Epidemic Dynamics in Urban-Like Areas (As an S-I-R Model)

Balla Surya Harshith

CS23B010
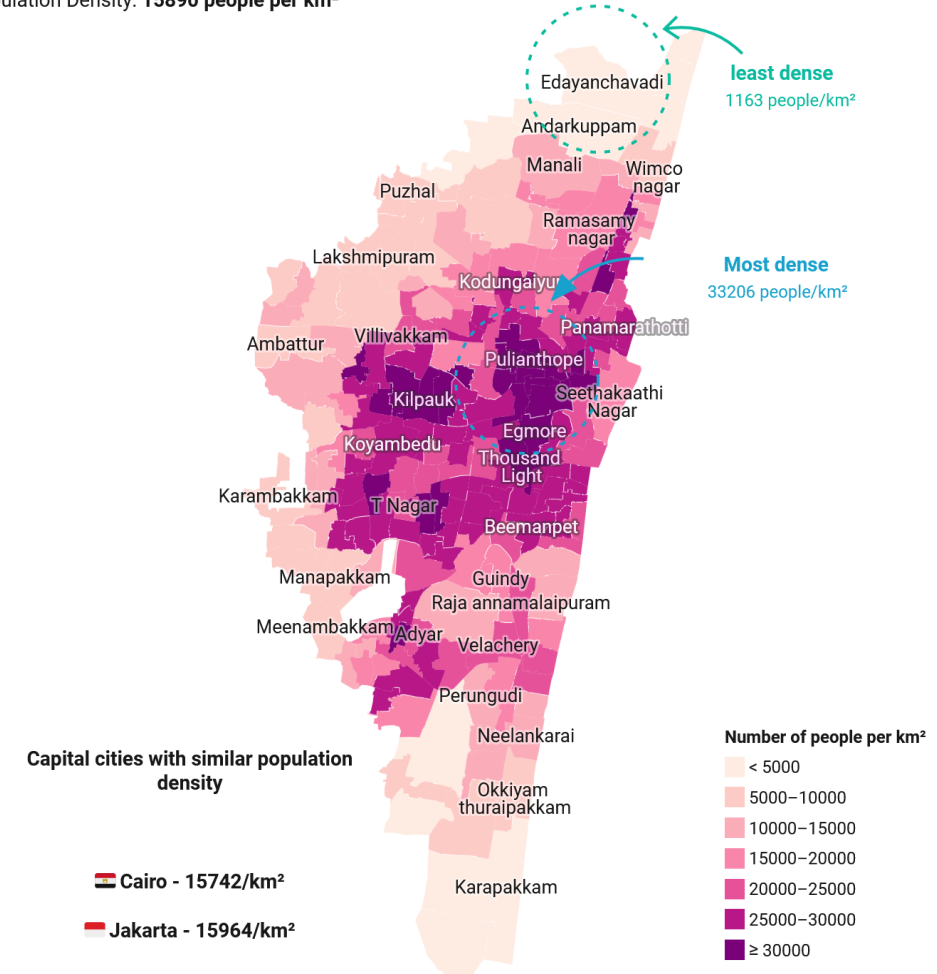
ID5090 final project

System:

- This is an agent-based simulation model of epidemic spread and vaccination strategies in an urban-like core-periphery environment. Transitioning between Susceptible, Infected, and Recovered states. Movement is biased toward their base (home) location, especially when outside it. These interactions form dynamic contact networks that shape disease transmission.

Population density of Greater Chennai Corporation

Estimated 2020 population of Greater Chennai corporation: **6868517 people** (6.9 million)
Area : **432.24 km²**
Population Density: **15890 people per km²**

least dense
1163 people/km²

Most dense
33206 people/km²

Capital cities with similar population density

🇪🇬 **Cairo - 15742/km²**

🇮🇩 **Jakarta - 15964/km²**

Number of people per km²

- < 5000
- 5000–10000
- 10000–15000
- 15000–20000
- 20000–25000
- 25000–30000
- ≥ 30000

Estimated 2020 population extracted from worldpop.org dataset using Qgis.
Map: @amasaesle • Source: GIS analysis • Get the data • Created with Datawrapper

Equations:

