# A Hybrid Model For Studying Spatial Aspects of Infectious Diseases

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# Introduction

In this presentation, I introduce the hybrid modelling for infectious diseases and make comparisons with continuum model.

# Why Hybrid Modelling? I

- Flexible
- More Realistic(But in our case, not that much realistic $R = 0$!!)

# What is Hybrid Modelling I

- Couple an agent based model with continuum based(ODE or PDE) model [3].

# What is Hybrid Modelling II

- Used not only for epidemic modelling but also any modelling field with spatial aspects occur e.g. [6](Retail Markets)
- Can also be applied in tumor growth [7]
- For more applications see [2, 4, 5].

# What is Hybrid Modelling III

We investigate our hybrid model in four cases:

- Transmission
- Motility
- Transmission+Motility
- Spatial Analysis

The main cases are transmission, and motility. Both have different continuum and agent-based component.

# The SIR Model I

For the continuum based component of the transmission mode, we need to introduce a famous model: SIR model. The SIR model is

# The SIR Model II

the solution of the following ODE with an initial condition.

$$\frac{dS}{dt} = -\beta S(t)I(t) \tag{1}$$

$$\frac{dI}{dt} = \beta S(t)I(t) - \gamma I(t) \tag{2}$$

$$\frac{dR}{dt} = -\gamma I(t) \tag{3}$$

where $S(t) + I(t) + R(t) = 1$.

# The SIR Model III

As in our hybrid model, when we assume no recovery, i.e. $\gamma = 0$, we get the following equations:

$$\frac{dS}{dt} = -\beta S(t) I(t) \tag{4}$$

$$\frac{dI}{dt} = \beta S(t) I(t) \tag{5}$$

where $S(t) + I(t) = 1$. Hence we can reduce this system of ODE into single ODE as

$$\frac{dI}{dt} = \beta I(t)(1 - I(t)). \tag{6}$$

# The SIR Model IV

Additionally this model is called the SI model. The solution for this model can be analytically given by

$$I(t) = \frac{I(0)e^{\beta t}}{1 + I(0)(e^{\beta t} - 1)}. \tag{7}$$

# Transmission Mechanism I

We have two components, continuum and agent based. For the continuum we get the solution of the model above.

# Transmission Mechanism II

For agent based we have the following illustration

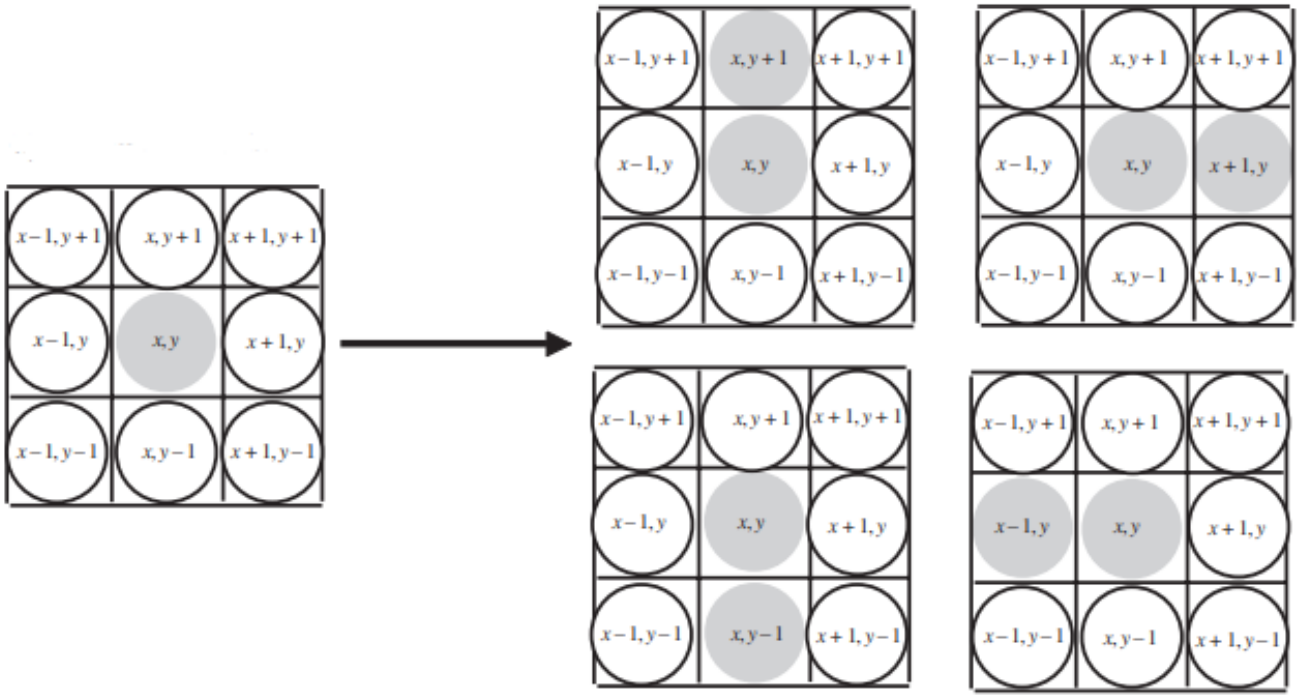


Figure: Illustration of the transmission, taken from [1]

# Transmission Mechanism III

The total number of infectious agents $n(t)$ at any discrete time $t$ is predetermined by the equation (7), and we have $n(t) = \lfloor I(t)LH \rfloor$ where $L$ and $H$ are the side lengths of the rectangular region. For each time step $t$ to $t + 1$, we run the agent based component process. This process is repeated until the total number of infectious agents in the domain is $n(t + 1)$.

# Transmission Mechanism IV

Simulation on $100 \times 100$ square region with uniformly distributed infectious agents with initial condition $I(0) = 0.1,\ \beta = 0.125$.

