

# Emergent Dynamics and Phase Transitions in a Grid-based SIR Epidemic Model

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1. Introduction	Marks: 5
Introduce your system. Describe the hallmarks of a complex system found here.	

## Introduction to the System

This MATLAB simulation models the spread of an infection over a two-dimensional domain using a grid-based approach. The system captures the dynamic interactions between susceptible, infected, quarantined, and recovered individuals. It incorporates several realistic epidemiological features, including:

- **Domain and Population:** The system is defined by a square grid of size  $N \times N$ , where individuals are represented as points.
- **Infection Spread:** An infection occurs probabilistically when a susceptible individual comes into contact with an infected individual within a defined radius of influence,  $R$ .
- **Recovery and Immunity:** Infected individuals recover after a set **Recovery Time (RT)** and are immune to reinfection.
- **Quarantine Measures:** A quarantine switch (qring) is activated if infections reach a threshold, isolating a portion of the infected population.
- **Asymptomatic Spread:** A fraction of infected individuals remains undetected (asymptomatic), affecting disease dynamics.

## Hallmarks of a Complex System in this Model

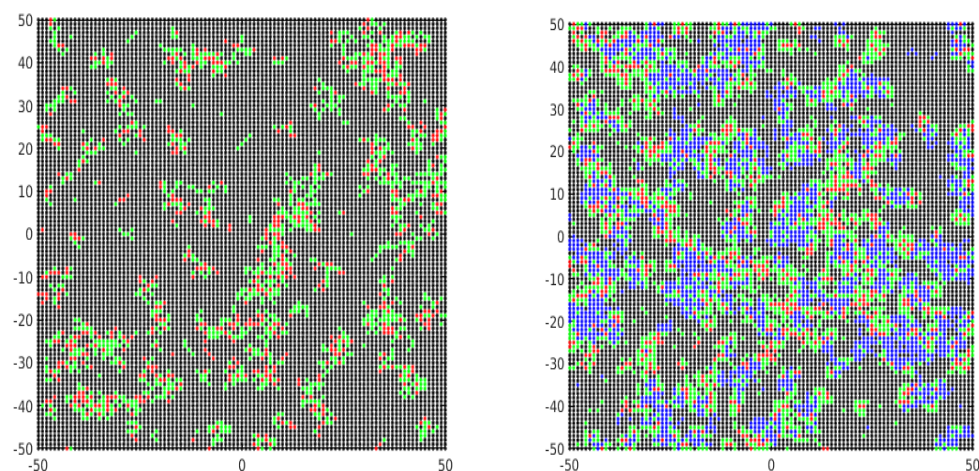
1. **Emergent Behavior**
  - The system exhibits large-scale infection patterns that emerge from simple local interactions. The spread is not predefined but arises dynamically based on probabilistic interactions.
2. **Non-Linearity**
  - Infection growth is non-linear due to probabilistic transmission and the influence of quarantine measures, which alter the system's behaviour when a critical threshold is reached.
3. **Stochastic Dynamics**
  - Randomness is inherent in the model through probabilistic infection chances, random initialisation of infected individuals, and variations in asymptomatic cases. This introduces uncertainty in outcomes.
4. **Adaptive Behaviour and Phase Transitions**
  - The system transitions when an infection is critical, triggering quarantine measures that shift the overall infection trend, mimicking real-world public health responses.
5. **Multi-Scale Interactions**
  - Individuals interact locally within a radius, but the cumulative effect is observed globally as the epidemic evolves.

<b>2. Model</b> (not more than 1 page)	Marks: 15
Write down your final model (eqns, algorithms, interactions, noise, etc.). Include all that is required to understand your simulations. Make schematics to explain them better.	

This simulation model is designed to capture the dynamics of infectious disease spread in a population through a purely algorithmic approach. The simulation begins by randomly infecting a fixed number of agents ( $k$ ) to initiate the outbreak. The infection spreads when an agent's immediate neighbour is infected, with a probabilistic chance of transmission. This local interaction forms the basis for how the disease propagates throughout the simulated environment.