Regarding movements:

$$(1) \quad \Rightarrow \quad x_i(t) = x_i(t-1) + v\cos(\theta) \quad \& \quad y_i(t) = y_i(t-1) + v\sin(\theta)$$

$$(2) \quad \Rightarrow \quad P_{jump}(d) = ce^{-cd}$$

$$(3) \quad \Rightarrow \quad x_i(t) = x_i(t-1) + v\cos(\Phi_i(t)+\alpha\Delta\theta) \quad \& \quad y_i(t) = y_i(t-1) + v\sin(\Phi_i(t)+\alpha\Delta\theta)$$

For the interaction radius, Location areas:

$$G(\sigma) \propto \sigma^{-\omega} \quad \& \quad L(\Sigma) \propto \Sigma^{-\gamma}$$

Condition for the interaction between 2 nodes

$$(x_i(t) - x_j(t))^2 + (y_i(t) - y_j(t))^2 \quad <= \{max(\sigma_i , \sigma_j)\}^2$$

we assume that if 2 nodes interact with each other then with the probability 'β' the infection passes if one is infected and the other is susceptible.

if an agent is infected then at any time after getting infected gets recovered with recovery probability 'μ'

Emergence and dynamics of the system:

Observation 1:

- The plots show the degree distribution of agents versus their interaction radius at three different points of time in the simulation. hotter agents indicate densely connected central locations, while coolest agents resembling the slightly connected peripheral regions, along with as the randomness increases this ideology vanishes as given below.
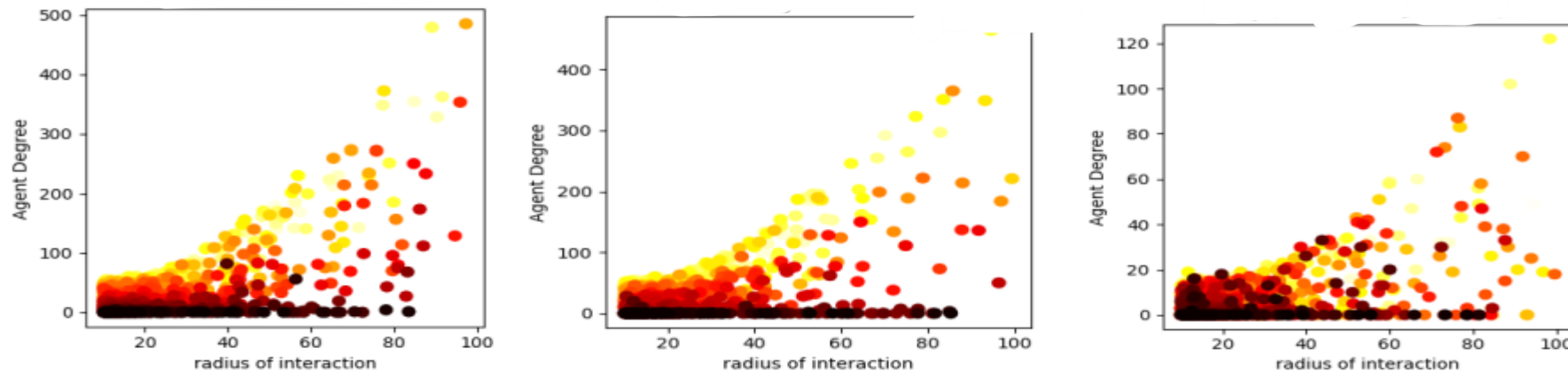

Here, N = 1500, L = 100, D = 100000, $\Sigma \in$ [10,1000] , $\sigma \in$ [10,100] , v = 50, c = 4 x 10^{-4}
With cases of α = 0, 0.2 , 0.8 correspond to p = 0.4 , 1 , 0.6 at the 1000 th time step.

Observation 2:

Based on the randomness parameter 'α' and leaving probability 'p' the trade off between the global and local interactions takes place. Which justifies the transmission ideology in an urban area type scenario and we discuss in detail in the next page. But here are the 3 scenarios where we have plotted the S(blue),I(red),R(green).Which tells that anyhow the transmission occurs (but changes on β and μ). Here α = 0, 0 , 0.6 correspond to p = 1 , 0 ,0.5. And the remaining are the same as above.