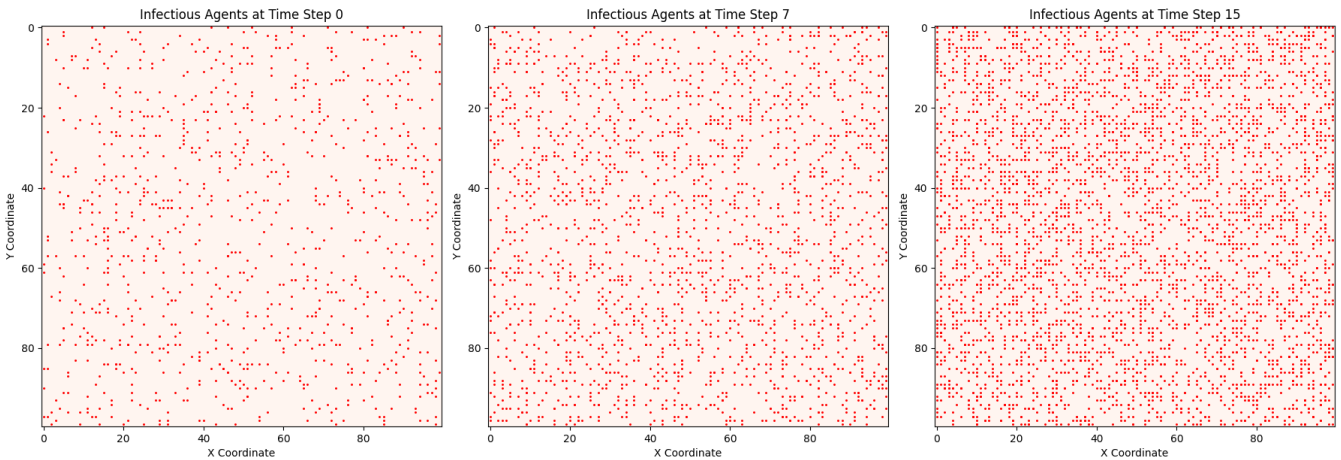


Figure: The simulation with initial condition $I(0) = 0.1,\ \beta = 0.125$

# Transmission Mechanism V

We check that the evolution of the proportion of infectious agents within the domain is the same as that of equation (7) for different $\beta$ values.

# Transmission Mechanism VI

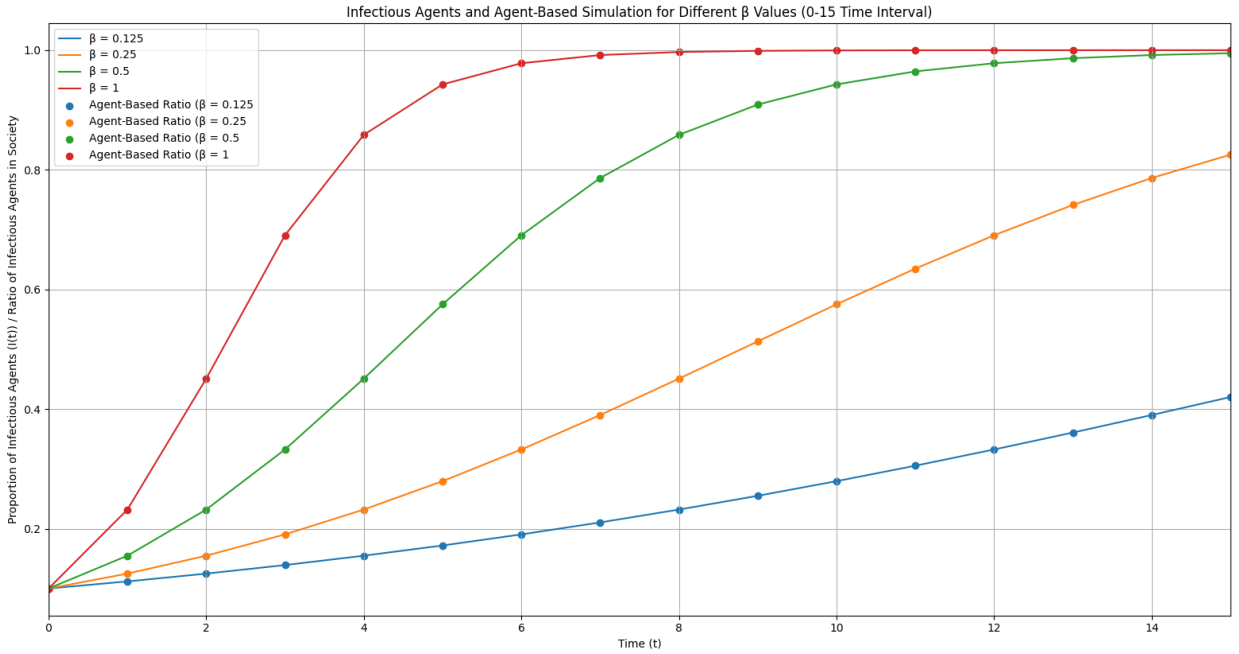


Figure: Evolution of the proportion of the population that is infectious for $I(0) = 0.1$. The markers are from the hybrid model and the solid curves are solutions of equation 7. From bottom to top, $\beta = 0.125, 0.25, 0.5, 1$.

# Transmission Mechanism VII

Clearly there is spatial dependence in the domain, forming clusters of infectious hosts. to see this we can do the following example with infectious agents located in the corners.

# Transmission Mechanism VIII

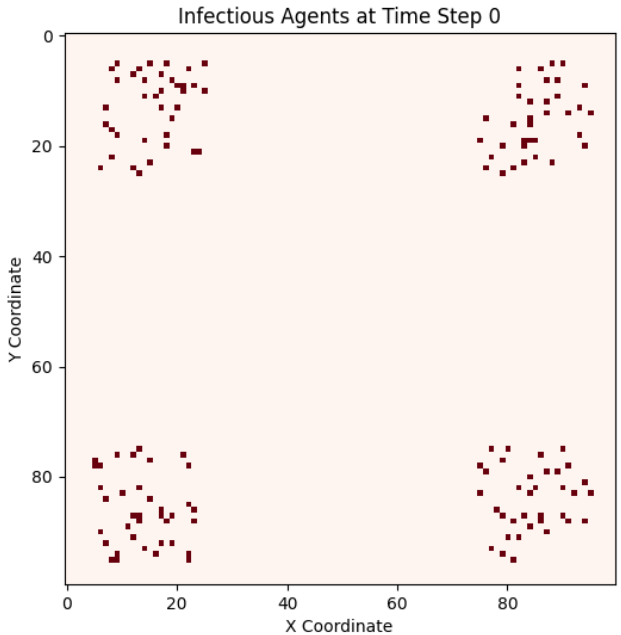


Figure: Initial condition for the simulation.

