

CITS4403 Project Report

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Infectious Disease Avoidance Modelling

1 Problem Statement

1.1 Background and Motivation

We are focusing on some of the ideas discussed in Weston et al. [13] concerning infectious disease modelling and the behaviour of individuals in such a model.

Specifically, the model chosen to simulate is that of the tendency of a population to avoid those they know are infected with a disease. We aim to investigate the isolation experienced by those both infected and not. We chose this system due to not only the recent COVID-19 pandemic but also to the current spread of infectious diseases through the authors' respective social groups. Both have noticed a higher occurrence of mild-to-severe illness in the community [3] and wished to examine the potential social effects this may have.

This work has the intended impact of investigating the isolation and loneliness experienced by individuals who become unwell, focusing on the social dynamics that emerge during disease outbreaks. There was a known mental health crisis during the 2020 pandemic [1][11], and by simulating these interactions, we aim to provide insights into how disease transmission can influence social behaviors and mental well-being in real-time scenarios.

1.2 Suitability for Agent-Based Modelling

Agent-based modelling is well-suited for simulating disease spread. Each individual can be represented by a single agent, and agent interaction allows for modelling disease transmission. This approach also shows the spread of disease and stigmatization within a community as it allows observation of the actions of healthy agents such as their tendencies to avoid sickness. We can introduce parameters which control avoidance behaviours and observe the impact on agent interaction.

A simple model may use binary sick/healthy states but may include other features like incubation, immunity, and transmission periods[12]. To create a more realistic representation of virus transmission, a typical agent may or may not interact with a neighbour, allowing a chance for transmission. Each agent must make a decision if and where to move each time step, meaning the model requires an Agent-Based system.

Mathematical models exist which simulate disease spread [6], but in a case where agents must behave individually and intelligently an agent-based system is more appropriate.

1.3 Complexity of the Case for Simulation

After the COVID outbreak, a renewed interest in disease modelling arose. Some key principles many of those papers complied with included a distinction between population- and individual-level models, and the need for an agent to gather information about disease states [12]. The requirement for agents to act intelligently adds further complexity, as they must understand and respond to various environmental factors.

These complexities—such as diverse disease states, agent interactions, and adaptive behavior—make the case valuable for simulation analysis. Understanding how agents process information and navigate a complex environment enhances our ability to simulate real-world disease spread and control measures effectively, as well as provide insight into the level of loneliness experienced over time.

2 Model Design

Our model draws on ideas introduced by the Schelling model of racial segregation [9]. In our system, agents move about a grid neighbourhood based on the agent states of the neighbourhood. In Schelling's model, agents tend to cluster with agents of the same race. In our model, agents tends to avoid and move away from visibly sick agents.

The model also takes inspiration from the vision radius code in the Week 7 Lab on Agent Based Modelling [7]. In our model, vision is used to determine an agent's 8 direct neighbors and, when moving away from a sick agent, to find an empty space that is not near another sick agent in a non-toroidal manner.

Our parameter selection is informed by existing literature in the field of disease modelling. The Kermack-McKendrick model is a well-researched case of disease transmission simulation [4]. In this model the key factors identified are the transmission rate and longevity of infection. Also informing our model development is the guideline published by Verelst et al. [12]. They note how an agents information gathering system is vital to their action in the simulation.

Stated simply, our model design follows a grid layout populated by several agents. Each agent has a health state and associated variables determining how long they remain in that state. At each time step, an agent may interact with any of its 8 neighbours - if it has any - providing an opportunity for disease transmission and contributing to a reduction in loneliness of the agents. After any transmission, agents may move to empty spaces in the grid as they try to avoid the disease. The initial configuration of this grid is a random assortment of cells populated by the agents, where some -usually 2- agents are initialised as incubating to begin the infection spread. Each agent also holds a loneliness attribute. At each step, the loneliness of an agent is given by the formula

$$1 - \frac{x_1 + x_2 + x_3}{24}$$

where x_1 is the number of neighbouring agents, x_2 is the number of neighbour-initiated interactions, and x_3 is the number of agent-initiated interactions.

2.1 Complexity Reflection

The model's complexity stems from the interaction between disease dynamics and social behavior, both of which are influenced by varying factors. By simulating these interdependencies, the model captures the unpredictable nature of human interactions during disease outbreaks and helps explore how agents prioritize physical health over social health in different contexts. The key contributing factors belong to two primary classes, disease modelling and social interaction modelling.

2.1.1 Disease Modelling Factors

There are several parameters implicit to the disease itself which can be modified to examine the resulting effect on interaction and loneliness. We can alter the incubation, immunity and transmission periods, changing the time agents remain in certain states and for how long they are able to transmit the disease. Each disease would also have a likelihood for transmission - contagion. Researchers have noted that many Disease Transmission models end up being disease dependent [12], so we shall consider several diseases to determine any model bias.