Note:- Here α is in between 0 and 1 of which upon increasing it we get more randomiised path towards the home location for a node.
And p is the probability that the node leaves it's home location.
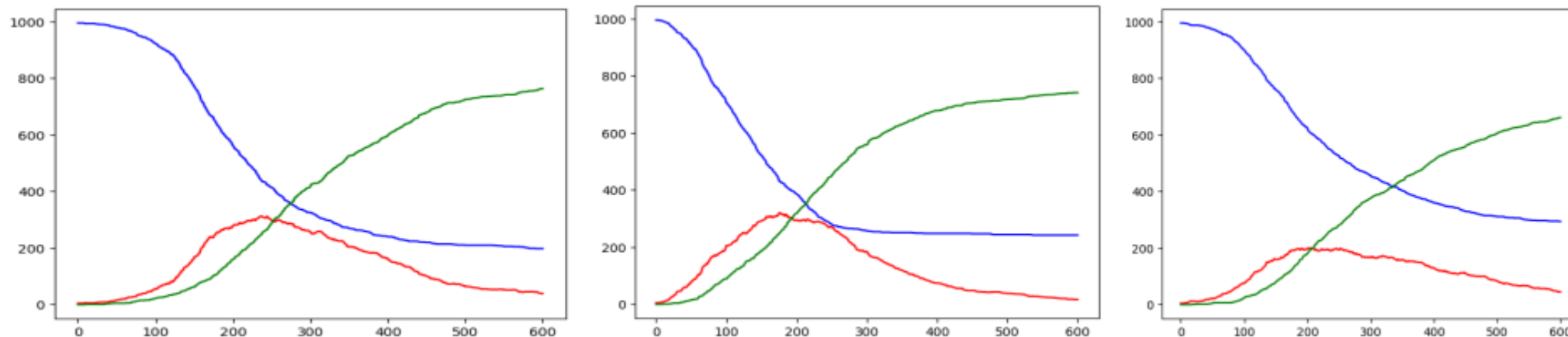
Data for Result 1:

- We take the network at some regular intervals of timestamps. The networks consists of all the nodes which are colored differently indicating the state they are in.(we neglect the edges having recovered node.)

- They have an edge between them if any of the pair of nodes are within the interaction radius of the other.

- The metric we have followed is generalized by simulating the model for different values of N, α, p, β, μ values. Some of them are shown here.

- Since the complex system is very dependent on the probabilistic distributions. A particular order parameter might not explain this.

# Result 1:Spreading Network Modularity(SNM)

Here we define an Order parameter SNM which is similar to the modularity in schelling model but the 2 two groups must be of infected and susceptible

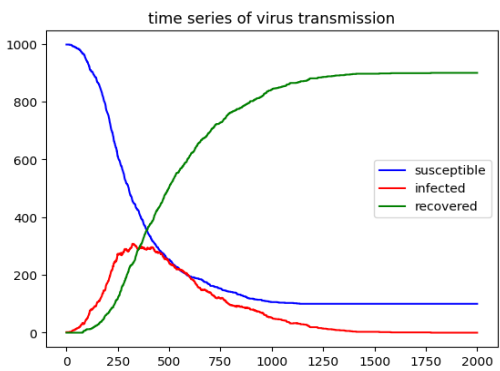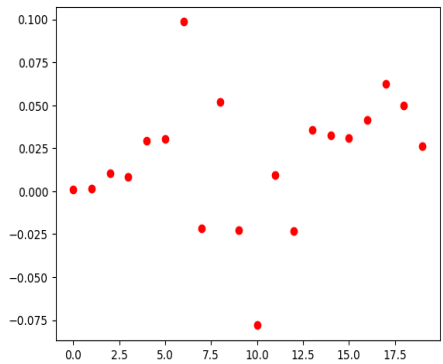$$SNM = (1/2m) \Sigma (A[i][j]-k[i]k[j]/2m)(1- delta[i][j])$$

So Here the rule is that based on how frequent the SNM is positive the rapidness of the infection propagation is higher. If it is less frequent then there will not be a very rapid growth (in other words we can say that it spreads slowly or it has vanished already.)