An important behavioural aspect of the model is the implementation of quarantine measures. Once the number of infected individuals exceeds a certain threshold, quarantine is activated. Infected agents identified as symptomatic are isolated, meaning they no longer interact with their immediate neighbours and cannot transmit the infection further. However, asymptomatic agents—determined by a probabilistic factor—continue to move freely and can contribute to the further spread of disease, adding complexity to the simulation.

Additionally, the model incorporates common-place dynamics to mimic environments where individuals congregate, such as markets or public transportation hubs. When this feature is enabled, a select number of agents are randomly chosen to visit a designated shared place, where all present are considered immediate neighbours. This increases the risk of rapid infection spread, as a single infected individual in the common place can expose many others. Notably, quarantined individuals are restricted from visiting these common places. Finally, the model includes a fixed recovery period for all agents, ensuring that individuals are immune to reinfection once recovered. This contributes to the overall dynamics and eventual stabilisation of the simulation. (For more details, refer to appendix 1).



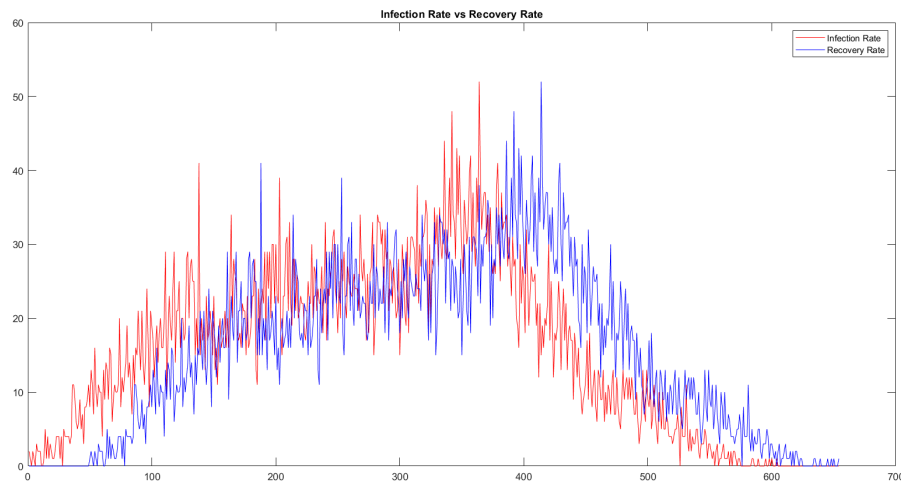
Black - Susceptible; Red - Infected; Green - Quarantined; Blue - Removed

### 3. Diagnostics and Initial Assessment (not more than 1 page)

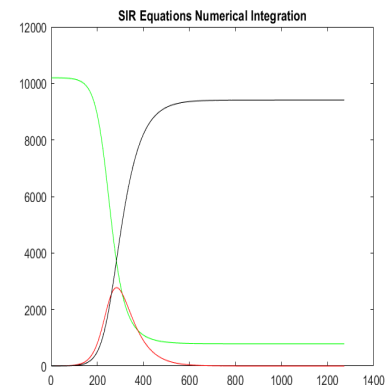
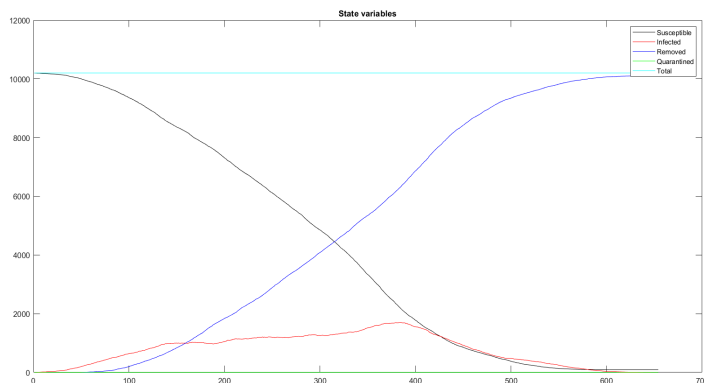
Marks: 20

Describe the **top two** diagnostics/tests conducted to verify the correctness of the model. Provide outputs/graphs showing expected (sketch or description) vs. observed behaviour (plot). Discuss any discrepancies and how they were resolved.