2.1.2 Social Interaction Modelling Factors

The primary aim of our simulation is to investigate the impact these illnesses have on the loneliness of the agents in the system. To better model this, it is important to consider several social factors when building our model. Depending on the severity of the illness being spread, an agent may choose to not interact at all if they are concerned they make others ill. Similarly, if the illness is severe, agents may be more likely to avoid sick agents in the model. The 'visibility' of the disease may make it harder or more difficult to tell who is sick, impacting who an agent chooses to interact with.

When calculating loneliness, a differentiation was made between agent and neighbor initiated interactions. This was done such that the model would be more accurate to the nature of social interaction as, most often, interactions are initiated by one person. This improves the realism of the model by more closely conforming to real-world scenarios.

3 Simulation Results and Analysis

3.1 Visualisation

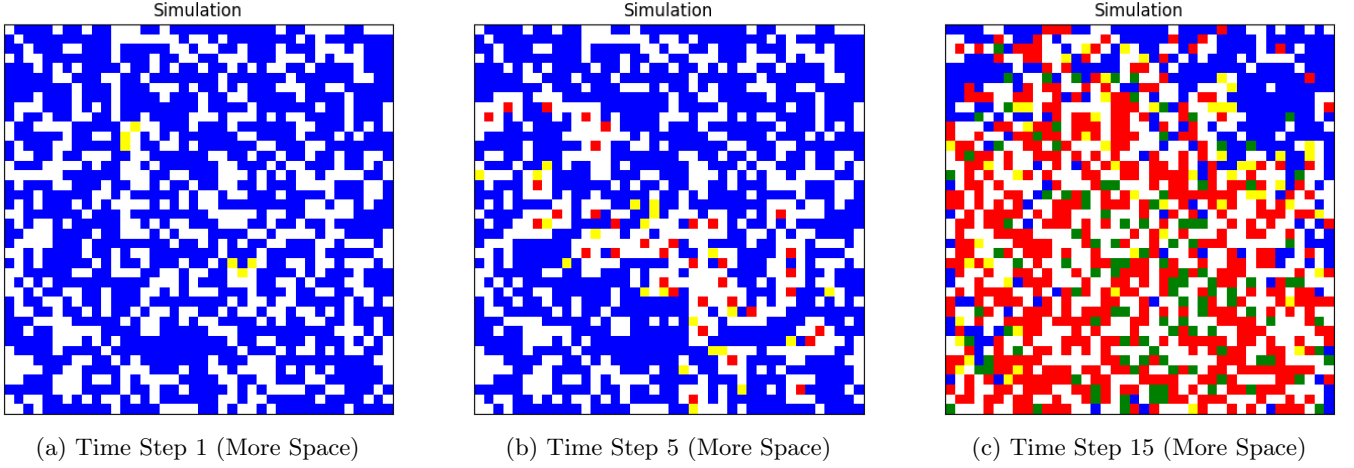
To see the evolution of the simulation over time we use a coloured grid as seen in Figure 1. Here, blue agents are healthy, red are infected, yellow are incubating and green are immune.

In this visualisation alone, particularly in Figure 1b, we can clearly see how visibly sick agents tend to be lonelier than others. Particularly, in environments where the spread of disease is more under control - such as the time step in Figure 1b - the few visibly sick agents are excluded from the general populous, and non-visibly sick agents have a tendency to cluster together. This clustering is an emergent quality of the model as it is not present in the code.

3.2 Quantitative Analysis

The desired dependent variable is the loneliness of the agents, reflected through a scaled weighted sum of their number of neighbours and number of interactions. This can then be represented as an average over time as depicted in Figure 2a. Another variable useful in quantitative analysis is the number of sick agents, as shown in Figure 2b. By having quantified these two variables, we can observe that they are closely related. A peak in average loneliness occurs at

