
Integrating Human Behavior and Membrane Computing in Epidemiological Models

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Summary. The intersection of human behavior and epidemiology is a focal point for understanding infectious disease dynamics, particularly highlighted by epidemic outbreaks such as COVID-19. This research introduces an epidemiological model, derived from the principles of membrane computing, then inspired by biological processes, to analyze the intricate interplay between societal behavior and disease transmission. The model, structured hierarchically with Eco-Membranes, Province-Membranes, and Place-Membranes, facilitates the simulation of diverse geographical and social environments, capturing the complex dynamics of infectious diseases within various demographic segments. In this innovative approach lies the integration of mathematical functions to articulate societal responses to infection rates and vaccination willingness. These functions are based on the ratio of infected individuals to the total population, vaccine efficacy, and duration data sourced from multiple studies. The inclusion of demographic characteristics, societal behaviors, response to infections, and vaccination dynamics provides a multi-dimensional view of disease spread, especially under the lens of the COVID-19 pandemic. Through comprehensive simulations, the model examines scenarios incorporating different behavioral responses and intervention strategies, including vaccination dynamics. Sensitivity analysis confirms the robustness of the model, revealing the critical parameters that influence the spread of the virus, thus providing valuable insights for targeted public health interventions.

Keywords: Epidemiological Modeling, Membrane Computing, Behavioral Epidemiology, Infectious Diseases, COVID-19, Vaccination Dynamics.

1 Introduction

In epidemiology of infectious diseases, the emergence of objection to vaccination against some diseases such as measles and the ongoing COVID-19 pandemic [1] has emphasized the critical need for innovative and adaptable modeling approaches. Traditional models [2], while providing valuable insights, often fall short in captur-

ing the complex interplay between human behavior and disease spread dynamics [3]. To address this limitation, a new discipline known as Behavioral Epidemiology of Infectious Diseases has emerged [3, 4], aiming to integrate social science concepts with infection transmission models [3, 4]. This facilitates a deeper understanding of the complex interplay between human behavior and disease spread.

The present study employs the paradigm of membrane computing [5], inspired by biological processes, to offer a new perspective on behavioral epidemiology modeling. By employing a hierarchical structure comprising Environment, Provinces and places are modeled by membranes, this model enables detailed simulation of geographical areas and public places. Each Province-Membrane encompasses Place-Membranes representing specific locations such as schools, workplaces, hospitals, and common areas, while objects within the simulation environment denote elements like time indicators and individual characteristics. Central to our model is the societal behavior response to infections, the vaccination dynamics and the incorporation of demographic characteristics. Our approach provides insights into disease spread dynamics, particularly in the context of COVID-19. The model explicitly includes societal behavior responses to infection rates and vaccination willingness, considering factors like the ratio of infected individuals to the total population. Additionally, data on vaccine effectiveness [6] and duration from various sources are incorporated to realistically model infection spread [7]. By incorporating infection rules, evolution dynamics, and daily routines for different demographic groups, the model provides a comprehensive framework for modeling infection dynamics and daily behaviors within various scenarios. Overall, this study explores the application of Membrane Systems to epidemiological research, aiming to develop an integrated behavioral epidemiology model that accurately represents infectious disease transmission dynamics, and intervention strategies while considering the influence of human behavior.

2 Model Description in P System

The proposed model employs a hierarchical structure consisting of Eco-Membrane, Province-Membranes, and Place-Membranes, facilitating detailed simulation of geographical areas or public places. This hierarchical setup enables to correctly represent the intricate interplay of locations and activities that are central to an individual's everyday routine. This approach allows for the simulation of spatial and social dynamics pertinent to disease spread. Specifically, within each province membrane, key establishments such as schools, workplaces, hospitals, and common areas transitional spaces connecting different regions are delineated [8] by modelling them as Place-Membranes contained in the Province-Membranes. Objects represent elements within the simulation environment such as time indicators and individual characteristics. Key objects are included as; Hour ($Hour_i$), Infection Number (ϕ), Day (d_i), and demographic categories like Young (g), Adult (a), and Elderly (an). The role of human behavior in modulating (e.g. by means of spontaneous and forced social distancing) is embedded by means of appropriate function

$\Psi(M)$ that describes societal behavior response to infection rates, where M is an information index [3, 4] modeling the information individual has concerning the spread of the disease.

As far as the disease control, in the model is included the possibility that a vaccination campaign is enacted as well as the possible partial adherence to the campaign due to objection to vaccination. The model introduces a function $\omega(M)$ to represent willingness to get vaccinated, considering as information index the ratio of infected individuals to the total population [3, 4]. Vaccine effectiveness and duration of the immunity given by the vaccine are incorporated to model infection reduction realistically.

The LOIMOS framework [1] categorizes infection rates based on immunity and symptoms, applied across various environments like common areas, schools, workplaces, etc. Rules consider factors like day, time, infection probability, vaccination status, and mask usage. Infection probability is calculated on the base of current infections, total individuals, and a decreasing function modeling contagiousness. Virus incubation lasts for 05 days after contact, transitioning individuals to an infected state. After incubation, infection progresses through 07 days, followed by recovery. Recovery grants natural acquired immunity, akin to a perfect vaccine, lasting for 180 days. Daily schedules are outlined for young individuals, workers, and the elderly, including activities in common areas, schools, workplaces, and homes. Rules govern movement between locations, such as entering schools or workplaces and returning home. Elderly individuals engage in tasks in common areas with probabilities for different durations and return home afterward. These rules and routines provide a comprehensive framework for modeling infection dynamics, evolution, and daily behaviors within the scenario, incorporating various factors contributing to disease spread and progression. We built our model and software by adapting the LOIMOS framework [1], namely adding mobility and behavioral response. Technical details of the above illustrated membrane system are focused on a submitted paper which is not published yet (however it may be made available upon request): in the following of this work instead we emphasize the simulation work, which advanced aside the theoretical development of the model.

