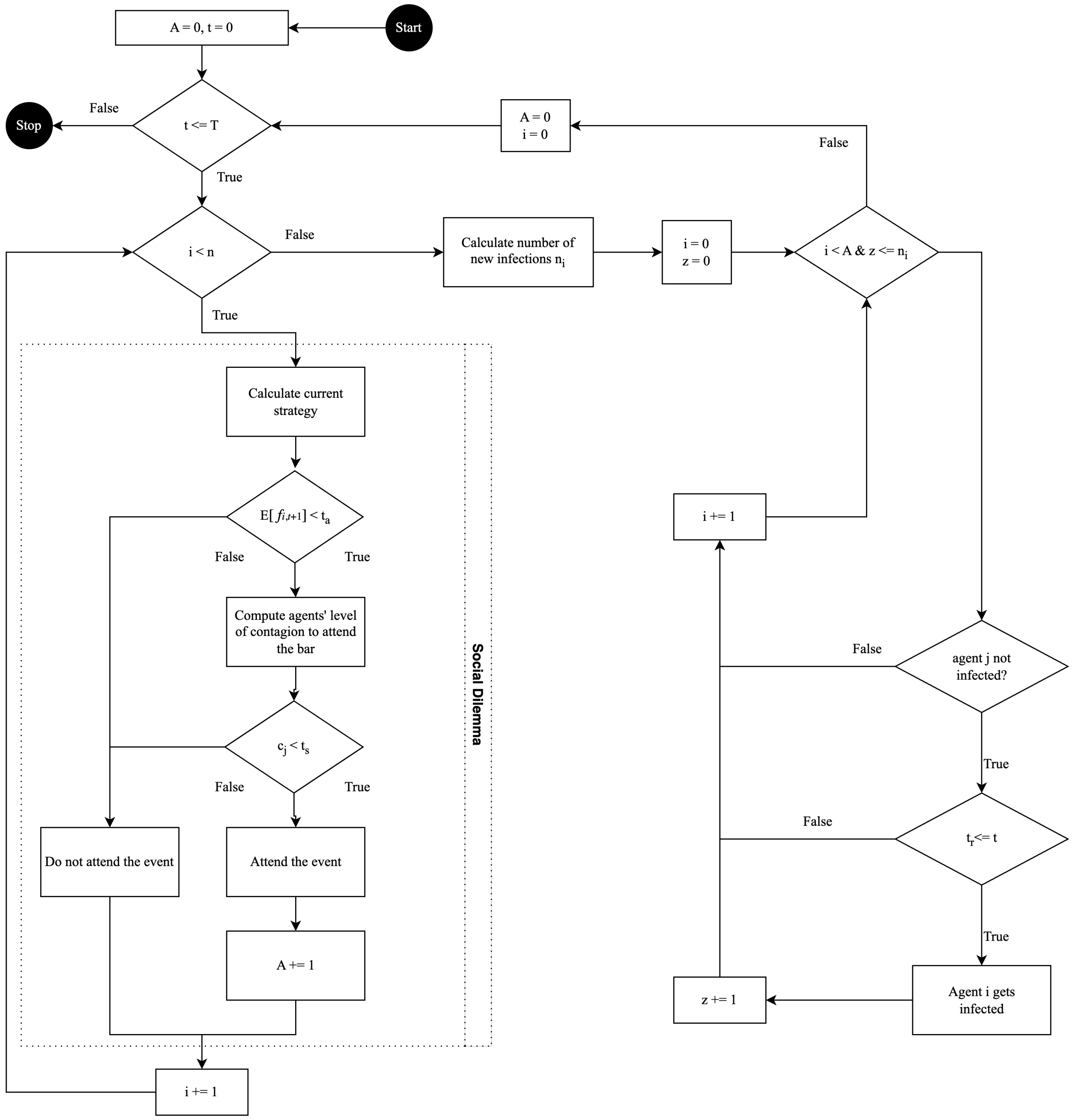

Figure 1: Scheduling process of the model.

the agents given their health states, where an infectious pathogen could be transmitted to those who decide to attend the bar, influenced by the density of the crowd and the duration of exposure.

Together, these two sets of actions capture a dual aspect of agent behavior: social decision making influenced by past experiences and the epidemiological implications of these social choices. The model thus provides a framework for examining the interplay between individual decision making based on memory of previous states and the collective outcomes in terms of disease transmission, offering insights into how individual behaviors aggregate to impact public health.