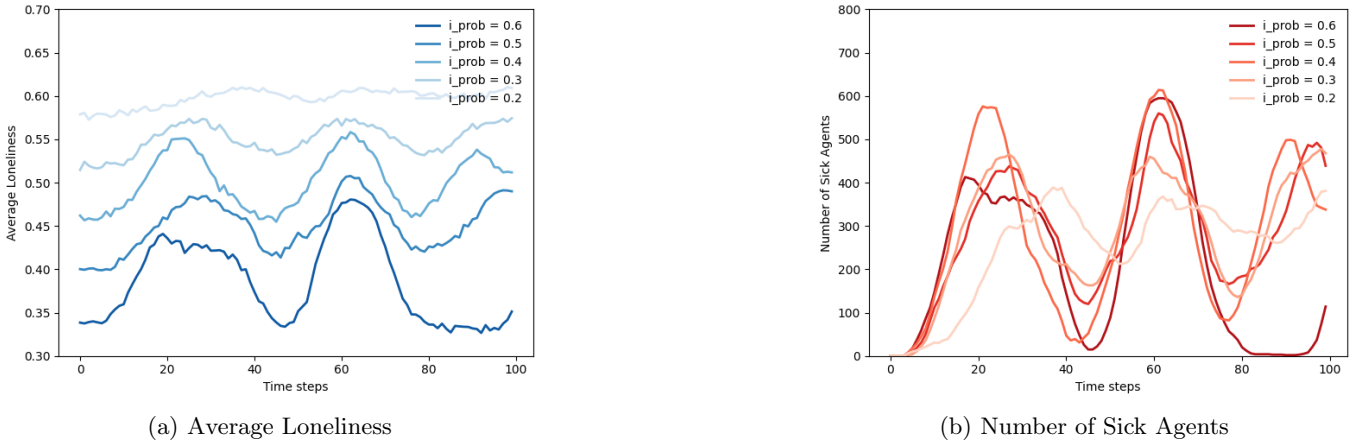
Figure 1: Modelling COVID-19



the same time as a peak in the number of sick agents. This tells us that the number of sick agents is proportional to the population's average loneliness. This is discussed further in Section 3.3 Parameter Impact.

In this quantitative analysis, we can also observe that, roughly, as the interaction probability increases, so does the number of agents, showing how social interaction comes at the expense of disease susceptibility, and validating motivations for social distancing within high-risk environments, such as the COVID-19 Pandemic.

Figure 2: Quantitative Analyses Over Time - COVID19



3.3 Parameter Impact

There are several parameters used to represent the complexity of the system. The probability of interaction between two agents is used to reflect both adherence to social distancing and fear of illness. For more severe diseases agents may be more likely to avoid interactions but may risk it if they do not feel much danger. The probability of transmission defines how likely the disease is to be spread during interaction. The immunity and incubation periods ensure more realistic depictions of disease transmission in a large environment, where illness doesn't manifest immediately and becoming 'well' prohibits an agent from becoming sick again immediately afterwards. The sickness period is disease dependent and describes the period in which an agent presents as sick to other agents and also when they are contagious. Alongside these agent parameters are simulation specific parameters. These are the number of time steps completed, the size of the neighbourhood grid and the population size within the model.

With these parameter choices, we model two representations of disease based on existing illnesses. The parameters for the common cold are informed from various sources. The transmission and immunity period are taken from medical journals and government sites [10, 8]. Other social parameters such as probability of interaction are informed by typical procedures put in place around outbreaks. In the case of the common cold, people may choose to isolate but are not likely to do so, reflected in this parameter. COVID-19 is also modelled as the more severe illness considered. The parameters for this case are modelled to reflect the more contagious, longer-lasting and more severe disease [2, 5]. For these reasons, the probability of transmission is higher, interaction is lower, and transmission period is longer. Each agent's maximum vision radius was also increased to model this sense of increased hyperawareness and a more conscious effort to practise social distancing. The results for each disease parameter set are provided:

3.3.1 Common Cold

Figure 3: Impact of Cold Parameters on Loneliness

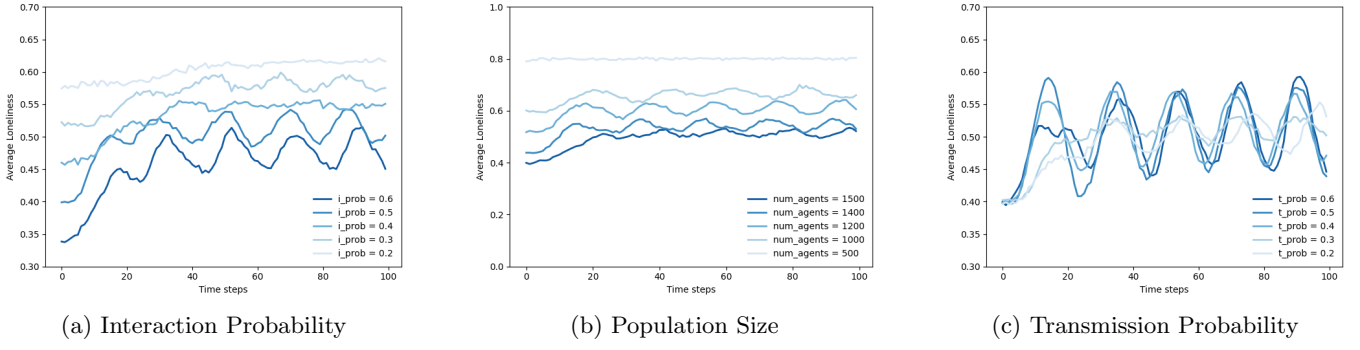
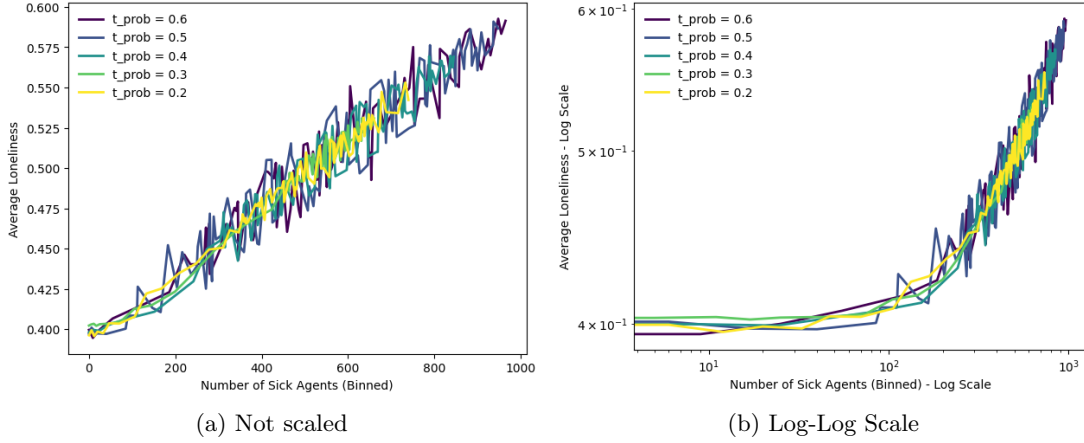
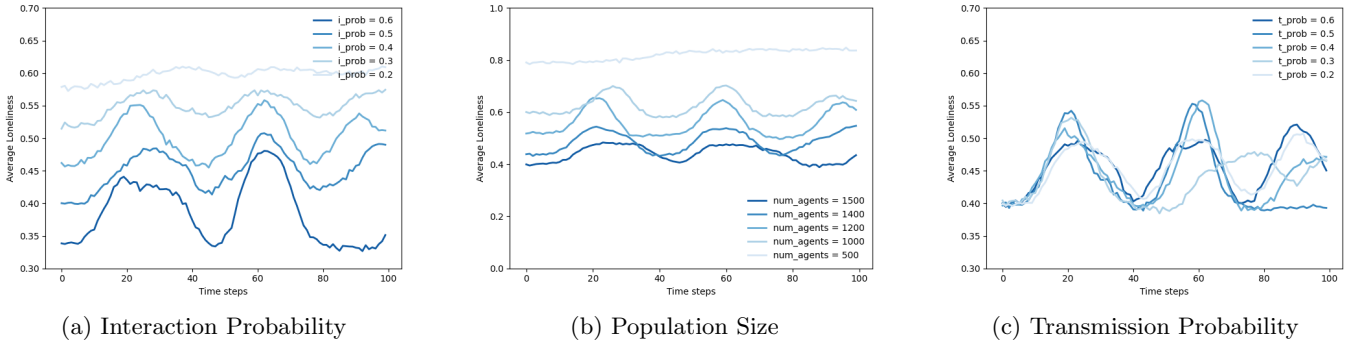


Figure 4: Modelling Average Loneliness against Number of Sick Agents, under the impact of transmission probability of Cold



3.3.2 COVID-19

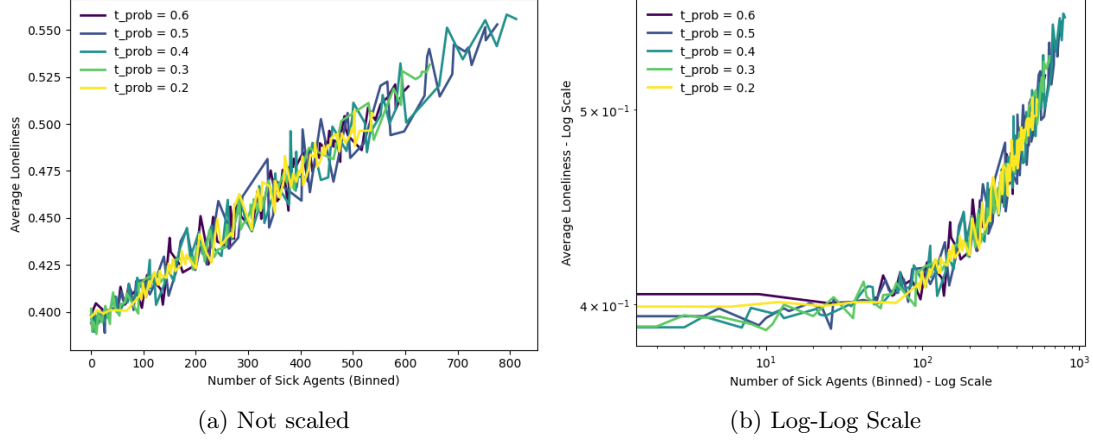
Figure 5: Impact of COVID Parameters on Loneliness



Figures 3 and 5 both show how loneliness and disease transmission are correlated. As more agents become infected, their interactions decrease and their loneliness score increases. The difference between the two lies within the frequency of peaks and the height of optima. The common cold parameters, with a lower severity and shorter sickness period, result in numerous optima during the simulation lifetime. The COVID parameters, while not peaking as often, have a higher impact on the loneliness of agents in comparison to the common cold.