One of the most basic diagnostics for the system is to perform sanity checks. For any moment in time, the rate of infection should be equal to the recovery rate with an offset of recovery time. This can be observed in the graph below. This means the correlation between infection rate and recovery rate is high. Upon calculating this value, it comes out to be 0.7272.



The differential equations for the SIR model can be found in reference 2. Upon solving these differential equations using numerical integration, a graph similar to the one obtained from the model is observed. These graphs are not precisely equal since the model has many limitations, but they can be observed to be qualitatively similar.



**4. Analysis of Emergence** (not more than 2 pages)

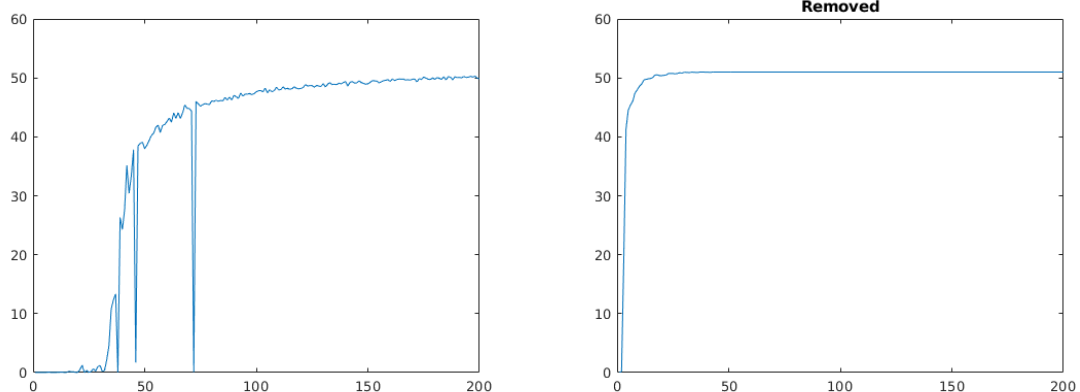
Marks: 35

What is the emergent behavior you observe in your system? – why is it emergent? (describe at least 2 distinct scenarios). What order parameters characterise your system well? Provide intuition for why certain emergent behaviours arise. Support explanations with simulations, graphs, or qualitative arguments. You can attach a google drive link to a max of two movie files. Make sure that movies will play on the browser without downloading it.

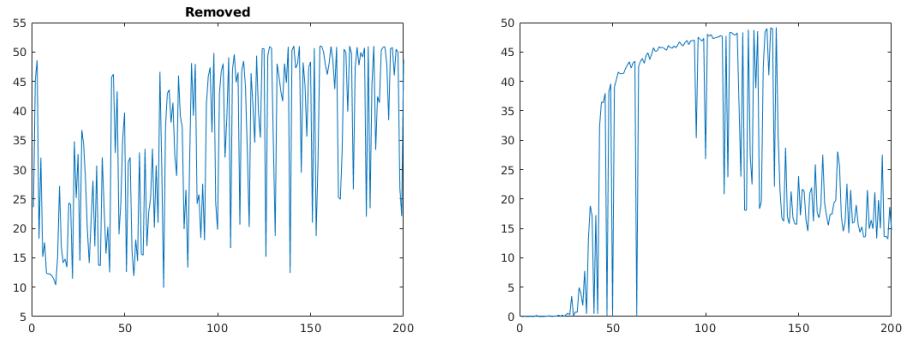
Two interesting emergent behaviours in the system are Epidemic Threshold and Peak Infection Rate.