# Transmission Mechanism IX

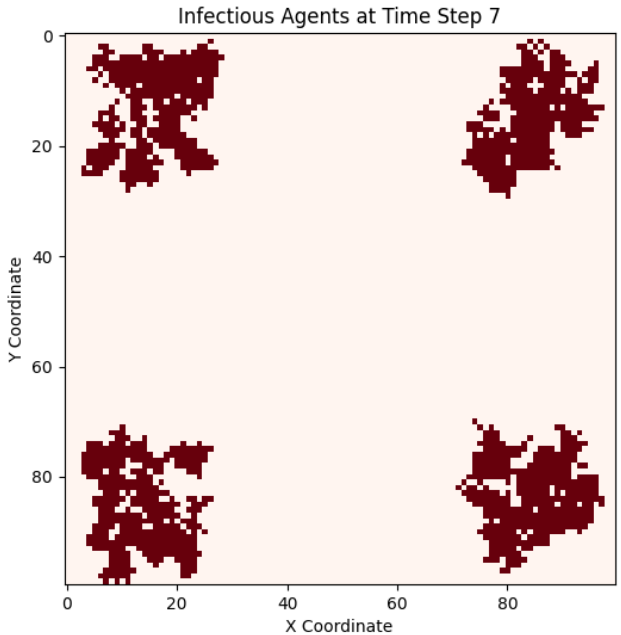


Figure: Simulation at time $t = 7$.

# Transmission Mechanism X


Figure: Number of infectious agents over time

# Motility Mechanism I

In continuum component we have diffusion equation as we have spatially dependence now. The evolution (in the x direction) of the proportion of infectious individuals within the population is $I(x, t)$. Assuming that the infectious hosts undergo an unbiased random walk, we have the linear diffusion equation

$$\frac{\partial I}{\partial t} = D\frac{\partial^2 I}{\partial x^2}$$

where $D$ is the diffusion coefficient. Here we analyze only motility so we assume no transmission. In this assumption number of

# Motility Mechanism II

infectious individuals remains constant at all time and for the agent based component this number can be given by

$$n = \left\lfloor H \int_0^L I(x,0)dx \right\rfloor$$

where $L, H$ are the length and height of the region, respectively.

# Motility Mechanism III

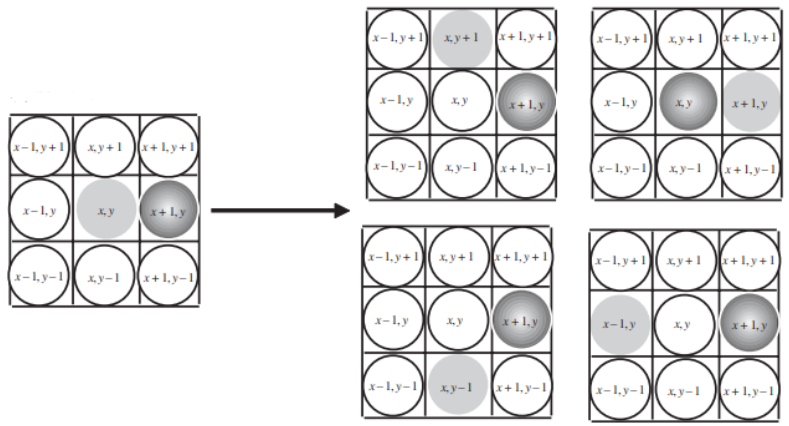


Figure: Motility Rule for the Agent-Based component of the Hybrid model. Taken from [1].

# Motility Mechanism IV

Now let us simulate the motility. To simulate it we first create an initial condition. Let us take $L = 100, H = 20$. The columns of the lattice, $c(x, 0)$, were populated uniformly at random with infectious agents according to

$$c(x, 0) = \frac{H}{2}(\Theta(x - 40) - \Theta(x - 60))$$

where $\Theta(x)$ is the unit step function.

# Motility Mechanism V

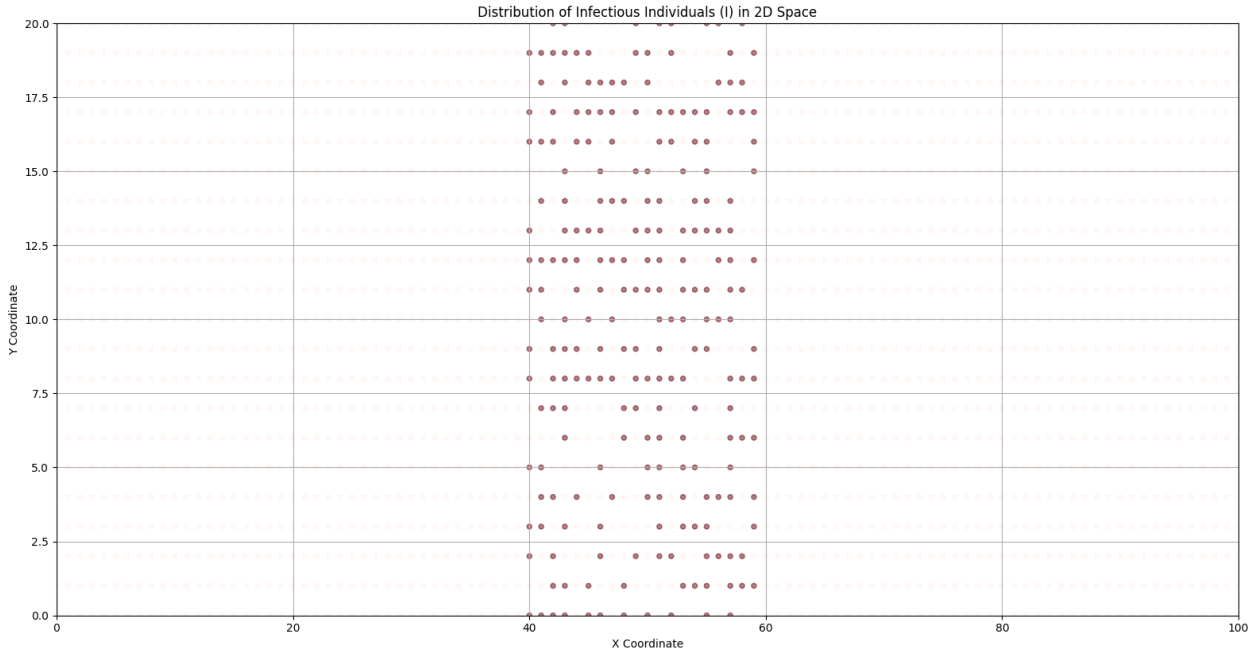


Figure: Initial condition of the motility simulation, with $D = 0.25$.

