Computational Model of a Vector Mediated Epidemic

PH599 Computational Physics

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- Epidemic spread is an important Social problem.
- Understanding the spreading pattern helps in formulating measures to control it.

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- \cdot Here, Mosquito \Longrightarrow Vector, Human \Longrightarrow Host

MODELLING A VECTOR-BORNE

DISEASE

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- Entities occupy the nodes of a Graph (N nodes)
- · Vectors are mobile, can hop to neighbour nodes
- Hosts are stationary
- · Only one host per node
- Hosts and vectors can either be infected or healthy

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- Vector infection rate I_v, if present at node with infected host.

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- No. of infected hosts in the system = \mathcal{H} .
- No. of infected vectors in the system = \mathcal{V} .



Simulation Algorithms

Transition rate of the system depends on the following transition rates:

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- Replacement of vector: For each infected vector, this transition is valid, therefore the total rate is $R_{\nu}V$.
- **Vector hopping between nodes**: Each vector hops at rate *D*, therefore the total rate is

$$D\sum_{i\in G}(v_{i,0}+v_{i,1})=DN_{v}.$$

Simulation Algorithms

Transition rate of the system depends on the following transition rates:

• Host Infection: Each uninfected host at node i gets infected at the rate $I_h v_{i,0}$. Therefore, the total rate is $I_h \sum_{i \in G} v_{i,1} (1 - h_i)$.

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- Host Infection: Each uninfected host at node i gets infected at the rate $I_h V_{i,0}$. Therefore, the total rate is $I_h \sum_{i \in G} V_{i,1} (1 h_i)$.
- Vector Infection: Each uninfected vector which is at a node i with an infected host becomes infected at rate I_v . Therefore, the total rate is $I_v \sum_{i \in G} v_{0,i} h_i$.

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- For example, $P_{host \, recovery} = \frac{R_h \mathcal{H}}{R}$
- $p(dt) = Re^{-Rdt}$. But, we can take $dt = \frac{1}{R}$, the average value. Improves performance significantly.

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- Replacement of Vector: Randomly selects an infected vector, based on weights of the vectors, and replaces one infected vector with a healthy vector.
- Vector Hopping: Randomly selects a vector, based on weights of the vectors, then uniformly randomly chooses a neighbour node from the adjacency list and transfers this vector to that node.

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- Vector Infection: Randomly select a node, based on weights of infected host in that node, and infect a vector.

Continuous Time Approach: Pseudo Code

VECTOR-BORNE DISEASE: CONTINUOUS TIME APPROACH

- 1| Initialize the system
- 3| Choose an event from EVENTS randomly based on weights of the events as described above
- 4| Handle the corresponding event based on the procedure given above for each event
- 5| Increment time t -> t + 1/R
- 6| Go to step 3

Continuous Time Approach: Time Complexity

$$O(t_{max} \times R_{max} \times N_{rep} \times N)$$

where, $R_{max} = 5 \times max(N_h, N_v) \times max(R_h, R_v, D, I_v, I_h)$ $N_{rep} = \text{no. of times the experiment is repeated.}$

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- Time taken by this single pass is a small but finite duration, denoted by Δt .
- In this method, no need to maintain a separate list for the vectors.

Discrete Time Approach: Events

• Host Recovery/Infection and Vector Infection: At node j, if the host is infected, then the host recovers with probability $r_h \equiv 1 - exp(-R_h\Delta t)$. And, if there are uninfected vectors at node j, then infect n of them with probability

$$P(n) = \binom{V_{0,j}}{n} (1 - e^{-l_v \Delta t})^n (e^{-l_v \Delta t})^{(v_{0,j} - n)}$$

for $n=0,1,2,\ldots,v_{0,j}$. If the host at site j is not affected, then the host becomes infected with a probability $1-exp(-v_{1,j}I_n\Delta t)$

Discrete Time Approach: Events

 Vector Replacement: At site j, n of the infected vectors are replaced by uninfected vectors, with probability

$$P(n) = \binom{v_{1,j}}{n} (1 - e^{-R_v \Delta t})^n (e^{-R_v \Delta t})^{(v_{1,j} - n)}$$

for $n = 0, 1, 2, ..., V_{1,j}$.