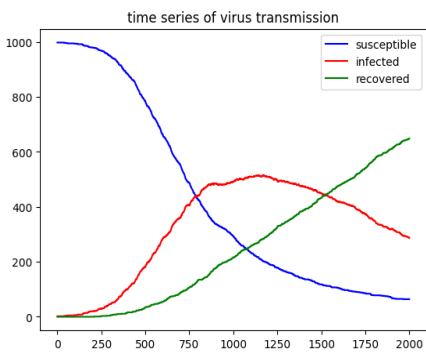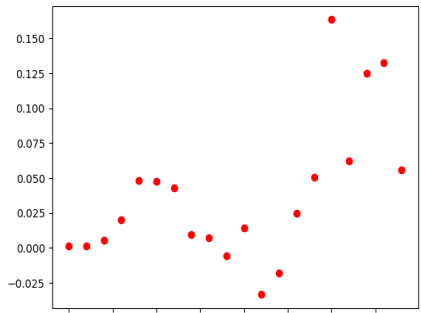Here we have some plot to demonstrate.

Plots for Result 1:
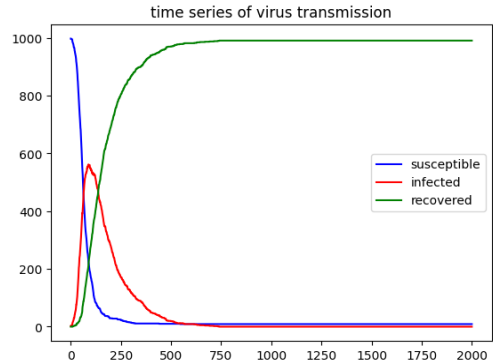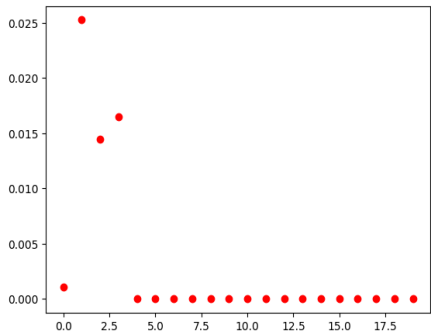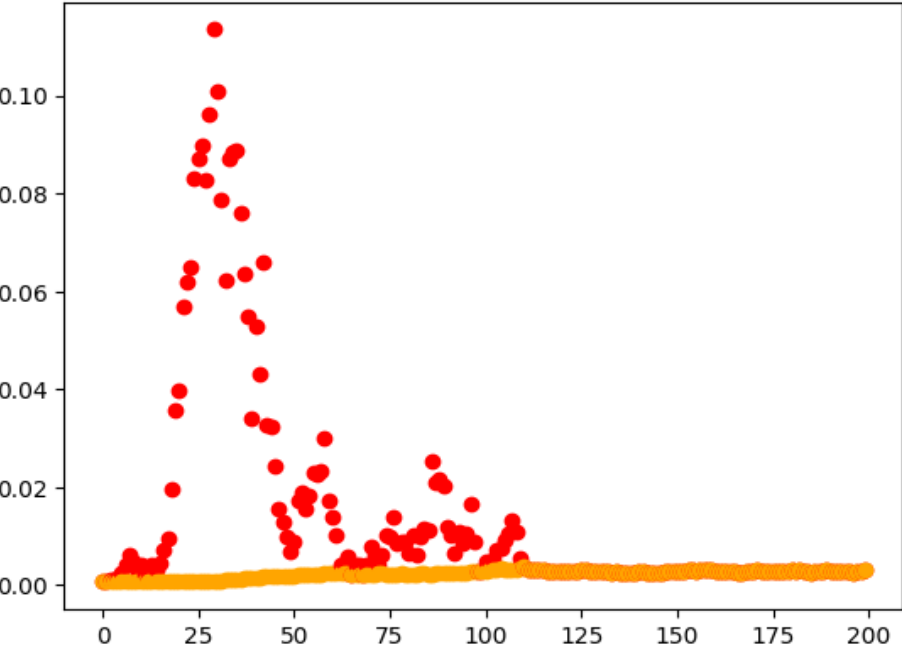
$α,p,β,μ = 0.3,0.6,0.01,0.005$

$α,p,β,μ = 0.7,0.3,0.004,0.001$

$α,p,β,μ = 0.1,0.8,0.06,0.01$

Data Required for Result 2: Equation Discovery

- We get the time series data of the total infected,total suscpetible at time t (i(t),s(t)) of the whole simulation.