3.1.1 Social dilemma

This model includes a single kind of agents, representing the individuals that could decide to attend the bar in any given week (the time step of the model) and thus possibly be infectious. The agents' behavior is modeled according to the hypotheses of the original El Farol Bar problem. First, the only decision each agent can make each week is whether to attend the bar, and the decision is always executed. Second, agents like to attend the bar, if it is not too crowded, and do it as much as they can: hence, each agent decides each week whether to attend the bar depending upon its expectation of the total number of agents who will attend. Third, agents interact with each other only at the bar, and therefore when their decision to attend has been already made.

The proposed model incorporates several hypotheses concerning agents' behavior. First, agents take a binary decision, as they can either choose to attend a bar or not; no other actions are included in the model, to focus on a specific aspect of social behavior. Second, agents inherently enjoy attending the bar and will do so as much as they can, but their preference is tempered by the bar's occupancy; agents are averse to overcrowding. Therefore, the decision to attend the event is influenced by their expectations regarding how crowded the bar will be. In time, this introduces a feedback loop where the average attendance of the bar inversely affects its attractiveness while it is directly influenced by it; a dynamic seen in many real-world social scenarios. Third, agents' interaction is solely defined by the shared presence in the crowded space of the bar, and there are no interpersonal communications or relationships affecting their attending decision.

The information about past attendance plays a crucial role in shaping agents' expectations, as it is used to estimate the number of agents likely to attend the bar in the subsequent week, as follows. For agents attending the event, the new value is the actual number of agents at the bar, while for agents that did not attend the new element of the memory is a random value, which stands for an educated guess made by agents which can not communicate with each other.

The agent's decision whenever to attend or not the bar is taken comparing an attendance threshold and the expectation regarding the future attendance. The attendance threshold t_a is a parameter of the model that depicts venue saturation level above which agents would consider unpleasant to be in the bar, consequently not attending the event.

Each agent i (where i goes from 1 to n, the total number of agents) generates an expectation regarding how many agents will attend the bar at the next time step memorizing the number of agents present at the bar the last m times it attended the bar, with m being the memory length, and weighing it to generate a prediction. In cases where the agent does not attend the bar, the value saved in memory is the one hypothesized by the agent, namely, the one generated with the 'expected attendance'. Let $s_{i,k}$ be the k-th element of the memory of agent i (with $k \in \{0, 1, ..., t\}$) and w the list of weight w_k used to the define importance of each memory element, which increases with k. So, the attendance – which is the number the agent i expects to be at the event at time $t+1$ – is therefore given by:

$$E_i[\sum_{j=1}^{m} a_{j,t+1}] = \sum_{k=1}^{m} s_{i,k} w_k \tag{1}$$

where a_j is the participation of the agent j to the event at time $t+1$, $\sum_{j=1}^{m} a_{j,t+1}$ is the total attendance at time $t+1$ and $E_i[\sum_{j=1}^{m} a_{j,t+1}]$ is the expectation of the total attendance from agent i at time $t+1$. Consequently, from the expected attendance is possible to determine also the expected filling f of the venue at the time $t+1$

$$E_i[f_{t+1}] = \frac{E_i[\sum_{j=1}^{m} a_{j,t+1}]}{C_{max}} \tag{2}$$

where C_{max} is the maximum capacity of the place. Given the expected filling, at each time step an agent i attends the event whenever $E_i[f_{i,t+1}] < t_a$.

3.1.2 Epidemiological transmission

In epidemiological models, each agent is typically into one of three states: susceptible, infectious, or recovered, a classification central to the SIRS (Susceptible, Infectious, Recovered, Susceptible) model of disease transmission dynamics. These class of models accounts for the possibility of waning immunity after an infection, and eventually become susceptible again, modelling diseases where immunity, either natural or vaccine-induced, can be acquired and diminishes over time.