# Motility Mechanism VI

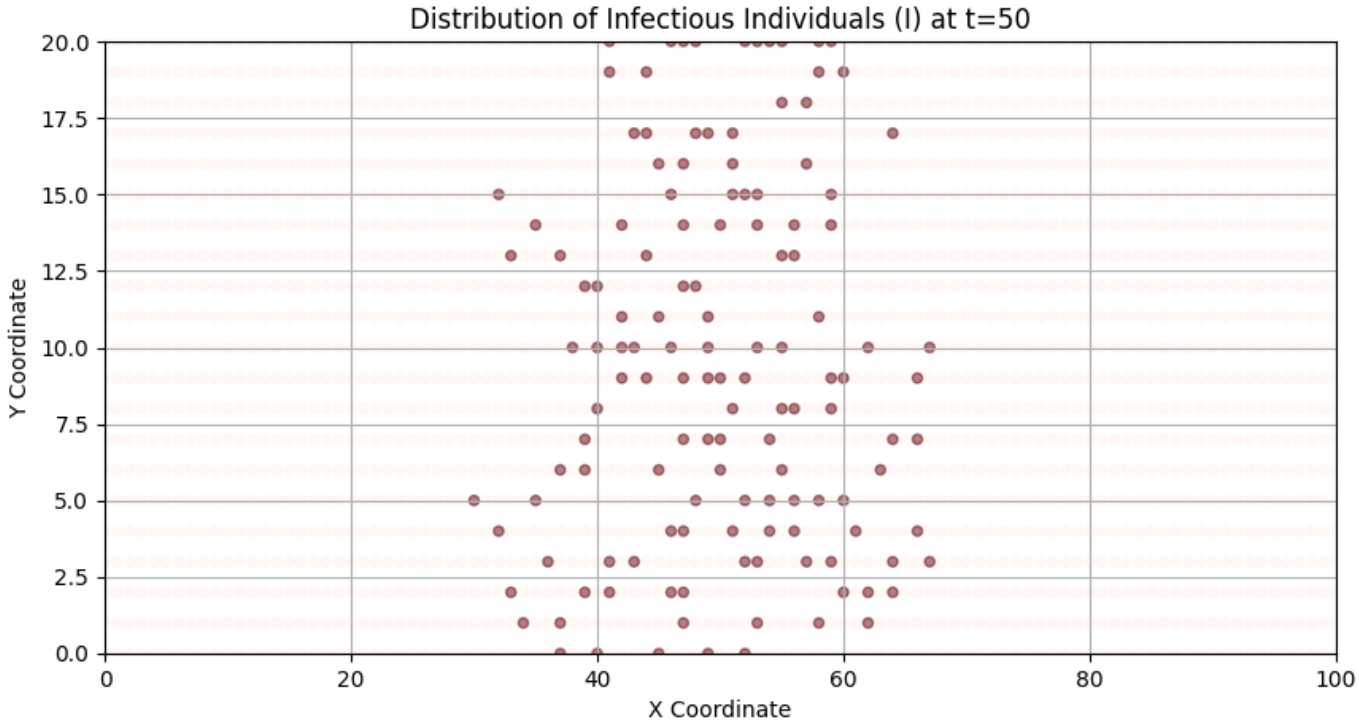


Figure: Simulation after 50 time steps.

# Motility Mechanism VII

We also want to investigate the motility of just one infectious agent in 500 days, which is completely a random walk as seen in the figure next slide.

# Motility Mechanism VIII

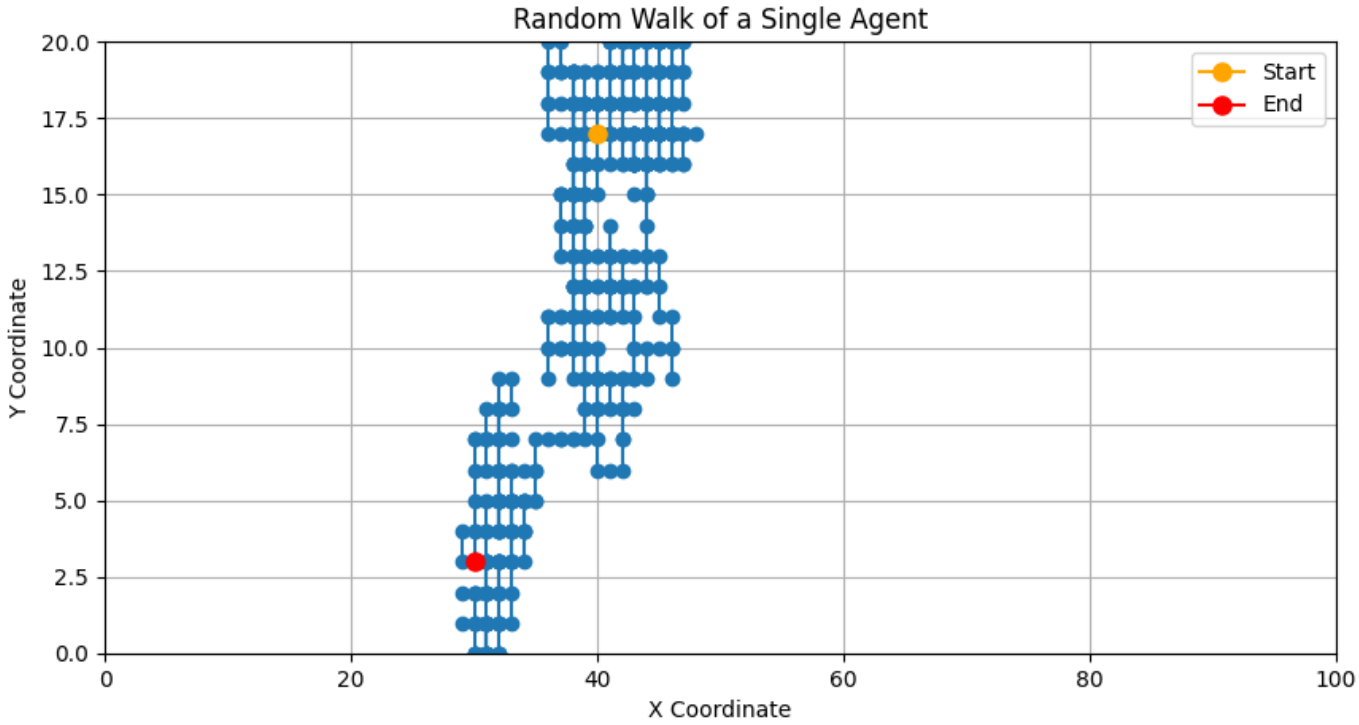


Figure: Random walk of one individual

# Motility Mechanism IX

The evolution of the squared displacements of this (tracked) infectious agent is given by