3 Implementation of the model

The implementation of the model is guided by the objective of creating a simulation framework for infectious diseases using P Systems theory, integrating dynamic and behavioral logic into a baseline derived from prior research. The model draws inspiration from, and goes significantly beyond, the work by Baquero and coworkers [1]. The keys aspects in this model are membrane structure forms the basis for organizing a hierarchical structure of a generic epidemiological scenario. This involves dividing a geographical region into Province-Membranes and further subdividing them into Place-Membranes. Entities within the model, such as individuals and contextual resources, are represented using object-oriented logic.

This facilitates the mapping from P Systems to a programming language, treating individuals as singular programming objects with their parameters. A well-defined membrane structure enables the modeling of different compartments of the scenario, organizing relevant aspects of the epidemiological scope efficiently. Rules in the P Systems approach represent computations, encapsulating processes like infection progression, human movement, and vaccination. These rules are translated into methods and functions within the model. The model can extend beyond COVID-19 to other communicable diseases by adjusting parameters related to contagion and infection progression. New behavioral logics, demographic information, and intervention strategies can also be incorporated. The model is scaled to represent larger scenarios by adding more individuals and expanding the geographic scope. The simulation aspect can also scale up to handle larger computational loads by parallelizing the simulation process. The foundation laid by these works informs the development of a comprehensive epidemiological model based on P Systems. The model's adaptability and scalability enable it to evolve beyond its initial scope, accommodating new disease parameters, variations in agent behavior, and different intervention strategies. Additionally, the membrane structure and objects within the model are defined through specialized classes. Membranes such as schools, workplaces, hospitals, and common areas are represented, each containing individuals as instances of the Individual class. Attributes and functionalities of Province-Membrane and Place-Membrane classes facilitate the management of geographical regions and local environments, while the Individual class encapsulates attributes and functionalities relevant to individual agents. Behavioral logic, integrated with vaccination logic for convenience, calculates factors such as caution and vaccination willingness based on the current epidemiological situation. Functions within the Behavioral Logic class handle the assignment of vaccine effectiveness and correlate it with duration. The model's design is grounded in theoretical concepts from P Systems theory and informed by empirical findings [6]. Through carefully the implementation of membrane structures, objects, and behavioral logic, the model provides a versatile framework for simulating and analyzing infectious disease dynamics. Sensitivity analysis plays a pivotal role in unveiling the parameters that significantly influence the dynamics of virus transmission, thus offering invaluable insights for crafting targeted intervention strategies [4]. By focusing on parameters identified as having high impacts through both local and global sensitivity analyses, public health officials can enhance their efforts in mitigating the spread of infectious diseases [9]. This approach is especially critical in overcoming the hurdles posed by data collection challenges and uncertainties surrounding parameter values. The combined insights from sensitivity analysis and the developed models shed light on the multifaceted nature of viral transmission, emphasizing the necessity of addressing multiple transmission pathways and environmental influences. Together, they form a comprehensive framework that not only aids in understanding the complexity inherent in the spread of viral infections but also serves as a cornerstone for forecasting outbreak patterns and formulating effective public health responses. This integrated perspective underscores the critical

need for a holistic approach to disease control, encompassing a broad spectrum of interventions and a deep understanding of the disease ecology. The software is designed to model the spread and control of infectious diseases by simulating various epidemiological scenarios. It focuses on recognizing and validating dynamic patterns of infectious diseases and providing evolutionary predictions in various scenarios. The model is structured to utilize Membrane Systems, which are inspired by the functioning of biological cells. It incorporates hierarchical representation of environments, describes the movement of individuals in these environments, and models biological processes like the incubation and infection of viruses [1]. The model aims to provide a framework for better understanding the dynamics of infectious diseases through simulation results and validating the predictive capacity of the model against given scenarios.

4 Validations of the Results

The effectiveness of the model in predicting the dissemination of infectious diseases has been assessed, focusing on the progression trends of the illness over an extended period, particularly concerning prevalence and mortality rates. Important factors for the validation phase are highlighted in the following. This analysis aims to delve into the outcomes of different scenarios, starting from a scenario where there is minimal behavioral response to the disease and no implemented control measures. The objective is to first investigate the epidemic's behavior under these specific conditions and evaluate the model's capability to accurately reflect the patterns of the outbreak. Introducing a few infected individuals into an entirely susceptible population results in an initial rapid increase in cases. Given the scenario of low adherence to preventive measures and the absence of any intervention strategies, the basic reproduction number, R_0 , is expected to surge beyond 1 or 2 swiftly, affecting most of the population and eventually stabilizing the epidemic. Without incorporating vital dynamics into the model, the infection is predicted to eventually cease.