**Epidemic threshold and phase transition**

Every agent in the system has only a probability of getting infected. There is a chance of an agent not being infected despite being next to an infected agent if the infection rate or recovery time is minimal. Hence, we can observe that if one of these parameters is a constant, the other displays a threshold value below which the epidemic does not spread and dies out in the initial stages. Close to this threshold, the system will behave in a nonlinear fashion and upon exceeding it, almost the entire population will end up getting infected. Quarantine measures play a very significant role in determining these thresholds as they can effectively convert an epidemic to an endemic. We have run multiple simulations to calculate these parameters, and the results are shown below.



1. Max Removed vs Recovery Time
2. Max Removed vs Infection Probability (0 to 0.05 linearly)  
(No Quarantine)



1. Max Removed vs Recovery Time
2. Max Removed vs Infection Probability (0 to 0.15 linearly)  
(Quarantine)

### Temporal Dynamics and Peak Infection Rate

Another emergent property dependent on the chance of infection and recovery time is the peak infection rate. While the epidemic threshold depends on both parameters sufficiently, PIR depends very highly on the chance of infection. Even if the recovery time is high, a low chance of infection will significantly slow the spread rate, affecting the temporal dynamics. In contrast, a longer recovery time will ensure that infection has sufficient time to spread, which can influence the epidemic threshold. The infection rate is also significantly affected by quarantine measures.

### Order parameters

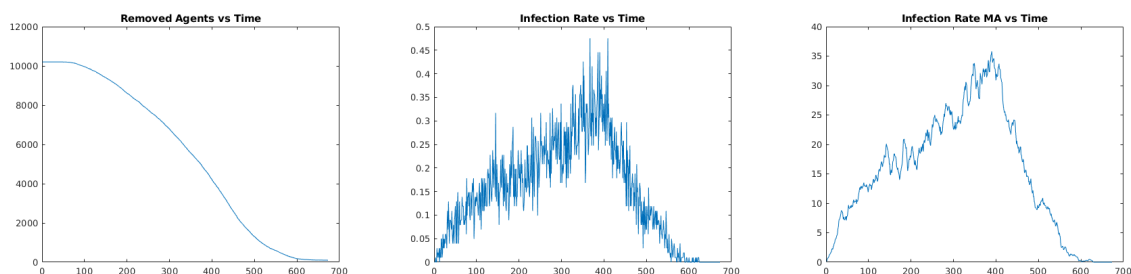
An order parameter that can be used to study the system is the maximum recovered agents. Order parameters can also be used to study system dynamics, such as maximum infected agents and peak infection rate.

### Recovered Agents

It shows the total number of agents that got infected and then recovered. Since our system runs till the infection dies out and since the system is limited, this also reflects all agents that ever caught the infection. This OP can take on very different values depending on whether the system is in the endemic phase or epidemic phase.

### Infected Agents

This can be used to predict the nature of the infection prior to it becoming an epidemic/endemic. It can be used as a benchmark for preventive measures. This data can also be used to measure infection rate and peak infection rate. Since the infection rate is very erratic in nature, we can use the moving average to study trends.



**5. Data from complex systems** (towards Phase 2) (not more than a page)

Marks: 20

What data do you get from this system with which you can perform data-driven analysis?  
Show plots of some data that is characteristic of the emergence observed. Explain why it is interesting to analyze such data.

## What Data Do You Get from This System?

We extract the following key data from our simulations.

### A. Time-Series Data

- Susceptible (S), Infected (I), Recovered (R), Quarantined (Q)** over time
- Helps track how the population transitions between states during the outbreak

### B. Peak Infection Metrics

- Maximum infection rate**  $\max(I(t))$ : Used to forecast the worst-case outbreak size
- Time to peak**: When the infection hits its highest point
- Epidemic Duration**: How long the infection persists in the population