$$X(t) = \sum_{i=1}^{t} (x(i) - x(i-1))^2,$$

$$Y(t) = \sum_{i=1}^{t} (y(i) - y(i-1))^2.$$

As expected, the gradients $X'(t)$ and $Y'(t)$ are related to the diffusivity by

$$X'(t) \approx Y'(t) \approx 2D.$$

# Motility Mechanism X

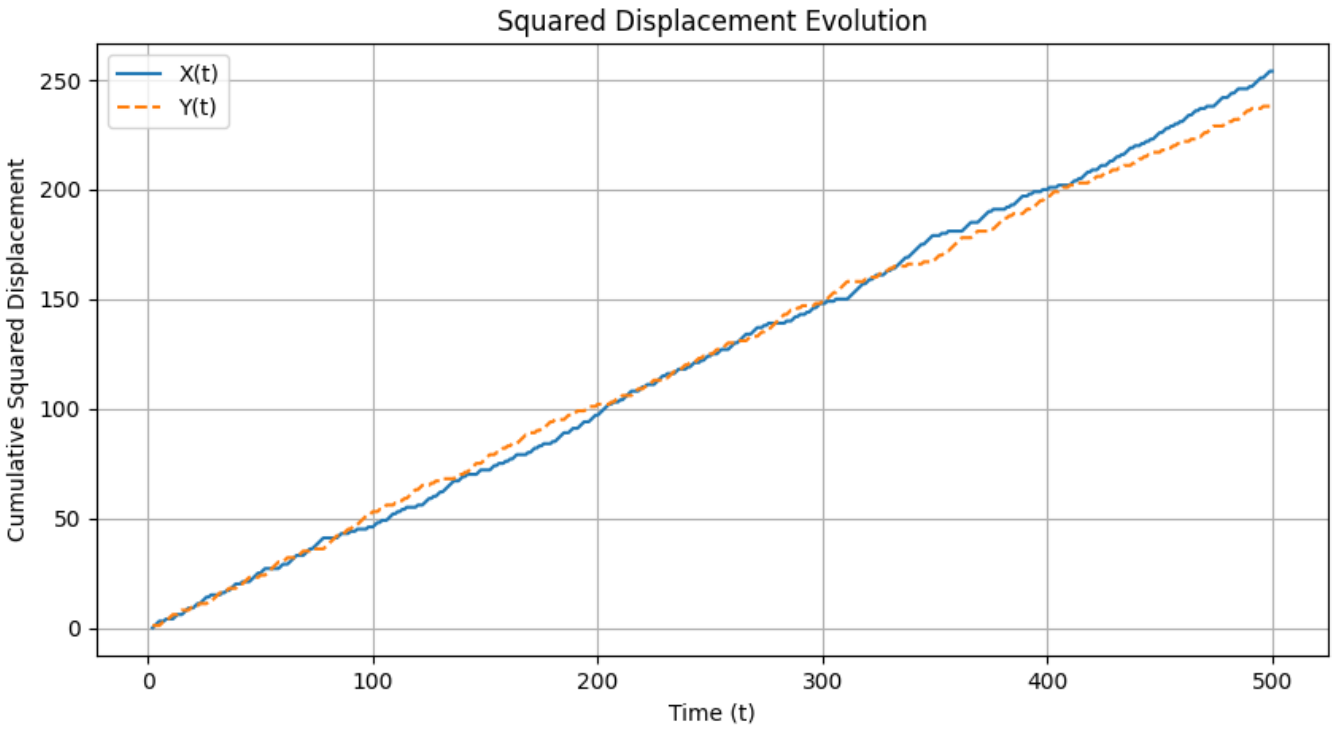


Figure: Square Displacements

# Motility Mechanism XI

Now we want to compare our hybrid model with diffusion equation solution by making 25 different simulation and taking its average We know that for $N$ realizations starting from the same initial condition, we can define an average column infectious agent proportion as

$$I_h(x,t) = \frac{1}{N}\sum_{i=1}^{N} c_i(x,t),$$

where $c_i(x,t)$ is the total number of infectious agents in column $x$ of the lattice after $t$ steps of the $i$-th realization.