The epidemiological dimension of this model is based on several key modeling hypotheses. Firstly, the contagion process is assumed to be uniform across all agents, characterized by a consistent duration and a uniform initial level of infectiousness. This simplification negates individual variations in disease progression and response to infection. Secondly, the model posits that the disease in question is non-lethal; agents cannot die as a result of contracting the illness. This assumption is critical as it focuses the model on the dynamics of disease spread rather than mortality rates, and the overall number of individual in the system remains the same. Furthermore, the model assumes the absence of long-term physical or psychological effects post-infection. Recovered agents are not hindered in their ability to participate in normal activities, such as attending a bar, indicating that the disease does not cause lasting health impacts. Psychologically, the model assumes that agents do not experience fear or behavioral changes as a result of the infection. They continue to frequent the events without any alteration in their behavior due to the experience of being infected. Finally, a crucial aspect of this model is the agents' ignorance of the epidemic. Agents lack information about the total number of infected individuals and do not consider the risk of infection in their decision-making process. This implies a lack of adaptive behavior in response to the epidemic, which significantly influences the model's predictions about disease spread. By ignoring potential changes in social behavior and risk assessment, the model strictly focuses on the mechanical spread of the disease under constant behavioral patterns. This approach simplifies the modeling process but may overlook important dynamics present in real-world scenarios where awareness and behavioral adaptations play a crucial role in disease transmission.

Agents can get infected only by participating to an event. So, the epidemic transmission happens solely at the bar, and only if at least an infectious is attending. The number of new infected agents i_t at time t is

$$i_t \propto \lfloor \frac{\sum_{j=1}^{n_i} c_j S_t}{C_{max}} \rfloor$$

where c_i is the level of contagion of each agent attending the bar (which is 0 when agents are not infectious) and S_t the number of agents in susceptible state attending the bar at time t. Notable, the contagious level is taken into account only for the n_i agents which are contagious enough, which is $c_j > t_c$.

In the proposed model, social relationships among agents are not considered, leading to a uniform infection probability for all individuals attending the bar at time t.

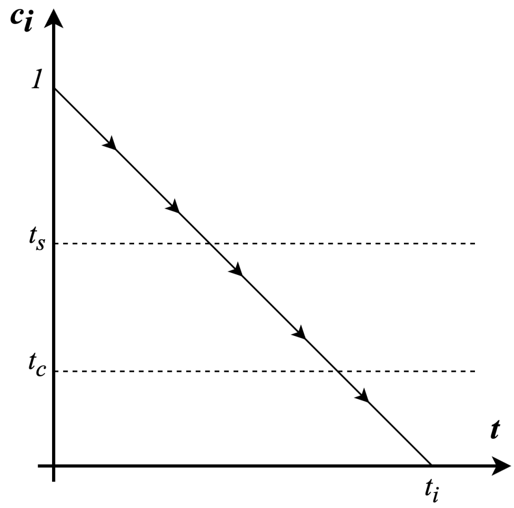

Figure 2: Decourse of contagious level for each agent

Consequently, the selection of new i_t infected agents at each time step is randomized from those present, not considering individual interactions or relationships.

Whenever an agent become infected, the infection follows this dynamics. Initially, the contagion level of the newly infected agent i is set to $c_i = 1$. Given an infection duration d_i, the contagiousity of agents decreases linearly by $1/d_i$ at each time step.

In the progression of the disease modeled, two critical thresholds, t_s and t_c, play pivotal roles in influencing agent behavior and the spread of the infection. The first threshold, t_s, represents the infection level at which an agent exhibits sufficient symptoms to deter them from attending the bar. The second, t_c, indicates the infection level beyond which agents can spread the infection The spread of the infection is most influenced by the agents with $t_c < c_i < t_s$, so with a contagious level between these two thresholds. This is because it encapsulates the period when agents are infectious but may not have anymore the level of symptom severity or self-awareness to avoid social gatherings, thereby contributing to the disease transmission dynamics.

In the modeled scenario, infected agents undergo a recovery process after a duration of t_i time steps. Upon recovery, these agents are conferred a temporary immunity lasting t_r time steps. However, this immunity is not permanent; after the elapse of t_r time steps, the agents once again become susceptible to infection. This cyclical pattern of recovery and renewed susceptibility underscores the transient nature of immunity in the context of the model.