As previously mentioned, it appears that the Average Loneliness of a population is proportional to the number of sick agents within that population. In Figures 4 and 6, these two variables have been plotted against each other (for both diseases modelled), whilst observing how changes in transmission probability affect this proportionality. Observably, the plotted graphs justify this aspect of the model - there is an evident trend that as the number of agents increases, so does average loneliness; and an increase in transmission probability further cements this understanding.

Figure 6: Modelling Average Loneliness against Number of Sick Agents, under the impact of transmission probability of COVID



This positive linear distribution is justified even further by the log-log scale plots in Figures 4b and 6b, showing an exponential growth curve in log scale, matching the positive linear distribution. Once again, accounting for how Average Loneliness is proportional to the Number of Sick Agents.

3.4 Real-World Reflection

Our results of a cyclical pattern of emergence with disease transmission is consistent with what is expected from literature [6], and also with what is observed in real-world cases. The several waves of the COVID-19 outbreak is reflected by the outcome of our simulation. The loneliness pattern is also reflective of real-world scenarios. During periods of isolation and quarantine, affected individuals exhibited a decline in mental health [11].

4 Conclusion

4.1 Summary

In this project we have developed an Agent-Based Modelling system to monitor loneliness of agents during disease transmission. Several parameters are used which address the disease modelling and social complexities of the system in order to best simulate real-world scenarios. Our findings through this model align with existing literature, where as the simulation continues the prevalence of the disease cycles alongside the loneliness of the agents. Each of the parameters has an impact on agent loneliness and disease transmission, where the primary effect can be summarised as the more 'severe' disease parameter sets have a greater impact on the loneliness of agents.

4.2 Limitations

Our model is limited in some aspects of sickness realism. One aspect in particular is the immunity period. In the real world, depending on the illness and the person's immune system, it may take a long time to become susceptible to the same illness once again. In our model, if we were to set the immunity period to a much higher value, it would cause the disease to die out. To prevent this from occurring we would have to make our population size much larger, and the simulation would have to run for a lot longer. If we were to do this, the process would have been much more computationally expensive, and thus we resorted to this simplified version of the immunity period such that the element of disease spread was present in our model.

4.3 Future Work

This work may be extended for the analysis of loneliness based on several features. Further mental health parameters may be used such as anxiety to simulate vulnerable classes and determine interaction, which may then have a relationship with how the loneliness attribute is updated. The loneliness calculation may also be altered to reflect a different measure of quantifying loneliness and fit better with the specific context.

The model could also consider how loneliness impacts the decision-making process. I.e., A more lonely individual may be more likely to risk an interaction with someone and is likely to follow a cyclical pattern of cresting and falling loneliness. This was considered for the model however, it is somewhat out of scope as it would explore how loneliness-motivated interactions affect the spread of disease, modeling a chain reaction between disease avoidance and disease spread rate.