# Motility Mechanism XII

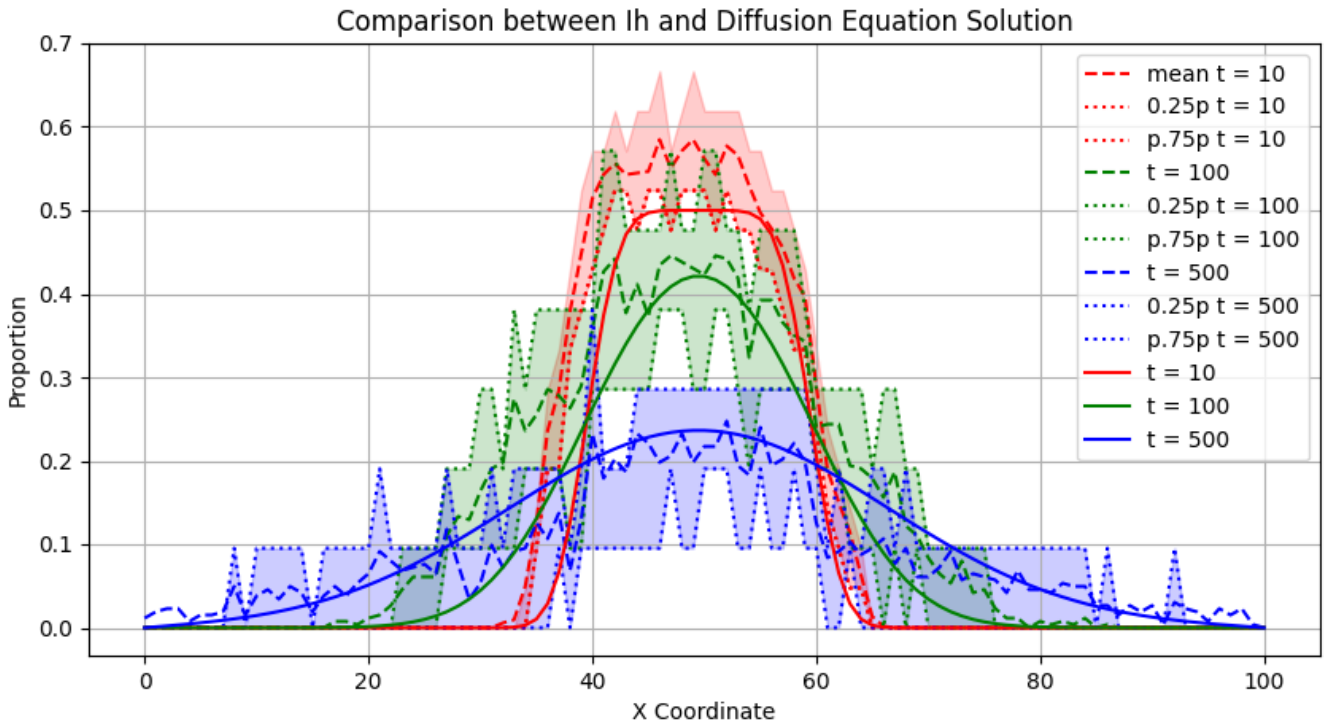


Figure: Comparison with diffusion equation

# Transmission+Motility I

Here we assume both transmission and motility can occur. The continuum component of this model can be given by Fisher equation

$$\frac{\partial I}{\partial t} = D\frac{\partial^2 I}{\partial x^2} + \beta I(x,t)(1 - I(x,t))$$

To make simulation, we choose $\beta = 0.1,\ D = 0.25$ as in the previous parts. If we choose the same initial condition with the motility case, we see the results at the $30^{th}$ and $100^{th}$ days as in the following.

# Transmission+Motility II

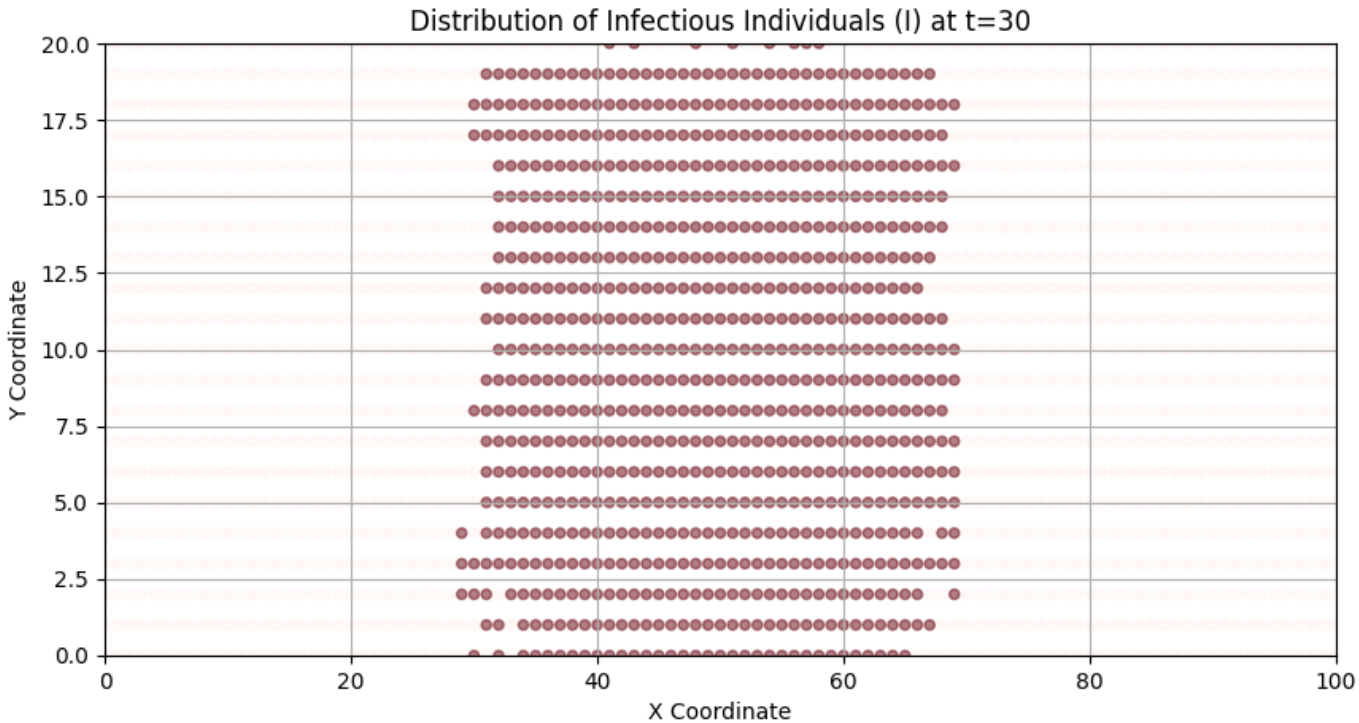


Figure: Transmission+motility after 30 days.

# Transmission+Motility III

The result of this algorithm after 100 time steps is as below.