Table 1: Description of model parameters

Parameter	Description
t_a	Threshold of share of expected agents above which an agent does not attend the event
t_s	Threshold of infection above which the infected agents have symptoms and do not attend the bar
t_c	Threshold of infection below which an agent can not transmit the disease anymore
w_{t-1}	Weight of the last memory in the decision-making process of agents
t_i	Duration of the infection
t_r	Duration of the immunity

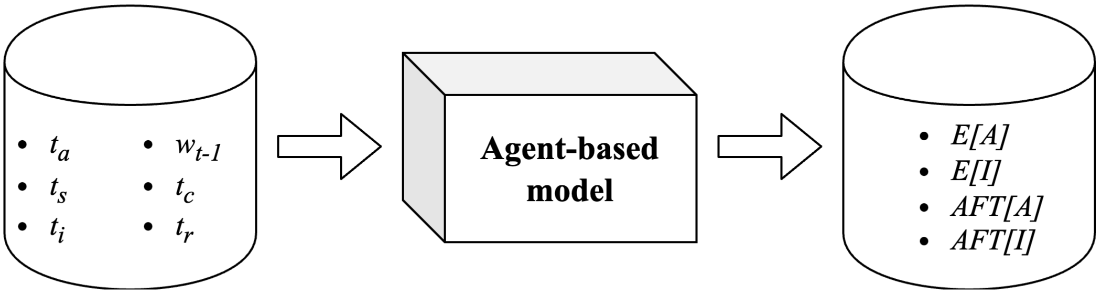

Figure 3: Black box diagram of the experimental setting

3.2 Model exploration

The model exploration consists of a grid sampling exploration of the parameter space, to collect the model outputs from different parameters' combination. Grid sampling from a parameter space involves systematically selecting a finite subset of parameter values that aims at comprehensively represent the entire parameter space. The idea underlying the use of this technique is to facilitate the exploration of system behavior across distinct parameter combinations, especially in cases where not a specific behaviour is expected or researched. Table 1 presents the parameters tested in the simulation and their explored ranges. The data are collected by simulation 10'000 times the agent-based model.

From each simulation, two time-series were collected: A, which is the number of attending agent at each time-step t, and I, the number of infected agents at each step of the simulation. Each time-series was computed before to be stored, to extract two output of interest: the mean value of the series $E[A]$ and $E[I]$, which are used to assess the overall status of the system in time, and the autocorrelation $AFC[A]$ and $AFC[I]$. The autocorrelation is a statistical tool that quantifies and

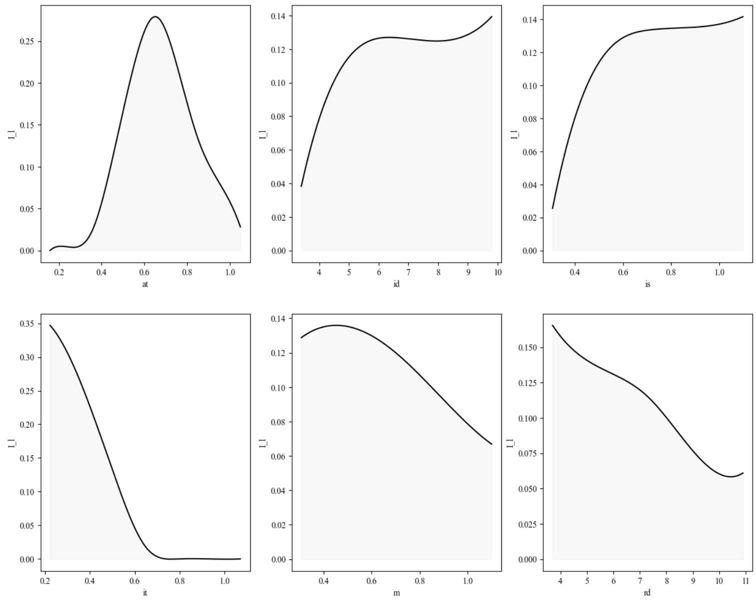

Figure 4: Probability for the infection to last until the final time step $t = 200$ for different parameter values, measured in shared of simulations in which the infection survives.

visualizes the degree of correlation of a given time series with its own past and future values as a function of time lag, and it is used to perceive seasonality in time-series. Specifically, for each simulation the higher value of the correlation between lagged sub-time-series is collected, and the lag windows used to computed it. Figure 3 depicts a black-box representation of the experimental setting. Even if the model is stochastic, each simulation was initialized with a specific random seed, that was stored as well. Consequently, the results were replicable later, and the time-series of each configuration of interest was observable.

The model, the exploration code and the data analysis are all implemented in Python 3.11. The code and the results are available upon reasonable request.