Discrete Time Approach: Events

 Vector Hopping: At site j, n vectors hop, with probability

$$P(n) = \binom{v_{1,j}}{n} (1 - e^{-D\Delta t})^n (e^{-D\Delta t})^{(v_{1,j} - n)}$$

for $n = 0, 1, 2, ..., v_{1,j}$. Choose the new site for each hopping vector from its set of neighbours using the adjacency list.

Discrete Time Approach: Pseudo Code

VECTOR-BORNE DISEASE: DISCRETE TIME APPROACH

- 1| Initialize the system
- 3| Perform all the events as explained above.
- 4| Store the values
- 5| Go to step 3

Discrete Time Approach: Time Complexity

$$O\left(\left\lceil \frac{t_{max}}{\Delta t} \right\rceil \times N_{rep} \times N\right)$$

where, N_{rep} =no. of times the experiment is repeated.

RESULTS

• High computational complexity of the operations as explained in the previous sections.

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- We will work with smaller, less computationally intense parameters.
- We define the vector density (ρ_v) as the average number of vectors per node.

Continuous Time Method: Parameters

Parameters:

- N = 100
- $t_{max} = 180$
- $N_{rep} = 10000$
- $R_h = 2.0$
- $R_{\rm v} = 1.5$
- $I_h = 1.0$
- $I_{v} = 2.0$
- D = 0.5

Continuous Time Method: Plots

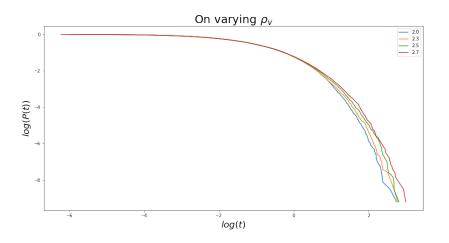


Figure 1: Log-log plot of P(t) vs t

Continuous Time Method: Plots

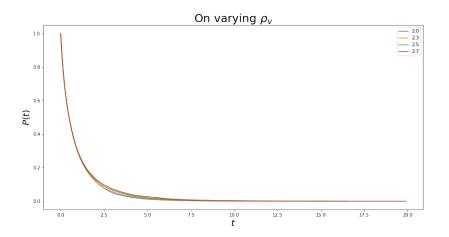


Figure 2: Plot of P(t) vs t

Continuous Time Method: Plots

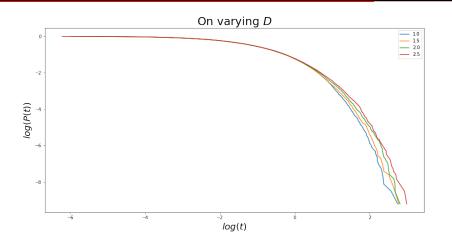


Figure 3: Log-log plot of P(t) vs t on varying D

Discrete Time Method: Parameters

Parameters:

- N = 5000
- $t_{max} = 4000$
- $N_{rep} = 1000$
- $R_h = 1.0$
- $R_{\rm v} = 1.5$
- $I_h = 1.0$
- $I_{\rm v} = 2.0$
- D = 0.5
- $\Delta t = 0.1$

Discrete Time Method: Plots

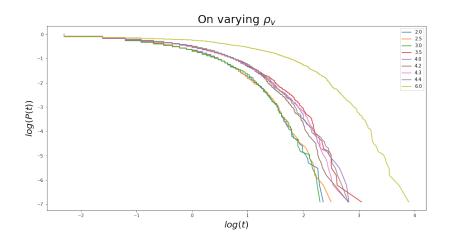


Figure 4: Log-log plot of P(t) vs t

Discrete Time Method: Plots

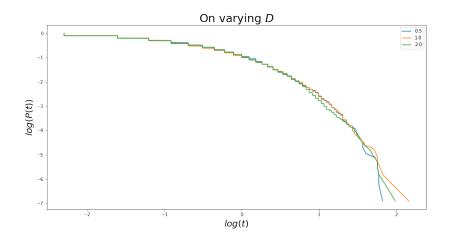


Figure 5: Log-log plot of P(t) vs t on varying D

References



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