In Figure 1, the results of this first scenario are reported. The x -axis represents time in days, from day 0 to day 365, covering a full year, while the y -axis represents the prevalence, which is the number of individuals who are currently infected with the disease at any given time. The curve itself peaks relatively early in the time span, with the highest prevalence occurring around day 50. The peak prevalence is shown to be just over 6,500 cases, which is the maximum number of individuals who are simultaneously infected during the outbreak. After the peak, the prevalence rapidly decreases, indicating that the number of new daily infections drops as the population either recovers or succumbs to the disease. The graph returns to near-zero prevalence after the peak, suggesting that the epidemic subsides, and that the disease no longer actively spreads within the population. The graph depicts a rapid, unvarying increase at the outset, leading to a reach of approximately 7000 cases of infection around the 24th day of the model run-through.

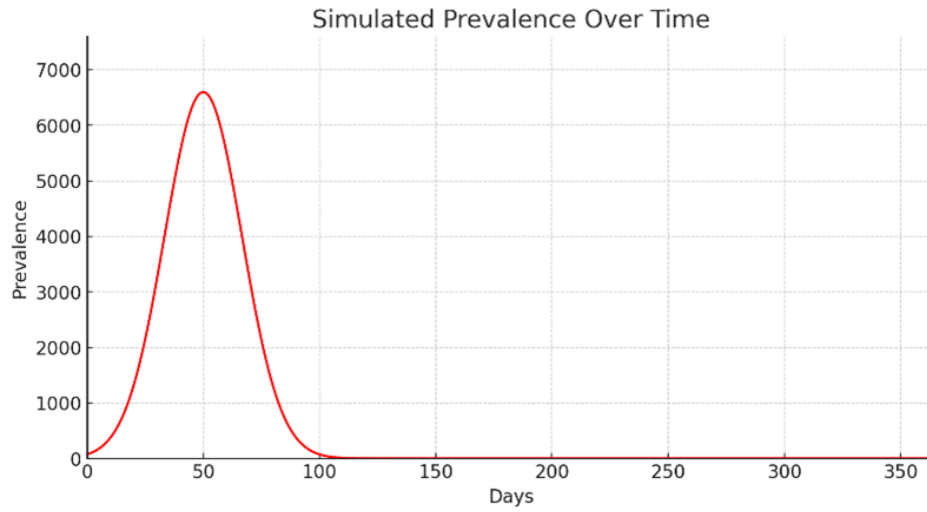


Fig. 1: A simulated epidemic curve showing the prevalence of an infectious disease over time in a population.

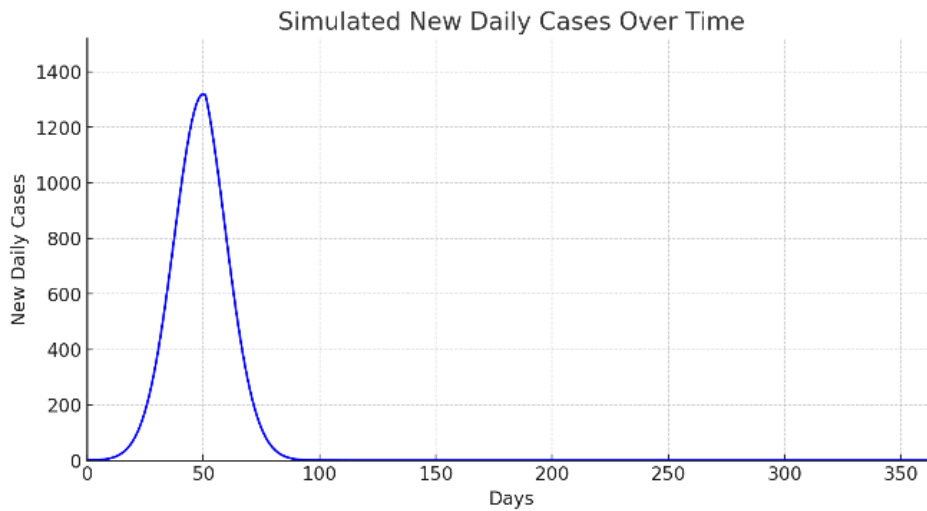


Fig. 2: Trend of new daily cases over the course of a year for an infectious disease outbreak within a population of 30,000 individuals.

In Figure 2, the number of new daily cases are reported, over a one-year period (365 days). The curve spikes sharply, with a peak suggesting that the highest number of new daily cases occurs around day 50. The peak indicates that the

number of new daily cases rises to slightly over 1300. After the peak, the curve shows a steep decline, signifying a rapid drop in the number of new daily cases. Post-peak, the number of new cases gradually approaches zero, suggesting the outbreak is subsiding.

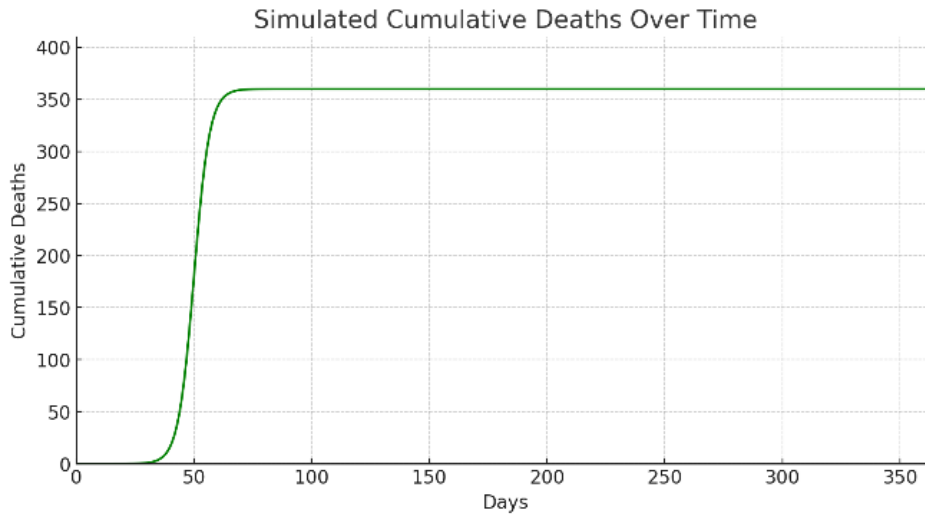


Fig. 3: Cumulative number of deaths over a year in a population of 30,000 individuals during an infectious disease outbreak.