### C. Comparison Between Scenarios

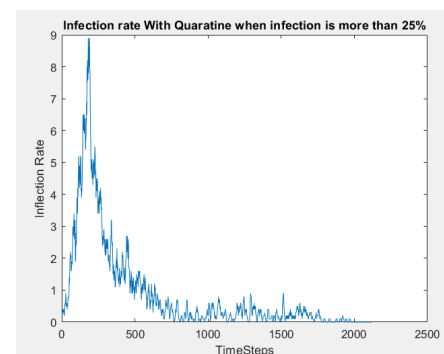
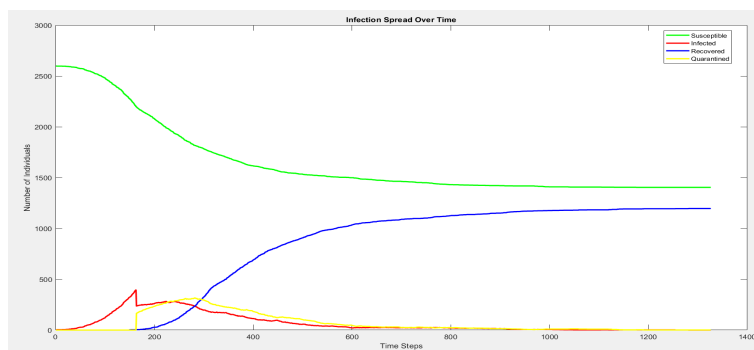
- We simulate both **quarantine** and **non-quarantine** environments to compare:
  - Peak infection rate
  - Time is taken for epidemic resolution

## Forecasting and Preventive Measures

Using the infection rate curve  $I(t)$ , we can:

- **Forecast peak outbreaks** by identifying the time and intensity of maximum infections
- Determine **when to implement interventions** (e.g., quarantine, social distancing)
- Optimise **preventive measures** based on expected outcomes:
  - Early quarantine → lower peak, slower spread
  - Delayed quarantine → overwhelming peak, faster spread

By analysing multiple runs with varied infection rates and quarantine parameters, we can build **predictive models** for real-world policy implications. The graph below is for the case B and C. And the graph of case A is combined, placed and after the case B and C



<b>6. References</b> (not more than half a page)	Marks: 5
Cite any papers, books, or online resources used in the study.	

1. Simulating an epidemic - 3Blue1Brown -  
<https://youtu.be/gxAaO2rsdIs?si=3LJiKXmjE3u8K7jV>
2. Differential Equation for SIR Model -  
<https://medium.com/@shaliniharkar/sir-model-for-spread-of-disease-the-differential-equation-model-7e441e8636ab>
3. MATLAB Functions Help -  
[https://in.mathworks.com/help/matlab/matlab\\_env/](https://in.mathworks.com/help/matlab/matlab_env/)



## Appendix

### Extra Emergence Pattern Observed in SIR Model

Another important Emergent phenomenon is the probabilistic spread of infection based on the initial location of infected individuals. In a  $70 \times 70$  grid of agents, if  $k$  agents are randomly infected in the centre, the epidemic grows larger than when those  $k$  agents are infected at the edges. This is because agents in the centre have more neighbouring agents to spread the infection to.

In the real world, this can be compared to **social networks**, where central agents (those with a high degree, meaning highly connected) are more likely to contribute to a widespread epidemic. In contrast, agents at the edges (those with a low degree, meaning fewer connections) are less likely to cause a significant outbreak.

Similarly, a **geographical interpretation** can be made: people living in **urban areas** are more likely to be infected than those living on the outskirts or in **rural areas**. Urban dwellers frequently interact with others through public transportation (e.g., buses and metros), increasing their exposure. On the other hand, people in rural or suburban areas have fewer interactions and connections, which naturally slows down the spread of the epidemic.

The **First case** is where the infection started at the corner **agents**, and the **second** is where the **middle agents** were infected.

Quarantine measures are introduced in the simulation **once the infection reaches 15%** of the total population. This mirrors real-world scenarios where **policy interventions** like lockdowns or ring quarantines are triggered **after infection reaches a critical threshold**. Once activated, agents are quarantined based on symptom visibility and contact tracing, which slows further spread.