4 Results and discussion

In Figure 4, the output of the simulation is visualized, demonstrating the infection probability for each individual at the end of simulations. This figure is of interest for two reasons. Firstly, it is necessary to clarify whenever parameters affects the behaviour of the model. Secondly, the figure reveals how even in a simplified model,

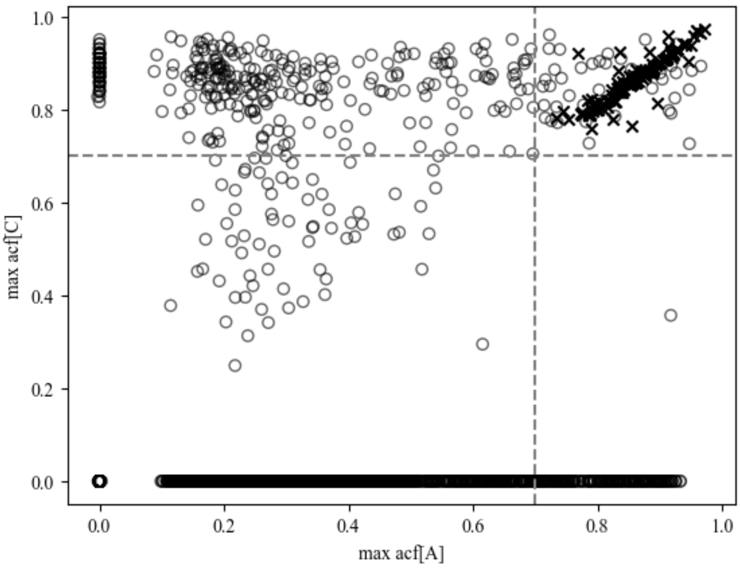

Figure 5: Scatter plot of the maximum values of auto-correlation for the time-series A and I for each simulation

nonlinear effects become evident, particularly in the context of parameters such as t_a and w_{t-1}.

The parameter t_a, which in here is taken as example, provides a compelling example of this nonlinearity. A low value for t_a results in limited attendance, restricting the spread of infection to a smaller subset of agents. This, in turn, curtails the progression of the epidemic, as per the modelling hypothesis that infection transmission occurs exclusively through event participation, and, if insufficient numbers attend, the contagion cannot disseminate effectively. Conversely, a high t_a value implies near-universal attendance at events, leading to simultaneous infection of a larger agent population. This synchronous infection increases the likelihood of a concurrent rise in immunity, thus diminishing the likelihood that the infection lasted until the simulation end. Such dynamics underscore the critical role of parameter settings in shaping the outcomes of the model and highlight the complex interplay between individual behavioral patterns and the broader epidemiological trends in this simulated environment.

Upon establishing that social parameters significantly influence infection dynamics, it became pertinent to investigate whether these interrelated behaviors lead to the emergence of non-punctual equilibrium states, commonly referred to as limit cycles in two-dimensional scenarios. This exploration is crucial for understanding the temporal evolution of the system under varying social conditions. The presence of limit cycles in such a system suggests a cyclical pattern of infection spread and containment, influenced by social parameters, even in absence of any central control. Identifying and understanding these limit cycles can provide deeper insights into the long-term behavior of the infection, offering valuable perspectives for understanding and predicting the impact of social behavior on disease dynamics.

The investigation into the existence of periodic fluctuations focused on the relationship between the main epidemiological output, denoted as I, and the principal social output A. This analysis was predicated on the hypothesis that an increase in the number of attendees (A) at social gatherings might correlate with a rise in infection rates (I). While this relationship aligns with the conceptual underpinnings of the model, it can be considered an emergent phenomenon, arising from the complex interactions and decision-making processes of the agents within the model, without being explicitly encoded either in the micro nor the macro behaviour of the model. This emergent behavior holds profound implications for the management of infection spreading in scenarios influenced by social behaviors. Specifically, the possibility that social dynamics, driven by individual decision-making processes, could inherently lead to cyclical patterns of infection rates is a significant insight.

The existence of a limit cycle is assessed by computing the maximum autocorrelation values for both time-series of the epidemiological output I and the social output A. The rationale behind this approach was to detect potential cyclic patterns within the data. A high maximum autocorrelation value in a time-series is indicative of cyclic behavior, signifying points in the series where periodicity or seasonality is pronounced. For the purposes of this study, a threshold value of 0.7 was established, above which autocorrelation is considered significantly high. The detection of high maximum autocorrelation values in both I and A time-series would be indicative of a non-punctual equilibrium within the system. Such a finding would imply that the dynamics of the system do not converge to a fixed point but rather exhibit ongoing cyclical fluctuations.