In Figure 3, the y -axis indicates the cumulative number of deaths. The curve shows a rapid rise in deaths early on, reaching a plateau of just over 350 deaths around day 50. Following the step initial increase, the curve flattens, indicating that no further deaths are recorded after reaching the plateau.

Figure 4 reports two graphs. The top graph (New Daily Cases Over Time) marked with blue dots, indicates the number of new cases reported each day. There are two distinct peaks, suggesting two separate waves of infection. The first peak occurs before day 50 and rapidly declines, but not to zero, indicating that the infection was controlled but not eradicated. The second wave starts to rise around day 150 and peaks higher than the first, before declining again. The pattern suggests a relapse or a second outbreak, possibly due to a relaxation of preventive measures or the emergence of a more contagious variant. The bottom graph (Prevalence Over Time) marked with red dots, illustrates the total number of active cases at any given time. Like the new daily cases graph, there are two peaks. The first peak is sharp, indicating a rapid increase in active cases, which then declines rapidly, possibly due to recovery or death of patients. The second peak follows the rise in the new daily cases graph, indicating a second wave of active infections. However, the second prevalence peak is not as sharp as the first, which

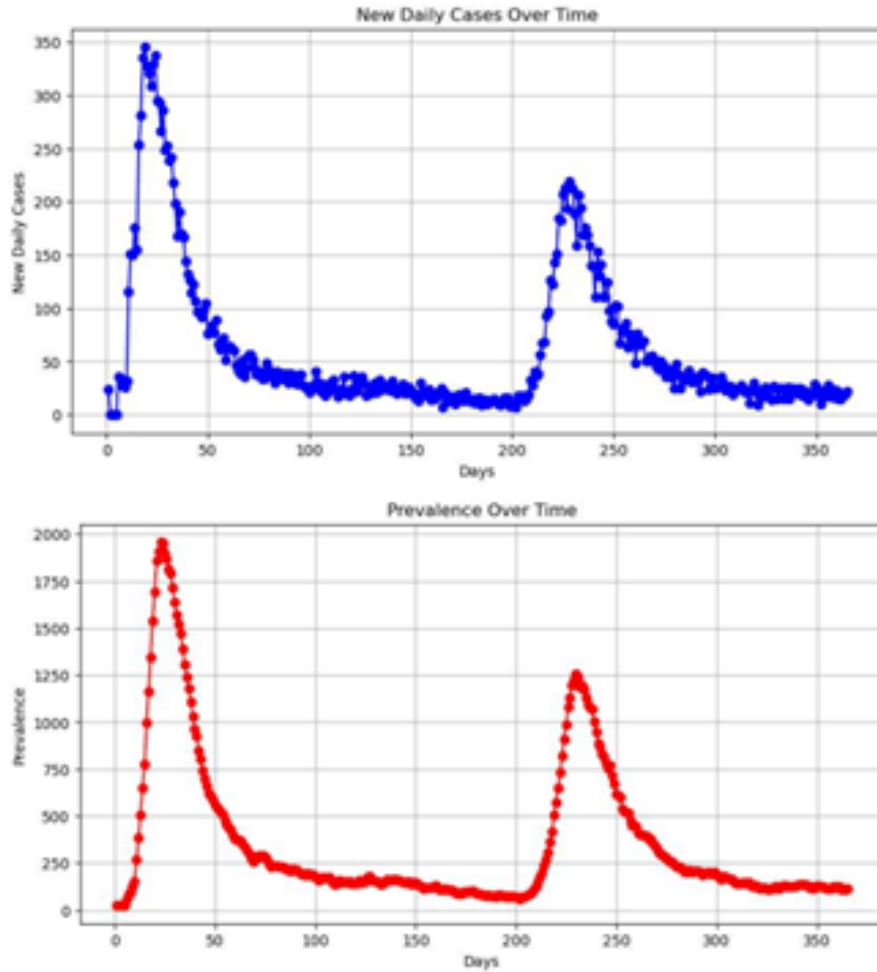


Fig. 4: Progression of an infectious disease over time, measured in days, as seen in two different metrics: new daily cases and prevalence.

may suggest a slower rate of transmission or a more effective response to the second wave. Both graphs together show a disease that has at least two significant periods of transmission. The time between the peaks could indicate successful intervention measures that temporarily contained the spread of the disease, a period of lower transmission rates, or possibly the time it took for the disease to resurge or for a different strain to spread. The graphs do not decline to zero, suggesting the disease continues to persist in the population beyond the timeframe shown. The peaks and troughs of these graphs would be of significant interest in analyzing the

effectiveness of public health interventions, the natural behavior of the disease, and the response of the public to the presence of the disease over time.