A Appendix

A.1 All Graphs for Common Cold

Figure 7: Impact of Cold Parameters on Loneliness

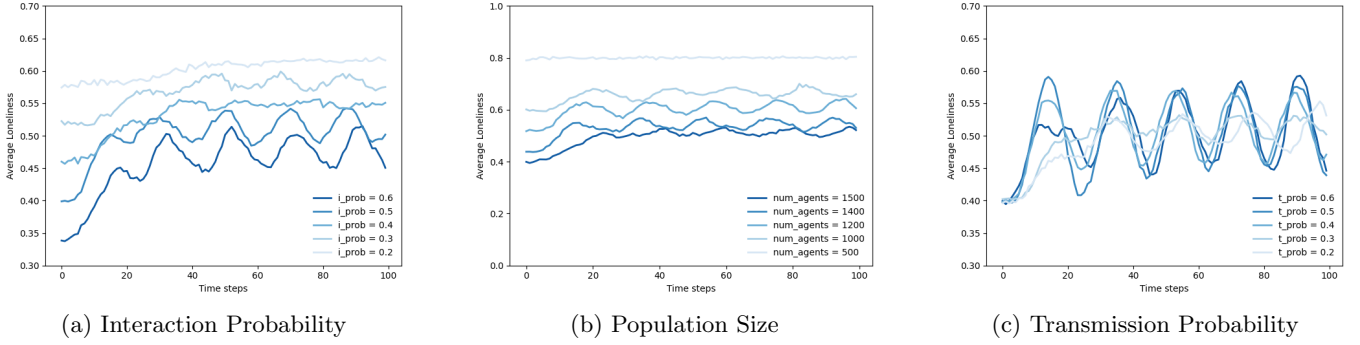


Figure 8: Impact of Cold Parameters on Sickness Proportion

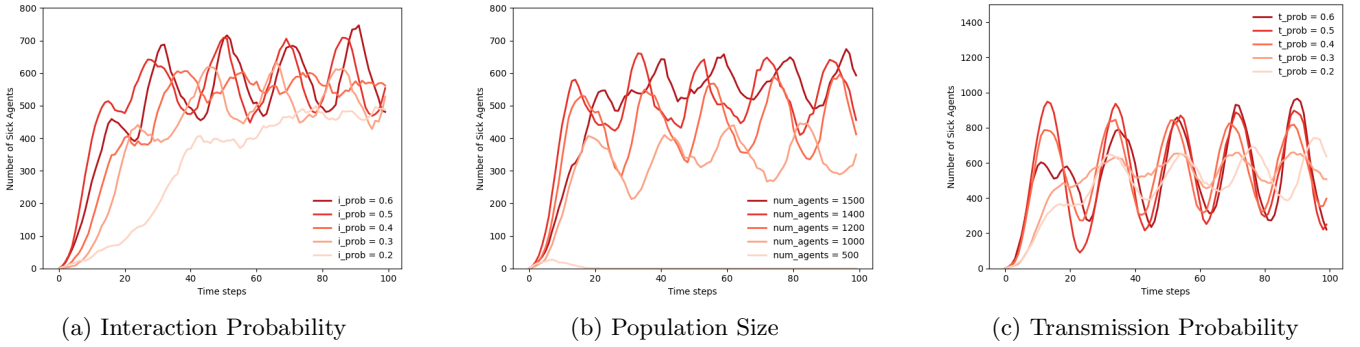


Figure 9: Impact of Cold Parameters on Loneliness vs. Sickness

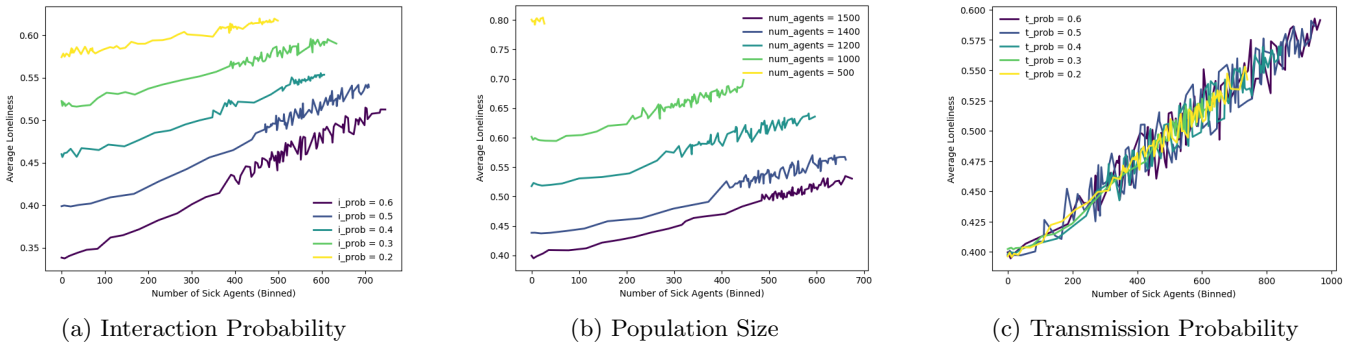
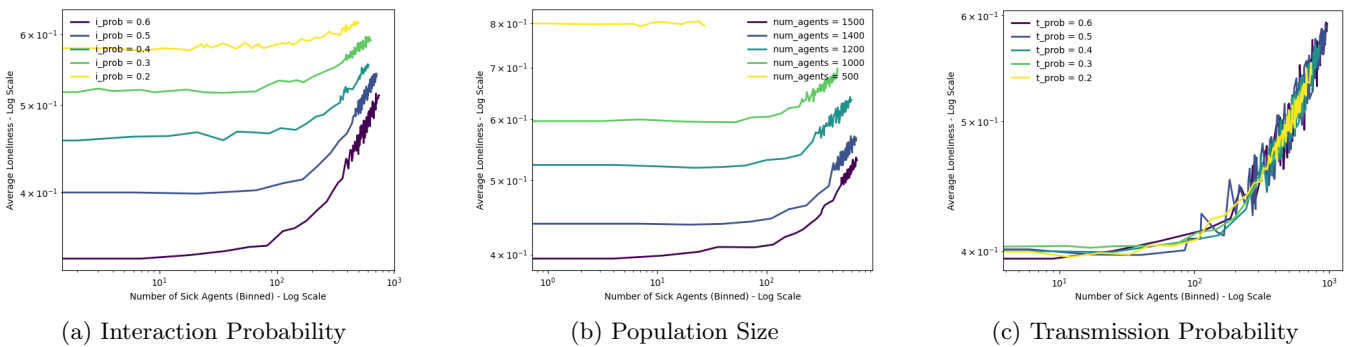