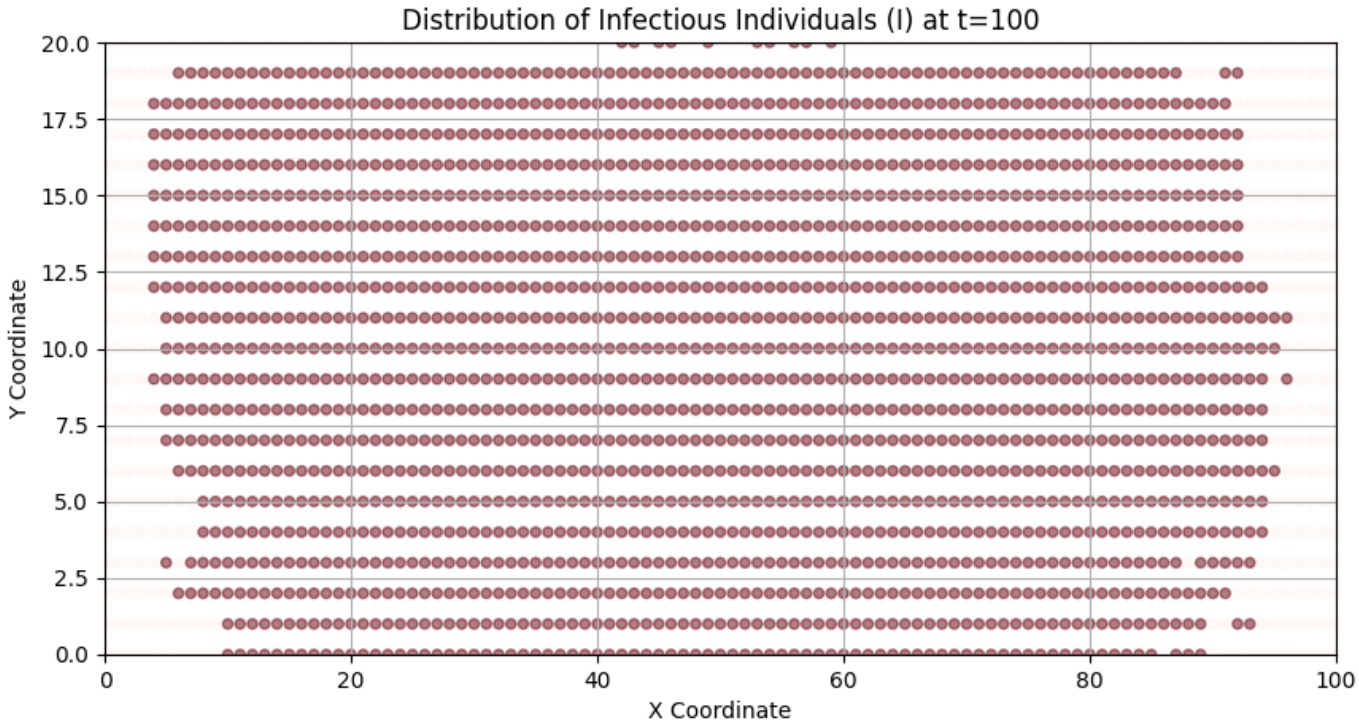


Figure: Transmission+motility after 100 days.

# Transmission+Motility IV

Now we run 25 simulation like in the motility case and compare the results with Fisher equation with the mean, 0.25, and 0.75 percentiles of the simulations.

# Transmission+Motility V

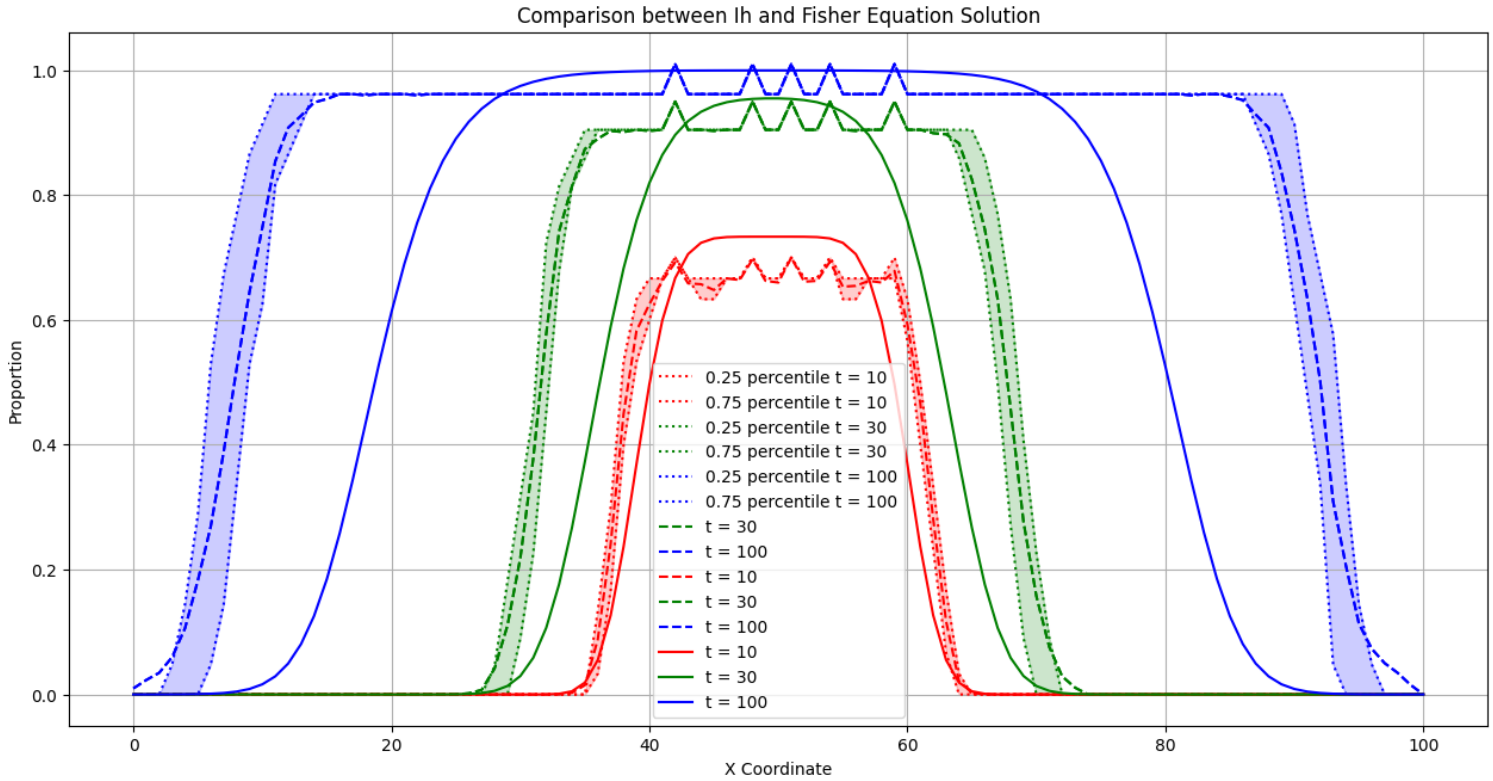


Figure: Comparison between Hybrid model and Fisher equation

# Spatial Analysis I

- Domain is divided into M equal square bins.
- At any time $t$, there are a total of $n(t)$ infectious agents in the domain.
- $b_i(t)$ is the number of infectious agents in bin $i$,
  - then the average bin count is $n(t)/M$,
  - the variance of the bin counts is

$$\sigma^2(t) = \frac{1}{M} \sum_{i=1}^{M} \left( b_i(t) - \frac{n(t)}{M} \right)^2 .$$

# Spatial Analysis II

The index is a scaled variance given by

$$j(t) = \frac{\sigma^2(t)}{\sigma_0^2(t)},$$

where

$$\sigma_0^2(t) = n^2(t)\left(\frac{M-1}{M^2}\right).$$

The index ranges from

# Spatial Analysis III

- unity, for a completely segregated state (when all infectious agents are in just one bin)
- to zero, for an evenly distributed state (when each bin contains precisely the average bin count)

**Warning**

Although the evenly distributed state is possible, it is not often realized. Instead, a more realistic situation occurs when each infectious agent is equally likely to reside in any bin. This is known in the literature as the complete spatial randomness (CSR) state.