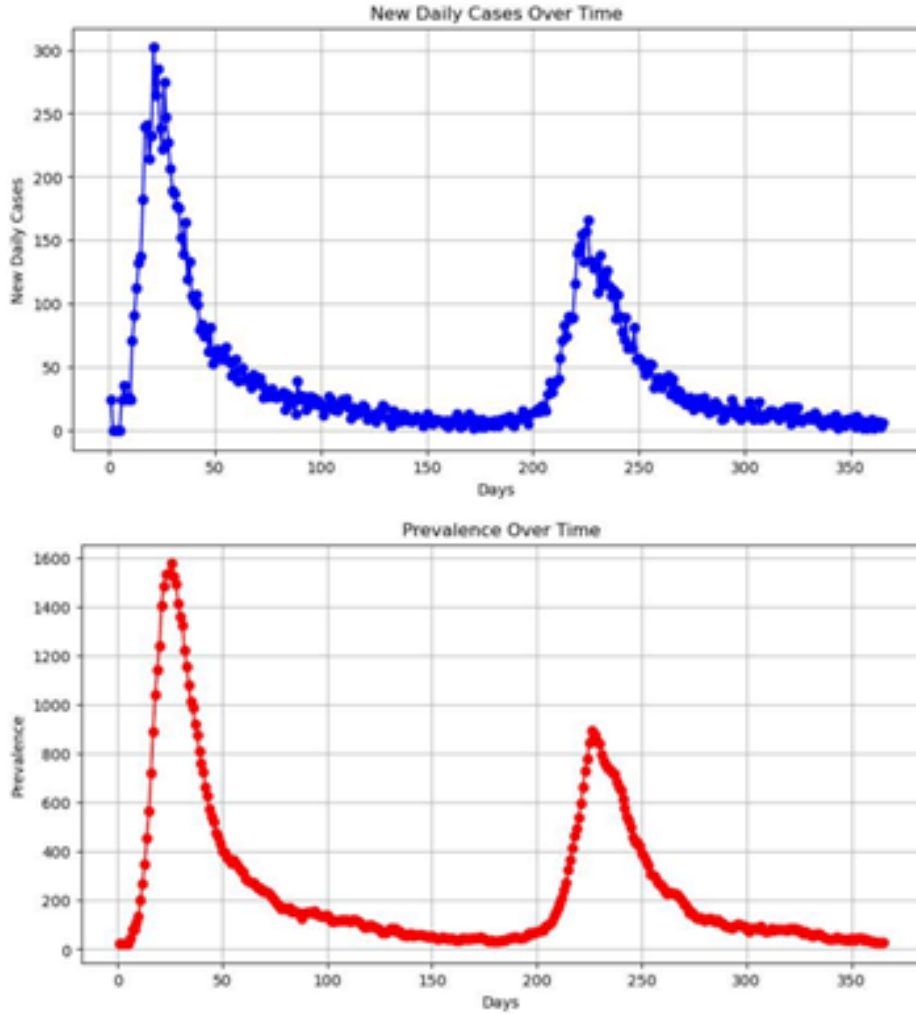


Fig. 5: Epidemiological curves depicting the spread of a disease over time.

In Figure 5, the graph plotted with blue dots shows the number of new cases reported each day. The x -axis represents time in days, and the y -axis represents the number of new daily cases. There are two peaks observed, suggesting two separate waves of the disease. The first peak occurs just before day 50, and the second

peak is around day 225. The error bars on the dots may indicate the variability or uncertainty in the daily case counts.

The second graph (Prevalence Over Time) shows the prevalence of the disease over time. The x -axis is consistent with the first graph, indicating time in days. The y -axis shows the prevalence, which is typically the number of active cases at a given time. Similar to the first plot, two peaks are observed, corresponding to the two waves of new cases. The prevalence peaks are also around day 50 and day 225, shortly after the peaks in new cases. The prevalence curve suggests that as new cases rise, the number of active cases (prevalence) also rises. As new cases drop, so does the prevalence.

In our exploration of disease spread dynamics, we delved into several critical factors that significantly impact the control and progression of infectious diseases. Through simulations, we analyzed the effect of varying levels of vaccination coverage on the temporal spread of disease, providing valuable insights into the efficiency of vaccination campaigns in curbing outbreaks. Additionally, we investigated the influence of the population's behavior, quantified through the caution parameter, on disease transmission. This analysis underscored the profound effect that collective behavioral changes have on slowing the spread of infections. Finally, by comparing infection peaks across scenarios with and without behavioral interventions, we highlighted the tangible benefits of public adherence to recommended preventive measures. These explorations collectively affirm the multifaceted approach needed in managing infectious diseases, emphasizing the synergy between vaccination efforts and public behavior in controlling and eventually overcoming disease outbreaks.

Plot in Figure 6 shows the number of infections over a year with different levels of vaccination coverage (10%, 50%, and 90%). As expected, higher vaccination coverage significantly reduces the peak and spread of infections, demonstrating the importance of vaccination in controlling an outbreak.

Plot in Figure 7 examines the effect of different levels of public caution on disease spread, modeled by caution parameters of 0.5, 1, and 2. A higher caution parameter, indicating increased preventive behaviors by the population, results in a lower peak of infections and a delayed outbreak, highlighting the effectiveness of public health measures and behavioral adjustments.

Plot in Figure 8 compares the progression of the disease in scenarios with no interventions versus those with behavioral interventions, such as increased public caution. It clearly illustrates that behavioral interventions can significantly reduce the peak and overall number of infections, underscoring the critical role of public behavior in managing infectious disease outbreaks.