Figure 10: Impact of Cold Parameters on Loneliness vs. Sickness Log



A.2 All Graphs for COVID-19

Figure 11: Impact of COVID Parameters on Loneliness

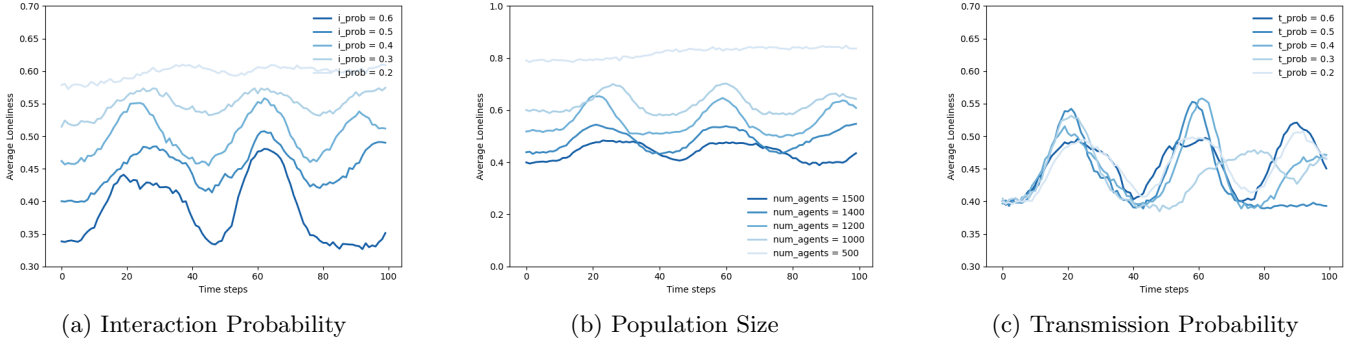


Figure 12: Impact of COVID Parameters on Sickness Proportion

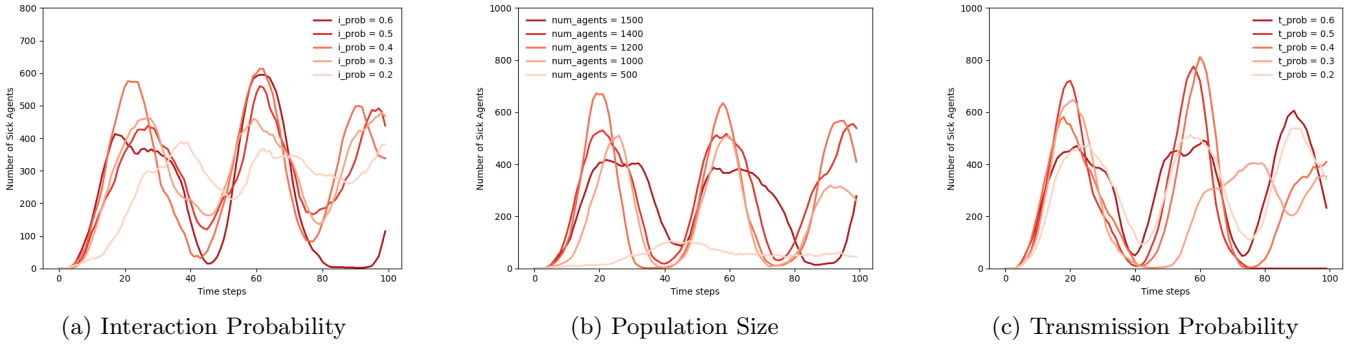


Figure 13: Impact of COVID Parameters on Loneliness vs. Sickness

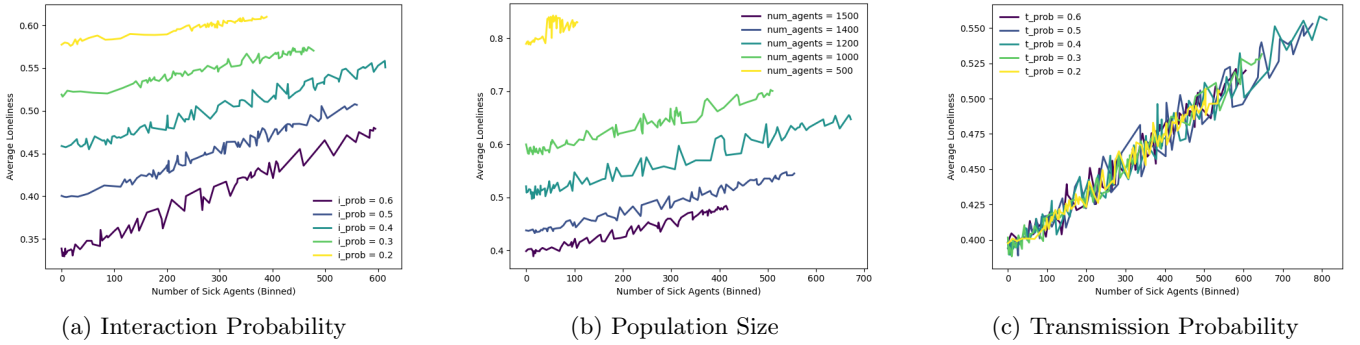
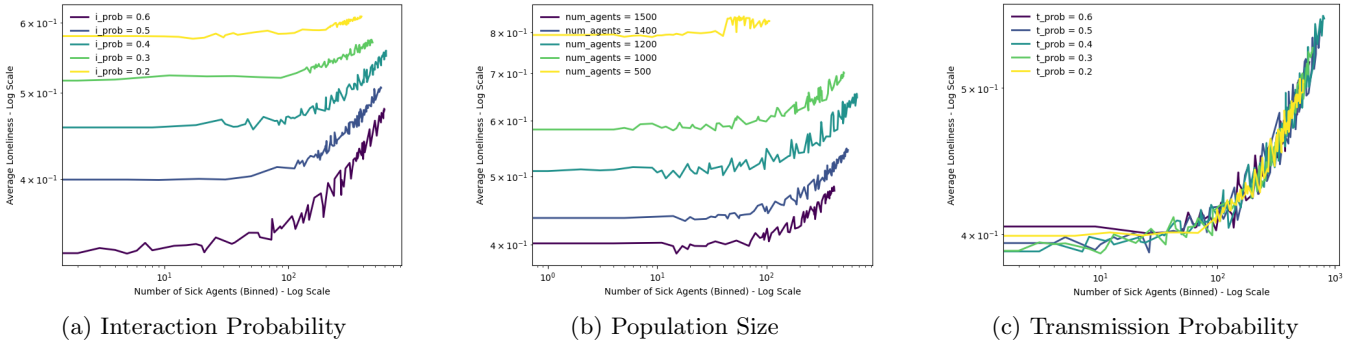


Figure 14: Impact of COVID Parameters on Loneliness vs. Sickness Log



References

- [1] COVID-19 pandemic triggers 25% increase in prevalence of anxiety and depression worldwide — who.int. <https://www.who.int/news/item/02-03-2022-covid-19-pandemic-triggers-25-increase-in-prevalence-of-anxiety-and-depression-worldwide>.
- [2] How to avoid catching COVID-19. <https://www.nhs.uk/conditions/covid-19/how-to-avoid-catching-and-spreading-covid-19/>.
- [3] Australian Bureau of Statistics. Health conditions prevalence. <https://www.abs.gov.au/statistics/health/health-conditions-and-risks/health-conditions-prevalence/latest-release>.
- [4] F. Brauer. The kermack–mckendrick epidemic model revisited. *Mathematical Biosciences*, 198(2):119–131, 2005.