From the observation of Figure 4, which depicts the results of this analysis, three groups of simulation outcomes can be identified:

1. simulations S_a, that include all the results;
2. simulations S_i, that include all the simulations in which I does not go to 0 at the end of the 200 simulated time-steps;
3. simulations S_c, that include the results in which a limit cycle between A and I appears, so that the $max(AFC[C]) > 0.7$ and $max(AFC[I]) > 0.7$.

Analyzing Figure 4, which presents the results of this analysis from our simulation

Table 2: Mean parameters values per each scenario

par	$E[par\|S_a]$	$E[par\|S_i]$	$E[par\|S_c]$	$\frac{E[par\|S_i]-E[par\|S_a]}{E[par\|S_a]}$	$\frac{E[par\|S_c]-E[par\|S_a]}{E[par\|S_a]}$
t_a	0.505900	0.582962	0.627943	0.152327	0.241241
t_s	0.506058	0.178483	0.140284	-0.647308	-0.722791
t_c	0.499642	0.594004	0.323688	0.188858	-0.352160
w_{t-1}	0.504864	0.445740	0.511489	-0.117108	0.013123
t_i	5.047981	5.895795	6.687943	0.167951	0.324875
t_r	5.552979	4.515539	4.652482	-0.186826	-0.162165

study, allows for the categorization of the simulation outcomes into three distinct groups based on their characteristics and behaviors. These groups are as follows:

1. Simulations S_a: This group encompasses all the simulation results, serving as a comprehensive dataset to which to make confrontations. It includes the entire range of outcomes observed during the study, providing a holistic view of the simulation's potential behaviors under various conditions.
2. Simulations S_i: This subset includes those simulations where the epidemiological output I remains non-zero at the conclusion of the 200 simulated timesteps. The persistence of I beyond this duration indicates scenarios where the infection continues to be present in the system, suggesting incomplete containment or ongoing transmission dynamics. This category is crucial for understanding the conditions under which the infection sustains itself over extended periods.
3. Simulations S_c: The final group comprises simulations where a limit cycle between social output A and epidemiological output I is evident. This is characterized by both $max(AFC[C]) > 0.7$ and $max(AFC[I]) > 0.7$, indicating significant autocorrelation and, thus, the presence of cyclical patterns in both social behavior and infection rates. This group is particularly significant as it highlights the dynamic interplay between social behaviors and epidemiological outcomes, manifesting as cyclic fluctuations over time.

These categorizations provide a structured approach to analyzing the simulation data, enabling a clearer understanding of the different dynamics at play.

Table 2 depicts the mean parameters values for each of the scenario. The analysis of table shows that the most influential factor in the emergence of limit cycles in model's outputs is the contagiousness threshold t_c, the value above which individuals become infectious, since it is consistently lower in S_c than in S_i. This suggests that the observed seasonality in the model is at least partially driven by maintaining a low threshold for contagiousness. Additionally, an high the duration of contagion t_i

is observed when cyclicity appears. This implies that within a socio-epidemiological context, a prolonged period of contagiousness might be a prerequisite for establishing stable oscillatory behavior in the whole population. It stresses the complex balance between the duration of infectiousness and the propensity to spread the disease, both significantly contributing to the emergence of limit cycles in this agent-based model.

Another influential parameter is t_s, which stands for the degree of health discomfort that prompts individuals to decide against attending the bar. Our findings suggest a difference in system behavior based on this parameter. Specifically, infections manifest without any noticeable cyclicity with an higher than average t_s.

Finally, a trend observed is the presence of cycles in scenarios where individuals better consider information from multiple past periods before making a decision, which in this model is given by an higher value of w_{t-1}, especially compared to the case in which infection is present. Essentially, when individuals incorporate a broader spectrum of historical data in their decision-making process regarding attendance, the system more frequently exhibits cyclical patterns. This suggests that the depth of historical context plays a significant role in shaping the system dynamics when there is an interplay between a social and an epidemiological dimension. By relying on a more extensive set of past data, individuals inherently introduce a delayed response mechanism. This delay can lead to periodic oscillations as individuals react to older information, causing a ripple effect in their collective behavior. The presence of these cycles underscores the importance of understanding the temporal depth of decision-making processes in socio-epidemiological models. It indicates that not just the immediate past, but a more extended historical context, can have profound implications on the emergent dynamics of such systems.