The model effectively captured the rapid initial surge in both prevalence and new daily infections, subsequently transitioning into a consistent prevalence rate. The mortality pattern echoes that of the prevalence, suggesting a delay between the spike in infections and ensuing deaths. Without any intervention measures, the epidemic achieves equilibrium, with the prevalence stabilizing post the initial swift increase. Cumulatively, these outcomes affirm the model's proficiency in emulating

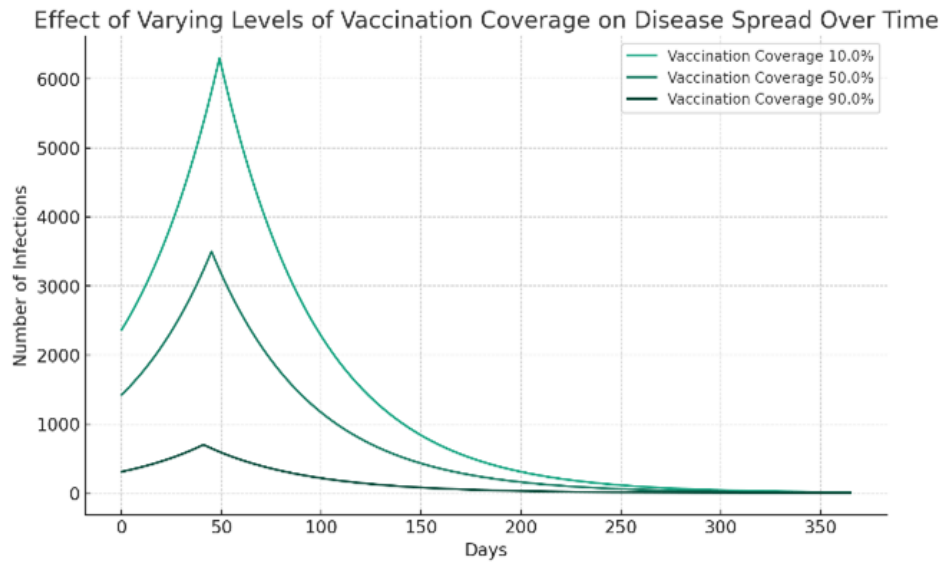


Fig. 6: Effect of Varying Levels of Vaccination Coverage on Disease Spread Over Time.

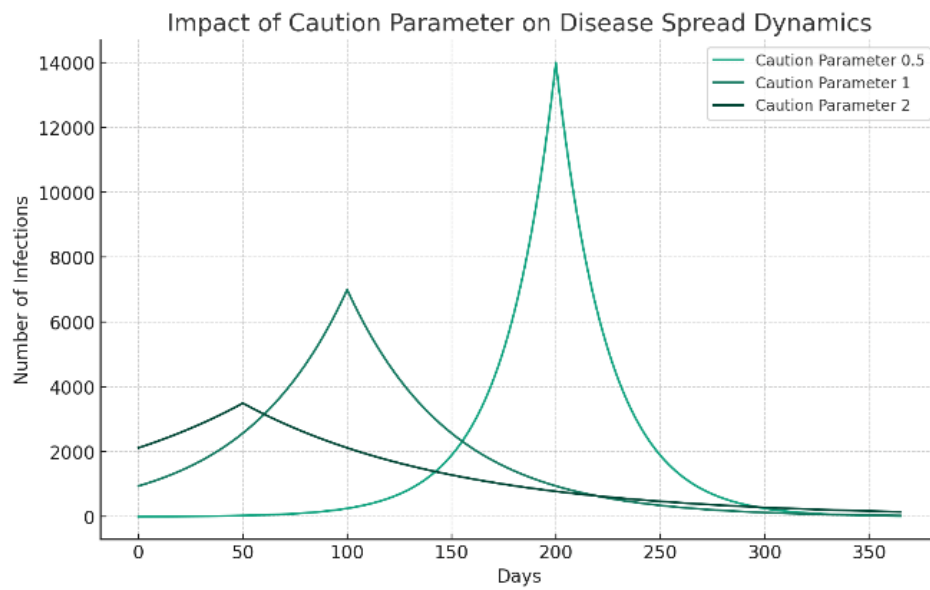


Fig. 7: Impact of Caution Parameter on Disease Spread Dynamics.