- [5] S. Collins and E. Starkman. Coronavirus incubation period. <https://www.webmd.com/covid/coronavirus-incubation-period>, Feb 2020.
- [6] J. F. Fontanari. A stochastic model for the influence of social distancing on loneliness. *Physica A: Statistical Mechanics and its Applications*, 584:126367, 2021.
- [7] S. Luo. CITS4403 week 7 lab code, 2024.
- [8] SAHealth. WWC Q&A. <https://www.sahealth.sa.gov.au/wps/wcm/connect/>.
- [9] T. C. Schelling. Dynamic models of segregation†. *The Journal of Mathematical Sociology*, 1(2):143–186, 1971.
- [10] J. Seladi-Schulman. How long is a cold contagious?, Jul 2024.
- [11] D. Talevi, V. Socci, M. Carai, G. Carnaghi, S. Faleri, E. Trebbi, A. di Bernardo, F. Capelli, and F. Pacitti. Mental health outcomes of the covid-19 pandemic. *Rivista di Psichiatria*, 55(3):137–144, 5.
- [12] F. Verelst, L. Willem, and P. Beutels. Behavioural change models for infectious disease transmission: a systematic review (2010-2015). *J. R. Soc. Interface*, 13(125):20160820, Dec. 2016.
- [13] D. Weston, K. Hauck, and R. Amlôt. Infection prevention behaviour and infectious disease modelling: a review of the literature and recommendations for the future. *BMC Public Health*, 18(1):336, Mar. 2018.