- We caculate the integral (i(t)), s(t) , s(t)*i(t).

- Here integral of i(t) can be interpreted as the area under the i(t) curve from 0 to t.

- We use the curve for the mean of the 20 simulation for each set of the parameters that we have taken.

- Here there is no obvious realization but we can observe that those 3 equations consists of the tanh() and log() functions as common.

- Here rate of the Integral of i(t) is considered as the i(t).

- Consider `X0 = infectedIntegral,X1 = Susceptible,X2 = Susceptible * infected`
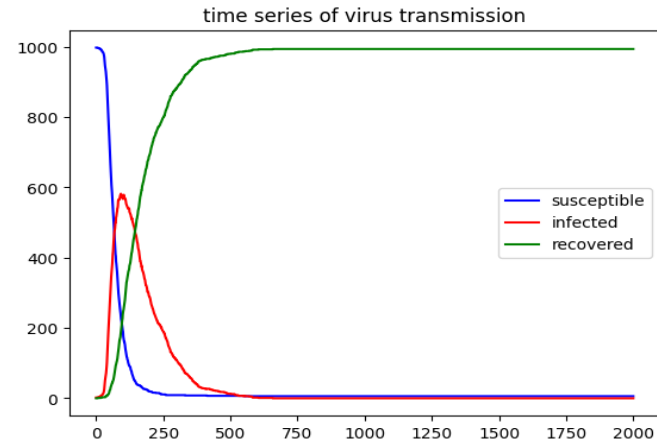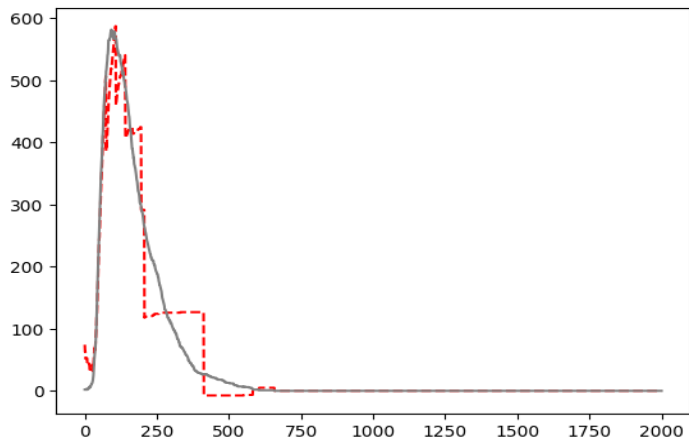
$$i(t) = -1.172\ x1 + 90.544\ \tanh(x1)$$
$$-36.386\ \log(x0) + 210.667\ \log(x1)$$
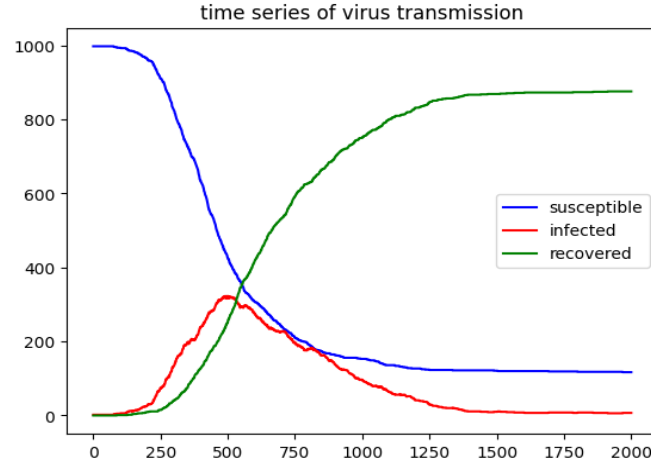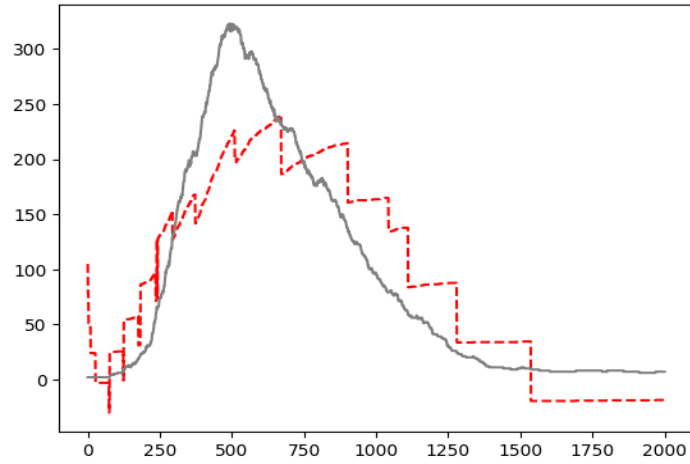
$$i(t) = -0.297\ x1 - 26.974\ \log(x0) +$$
$$3.930\ \log(x1) + 54.015\ \log(x2)$$
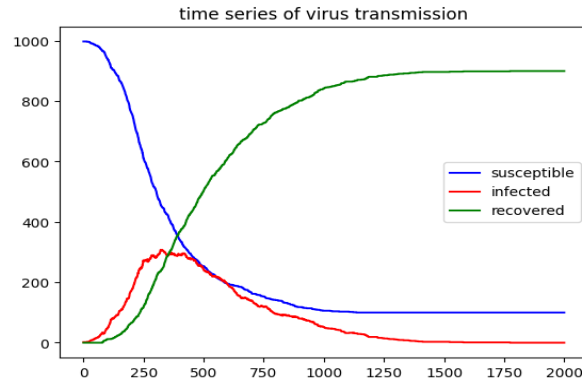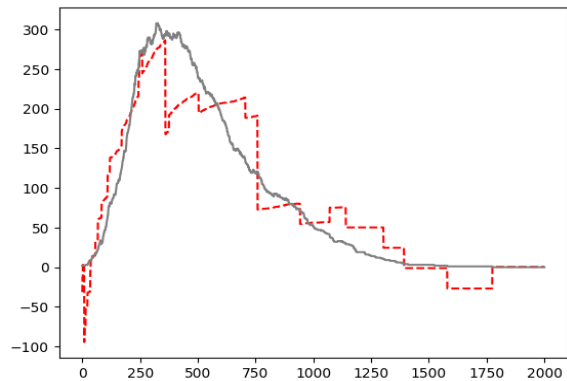
$$i(t) = -0.224\ x1 + -54452.734\ \sinh(x1) +$$
$$15.028\ \tanh(x1) - 32.450\ \log(x0)$$