# Spatial Analysis IV

The CSR limit for the index is

$$J_{CSR}(t) \approx \frac{1}{n(t)} - \frac{1}{LH}.$$

We compare this limiting value to the average index, defined as

$$J(t) = \frac{1}{N} \sum_{i=1}^{N} j_i(t),$$

where $j_i(t)$ is the $i$th realization of the index.

# Spatial Analysis V

Now we make spatial analysis for two different $\beta$ values 0.01 and 0.2 with initial condition $c(x, 0) = 0.1H$.

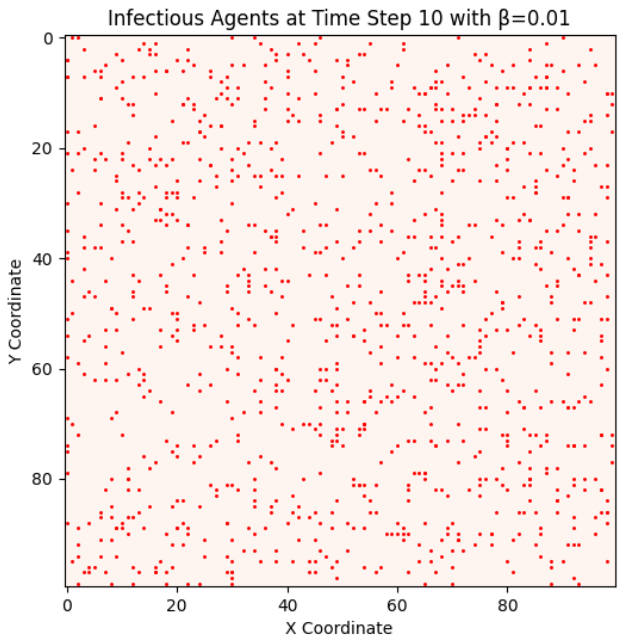


Figure: Simulation for $\beta = 0.01$

# Spatial Analysis VI

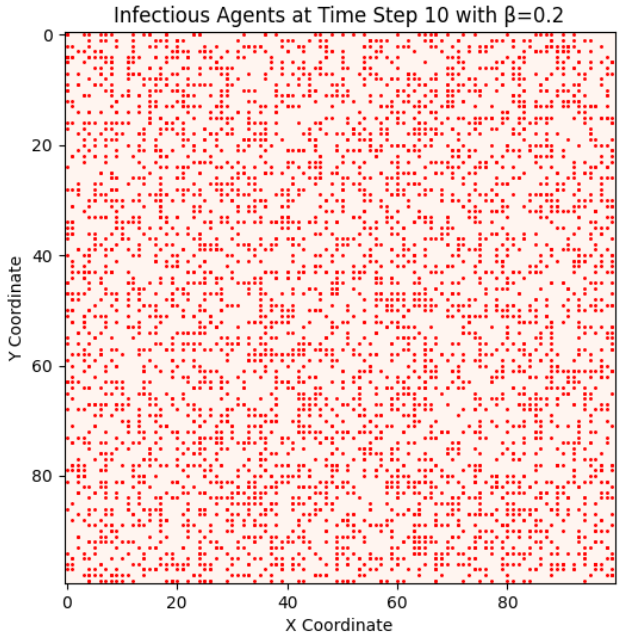


Figure: Simulation for $\beta = 0.2$

When we compare the limits, we get the following result.

# Spatial Analysis VII

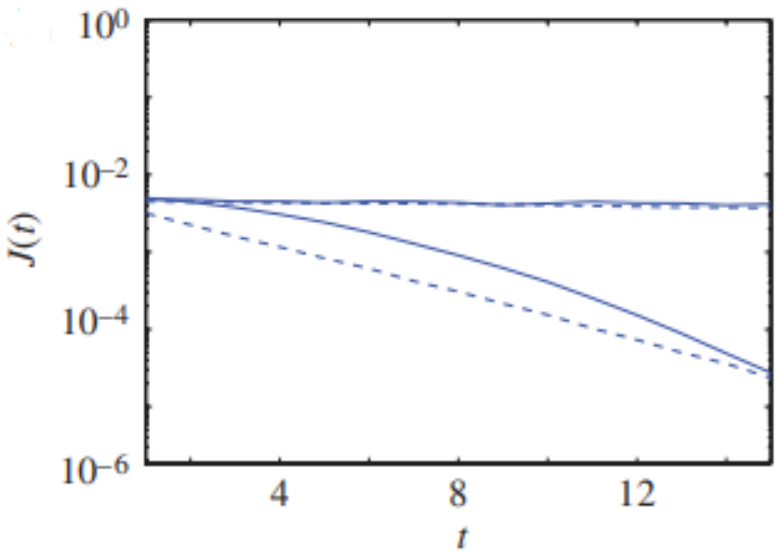


Figure: Average index with $M = 80$ equal-sized bins (solid curves, $N = 25$) and CSR limiting value (dashed curves). From bottom to top, $\beta = 0.2, 0.01$. Taken from [1]

# Spatial Analysis VIII

For the lower value of the transmission rate parameter, $\beta = 0.01$, the spatial domain of infectious agents is well homogenized as the average index is close to the CSR limit. This contrasts with the higher value of the transmission rate parameter, $\beta = 0.2$, where the spatial distribution is non-homogeneous, as the average index deviates from the CSR limit. Only when $t = 0$ (that is, the initial condition) and when the lattice is completely occupied with infectious agents is the CSR state achieved.

Thank you for listening...

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