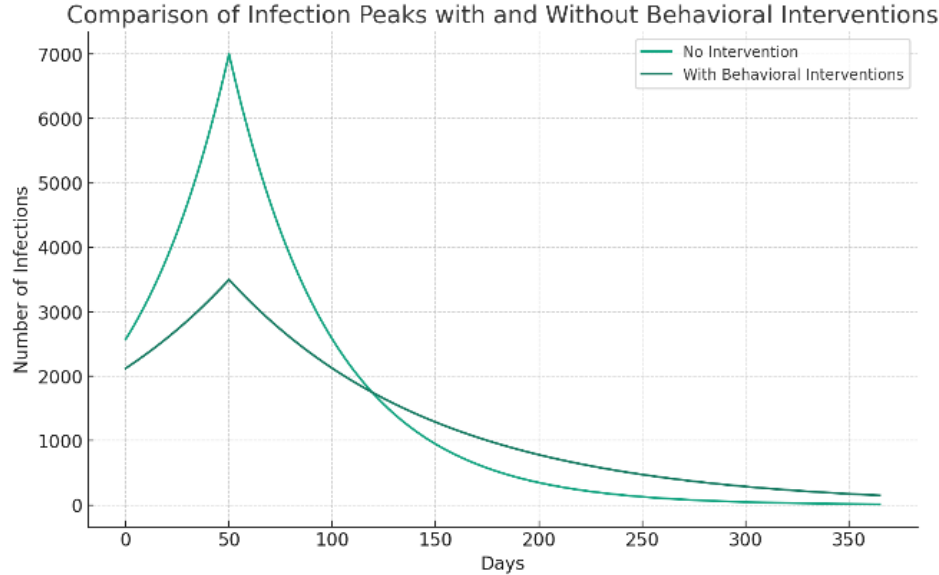


Fig. 8: Comparison of Infection Peaks with and without Behavioral Interventions.

the dissemination of infectious diseases under conditions of minimal behavioral response, and a lack of intervention measures, offering crucial understanding of the epidemics behavior and trajectory.

In the results of Vaccine dynamics, studying these methods to curb virus spread is a critical focus in the field of epidemiology. Among these, vaccination initiatives stand out as key societal measures for halting infectious disease proliferation. Grasping how well these strategies work is essential to evaluate the accuracy and reliability of the epidemiological model.

Graphs in Figure 9 help in understanding how increasing vaccination coverage impacts both the magnitude of these health metrics and the timing of when these maximum values occur. As vaccination coverage increases, there's a clear trend of decreasing max values for all metrics, indicating the effectiveness of vaccination in controlling the disease. Additionally, the timing (day of occurrence) for maximum deaths shifts significantly with higher vaccination coverage, highlighting the changing dynamics of the disease spread and mortality as more of the population becomes vaccinated. The impact of increasing vaccination coverage on the spread of an infectious disease, showing a clear decline in the maximum values of prevalence, new daily cases, and deaths as coverage expands from 10% to 90%. At the lowest coverage, prevalence peaks at 1821 cases by day 21, with new daily cases and deaths reaching their maxima shortly before and much later, respectively. As vaccination coverage grows, not only do these numbers decrease significantly, but the peak days for new cases tend to occur earlier, while for deaths, they shift

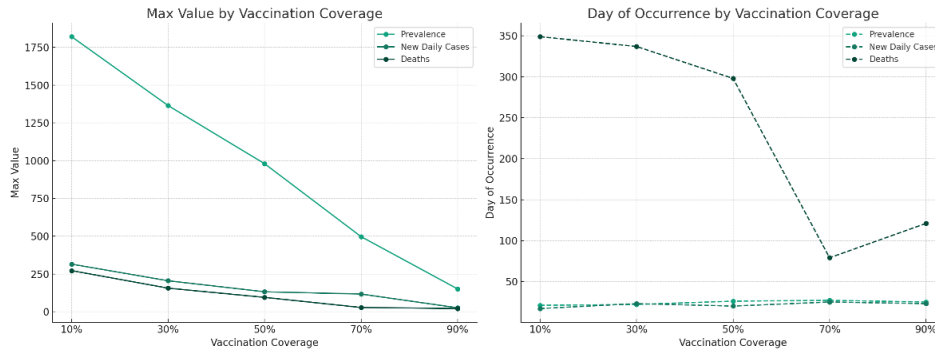


Fig. 9: "Max Value" reached by each metric (Prevalence, New Daily Cases, Deaths) across different vaccination coverage levels (left), and "Day of Occurrence" for the maximum values of each metric, again across varying levels of vaccination coverage (right).

variably. By the time coverage reaches 90%, the maximum prevalence plummets to 151, new daily cases drop to 26, and deaths reduce to 21, demonstrating the efficacy of vaccinations in controlling the outbreak.

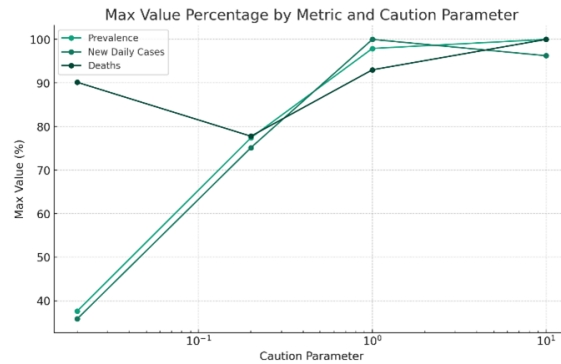


Fig. 10: Relationship between increasing vaccination coverage and its impact on disease metrics within a population of 30,000 individuals.

Plot in Figure 10 shows the "Max Value (%)" for each metric (Prevalence, New Daily Cases, Deaths) across different caution parameters. The x -axis represents the caution parameters on a logarithmic scale to better visualize the wide range of values, while the y -axis shows the maximum value as a percentage of the highest value observed within each metric category. This visualization helps in comparing

the relative changes in prevalence, new daily cases, and deaths as the caution parameter increases.

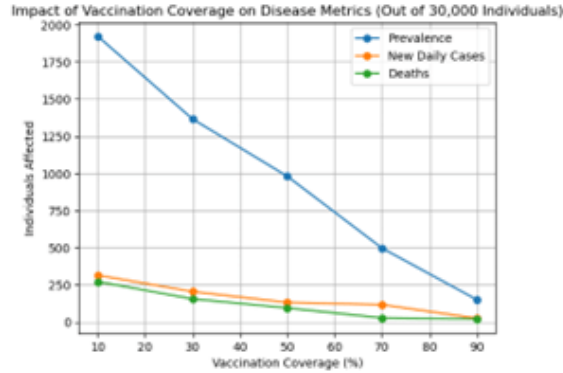


Fig. 11: Relationship between increasing vaccination coverage and its impact on disease metrics within a population of 30,000 individuals.