New questions to ask in the system (max 2 slides)

- Can we propose any other Order parameters with a formal mathematical proof rather than by observation for this system?

  And also, can any assumptions facilitate this?

- If we propose any vaccination facility for this area, then how can we propose the strategies to tackle the disease, and also can there be any order parameter that signifies the effectiveness of the vaccination?

Quick snapshot of other analyses you have done

- This framework offers mathematical insights through a simplified 1D version of the model, rather than relying on data-driven approaches. By interpreting the dynamic contact network as a Markov chain—a core concept in probability theory—it enables rigorous analysis of disease spread. This perspective provides a tractable way to understand epidemic dynamics and evaluate intervention strategies. Key analytical results emerge naturally from this formulation.

$$\Lambda_\ell(t) = 1 - (1 - \lambda i_\ell(t))^{q_\ell N} = 1 - (1 - \lambda q_\ell i(t))^{q_\ell N} .$$

$$\Lambda_{\text{out},d}(t) = 1 - \left(1 - \lambda q_{\text{out},d} i(t)\right)^{q_{\text{out},d} N} .$$

$$E[k_{\text{in},i}] \approx \frac{q_{\text{in}}^2}{\Sigma_\ell^2} (n - 1) \left(\sigma_i^2 + \frac{\sigma_i^{1-\omega} - \sigma_{\text{max}}^{1-\omega}}{\sigma_{\text{min}}^{1-\omega} - \sigma_{\text{max}}^{1-\omega}} \left(\frac{(\omega - 1) \left(\sigma_{\text{max}}^{3-\omega} - \sigma_i^{3-\omega} \right)}{(3 - \omega) \left(\sigma_i^{1-\omega} - \sigma_{\text{max}}^{1-\omega} \right)} - \sigma_i^2 \right) \right) .$$