Finally, Figure 6 and Figure 7 present two examples of simulations in which a cyclical equilibrium appeared. In both cases, it was considered more appropriated to present both the time-series representation and the behaviour on the state-space. The jagged nature of the observed cycles can be attributed to the high temporal granularity chosen for the study. As a consequence of this granularity, many discontinuities are apparent, which are not observed in classic limit cycles derived in continuous functions or in continuous time simulations. However, the very fact that we observe such sharp-edged cycles indicates the underlying dynamics generating these non-static equilibria are notably robust. In essence, despite the coarse temporal resolution introducing apparent irregularities, the inherent stability of the system's dynamics is evident. This robustness provides assurance in the reliability of the observed patterns, and suggest that an analogue real-world system could have a given resilience to external perturbations, given for example by policy-maker interventions or epidemiological setting variation. Nevertheless, further mathematical analysis and simulations are required to quantify the precise nature and stability of this limit cycle.

5 Conclusions

The results of this paper demonstrate how an intertwined socio-epidemiological toy model can be utilized to enhance the understanding of how individual behavior and its thresholds impact the spread of infections in socio-epidemiological models. More precisely, it shows that a non-stable equilibrium can exist in this type of system, and that these cycles are significantly influenced not only by the epidemic aspect of the system but also by the social aspect, even in conditions where there is no central authority to implement controls and make decisions, and where the agents exhibit greediness without considering potential consequences.

The limitations of this work include a strong reliance on specific modeling assumptions, such as agent homogeneity and the specific rules of behavior, including when to attend the bar in case of infection levels above or below a certain threshold, or agents' inability to estimate the number of infected individuals who will attend the bar the following week. Furthermore, the results should be validated in more realistic scenarios.

Future developments entail the introduction of a social network to assess how the presence of specific relationships that determine when an agent attends the bar affects the intertwined relationship between the social and epidemiological components of the system. Additionally, the model could be employed to study potential healthcare policies, such as mandatory reductions in capacity at public places or awareness campaigns for citizens. Finally, an analytical treatment of the model could be performed to gain a better understanding of the oscillatory behavior observed in the model's output.

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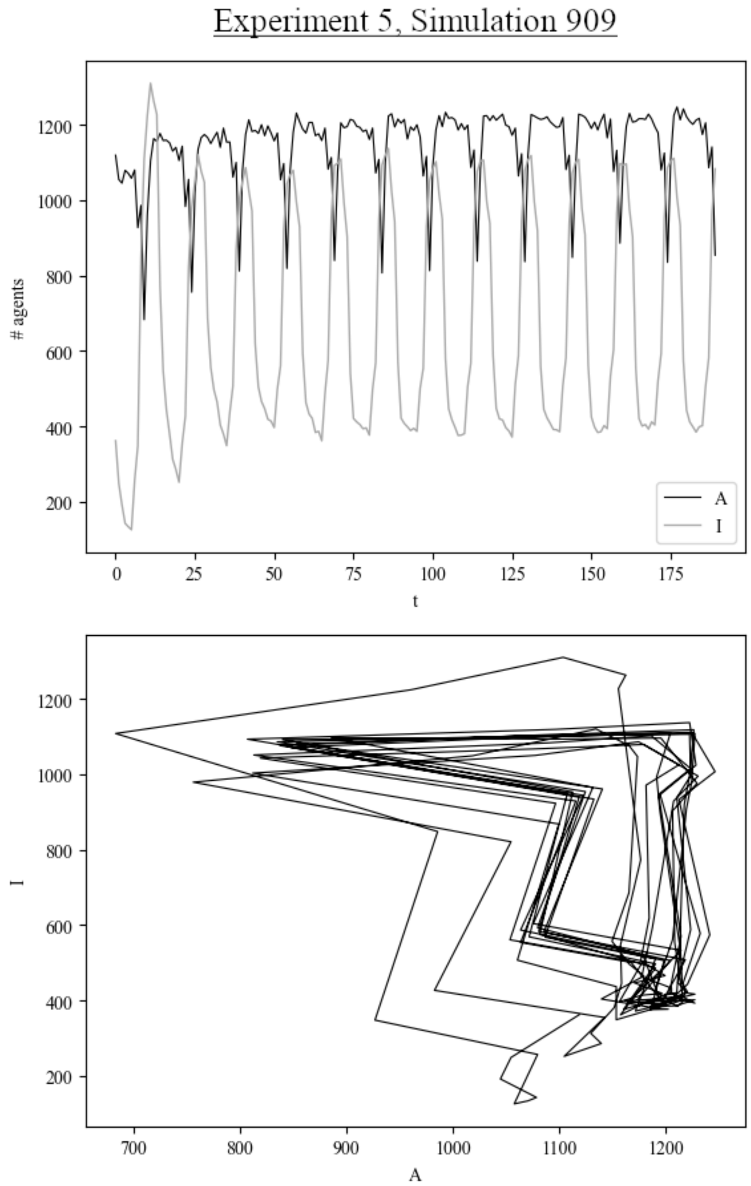