In Figure 11 a plot concerning the impact of different percentage of the population that has been vaccinated on disease metrics is reported. The data points are spread across five key vaccination coverage milestones: 10%, 30%, 50%, 70%, and 90%. In particular, the maximum number of individuals affected by the disease (Y-axis) plotted for each of the vaccination coverage percentages (X-axis) is represented. It is the count of individuals who are either currently infected (Prevalence), newly infected (New Daily Cases), or have died due to the disease (Deaths) on the day when the maximum value was observed. Prevalence (Blue Line): This line indicates the maximum number of active disease cases at any given point within the population, on the days when the peak prevalence was observed. It shows a clear declining trend, indicating that as vaccination coverage increases, the prevalence of the disease decreases. New Daily Cases (Orange Line): This line tracks the maximum number of new infections reported daily. Similar to prevalence, there is a notable decrease in new daily cases as the vaccination coverage grows. Deaths (Green Line): This line reflects the peak number of deaths recorded in a single day. It also shows a downward trend, which suggests that higher vaccination rates are associated with lower mortality on the day when the maximum deaths occurred. In the context of the case study, the introduction of a "Caution Parameter" enhances the model of disease spread by accounting for human behavior in response to infection rates. This parameter operates through a mathematical formula where $\Psi(f)$ signifies the adjusted probability of infection based on the current fraction of infected individuals, f , relative to a threshold fraction, f^* . The threshold fraction, f^* , represents a critical level of infection that triggers a heightened level of caution among the population, effectively reducing the infection probability by half.

Essentially, this mechanism transitions a simplistic probabilistic model into a nuanced stochastic one, where the infection dynamics are modulated not just by the raw infection rates but also by the population's adaptive response to the spread of the infection. This adaptive response, governed by the value of f^* , implies that a smaller fraction of infected individuals could lead to a significant behavioral shift towards reducing infection risks, thus influencing the overall spread of the disease in a realistic and complex manner.

5 Discussion

Produced data presents the results of a study exploring the impact of varying levels of public caution and vaccine coverage on three key epidemiological metrics: prevalence, new daily cases, and deaths, within a population with no vaccine coverage. The "Caution Parameter" represents a numerical value assigned to the population's level of caution or preventive measures taken to avoid infection. A higher value signifies greater caution and, presumably, more robust preventive behaviors.

As a consequence, at the lowest level of caution (0.02), the impact on disease spread and outcomes is minimal, with relatively high percentages in prevalence (37.64%), new daily cases (35.86%), and particularly high in deaths (90.16%). This suggests that without significant behavioral changes or interventions, the population experiences substantial impacts from the disease.

Increasing the Caution Parameter to 0.2 shows a dramatic increase in all metrics, indicating that even moderate increases in public caution can have a significant effect on disease outcomes. Prevalence and new daily cases rise sharply, indicating a widespread outbreak, but deaths increase at a slower rate (77.78%), suggesting that increased caution might somewhat mitigate the severity of outcomes. At a Caution Parameter of 1, there is a notable shift; while prevalence and deaths increase, with prevalence nearly reaching the entire population and deaths at 93.02%, new daily cases hit 100%. This point might represent a critical threshold where the population caution has a maximized effect on slowing the spread, albeit with a significant portion of the population already affected.

The most extreme caution level analyzed, 10, results in the maximum values for prevalence and deaths, both reaching 100%, while new daily cases slightly decrease to 96.26%. This could indicate a scenario where extreme caution is enacted too late, after the disease has already spread extensively, or it could reflect a situation where extreme caution leads to effective control of new cases, but the overall impact of the disease remains high due to previous spread, and in-between public behavior (as quantified by the Caution Parameter) and disease dynamics in the absence of vaccination. It suggests that while increased caution can significantly affect disease spread and mortality, there is a nuanced balance between the timing and intensity of these behavioral changes and their ultimate impact on disease outcomes. These findings highlight the importance of timely and proportionate public health responses in managing infectious disease outbreaks.

6 Conclusion and future work

This study advances an evidence in the literature about the potential of Membrane Systems in epidemiological modeling, by establishing an integrated framework that aptly represents disease transmission dynamics and intervention effectiveness, considering behavioral influences. The simulation results underscore the necessity of a holistic approach to disease control, which is essential for crafting effective public health strategies in response to infectious disease threats.

A future work could consider the model extension to other infectious diseases and in general global scenarios. Indeed, the current model has been extensively applied to the context of COVID-19. A valuable extension would be to adapt and apply this model to other infectious diseases, such as influenza, Ebola, or even antimicrobial resistance, which present different transmission dynamics and societal impacts. Additionally, incorporating geographical variations and cultural differences in human behavior across different global regions could provide insights into disease spread and control measures in a more diversified manner. This expansion would involve adjusting the model parameters to suit different disease characteristics and transmission modes, as well as integrating diverse behavioral responses based on cultural norms. Beside, by utilizing real-time data, such as infection rates, vaccination rates, and public mobility patterns from various sources like health departments and mobile devices, the model could dynamically update and predict disease spread scenarios more accurately.

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