Figure 6: An example of simulations presenting a periodical behaviour (time-series and state-state)

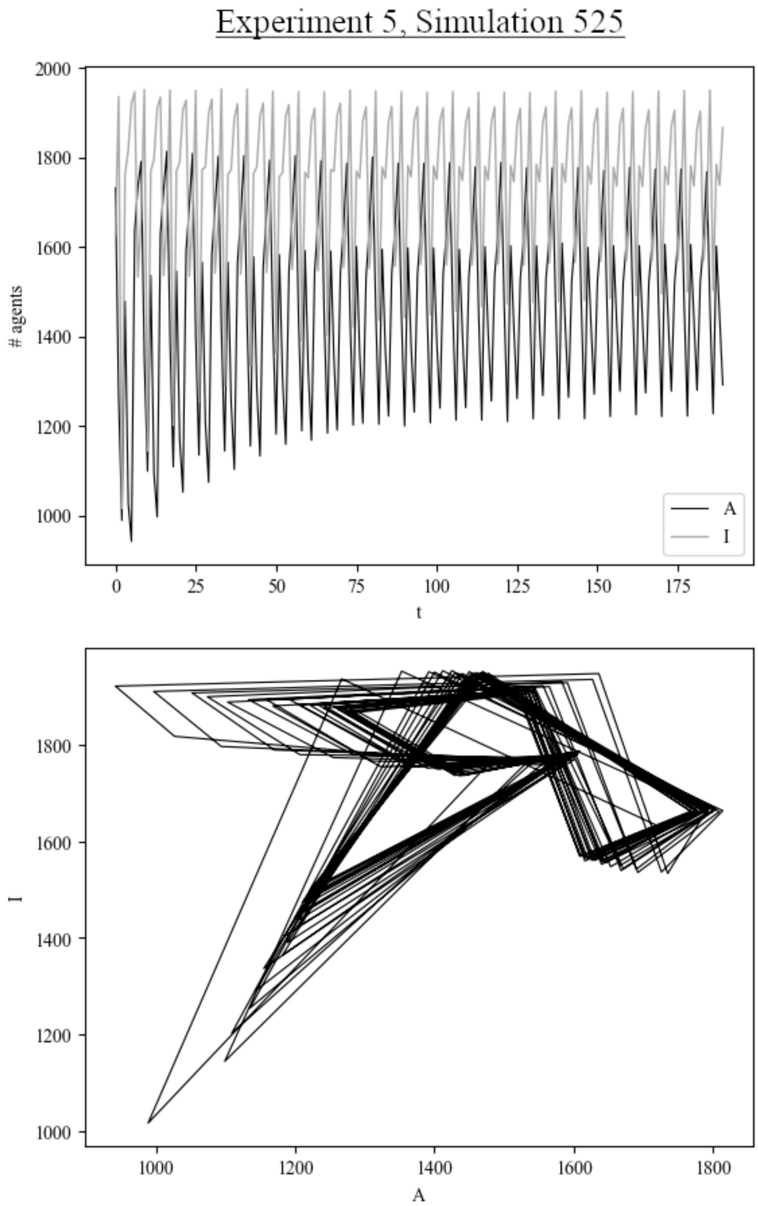

Figure 7: An example of simulations presenting a periodical behaviour (time-series and state-state)

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