

## ECE 5110 Mini Project #2

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### PROMPTS

a) Argue that this random process is a CTMC.

This SIR process is a CTMC because the underlying mechanics are memoryless. Recovery follows an exponential distribution with rate 1, and transmission occurs via independent Poisson processes with rate  $\lambda$ . Because these distributions are memoryless, the time the system has already spent in its current state does not influence the timing or probability of the next event.

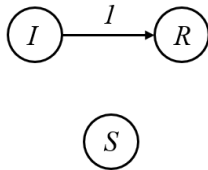
Besides, the system evolves in continuous time with state-dependent rates. Multiple possible transitions (infection or recovery) compete based on the current population state, resulting in exponentially distributed inter-event times.

Draw the transition rate diagram for  $n = 1$  and  $n = 2$ .

If  $n = 1$ , then there are  $3^1 = 3$  states:  $\{S, I, R\}$ ;

If  $n = 2$ , then there are  $3^2 = 9$  states:  $\{SS, SI, SR, IS, II, IR, RS, RI, RR\}$ .

$n = 1$ :

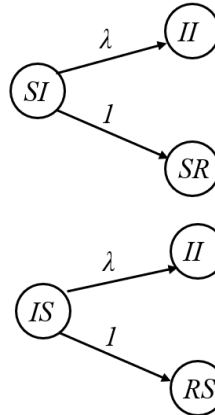


$n = 2$ :

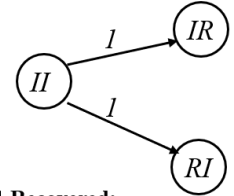
**2 Susceptible:**



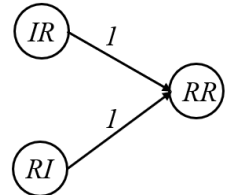
**1 Infected:**



**2 Infected:**



**1 Recovered:**



**2 Recovered:**



Figure 1. Transition Rate Diagrams for  $n = 1$  and  $n = 2$

For  $n = 5$ , describe the set of possible next states for each of the 3 states mentioned above.

The 3 states mentioned above are {IIIII, IISSS, IRSSR}.

i) IIIII: the set will be {RIIII, IRIII, IIRII, IIIRI, IIIIR};

ii) IISSS: the set will be {RISSS, IRSSS, IISSS, IISSI};

iii) IRSSR: the set will be {RRSSR}.

b) Explain why we have  $E[T] = f(n)$ .

Since the expected time to go from  $k$  infected to  $(k-1)$  infected is the mean of that exponential distribution, by summing up all the possible  $k$  ( $k = 1, 2, \dots, n$ ), we can find that the expectation of  $T$  equals  $f(n)$ .

Plot the eradication time  $T$  averaged over many runs for  $n$  and  $f(n)$  for various choices of  $n$  in the range 1 to 1,000. Are the curves close? Explain why the value of  $\lambda$  is immaterial for this simulation.

While averaging the eradication time  $T$  over many runs, according to the Law of Large Numbers, the sample average will converge to the theoretical expected value  $E[T]$ . Any small deviations are due to variance in the random simulation and would decrease further if we increase the number of "many runs".

The value of  $\lambda$  is irrelevant for this specific simulation. The system acts solely as a pure death process (only recoveries occur), which is governed by the recovery rate (mean 1 week), not the transmission rate.

c) Compare the 3 scenarios by plotting  $M$ , averaged over many runs, with  $\lambda$  ranging between .1 and 200. Does inoculation help?

$\lambda$	Consequences
$\lambda$ is very low ( $\lambda < 1$ )	All three curves will converge to the same low value (likely $M = 1$ or 2)
$\lambda$ is very high ( $\lambda > 10$ )	All three curves will converge to the same high value (likely $M = 5$ )

Chart 1.

Yes, inoculation helps by reducing the number of immediate susceptible targets, and thus providing a "firewall" against the spread of the disease.

*Does it make a difference whether we inoculate a neighbor or a randomly-chosen individual?*

Neighbor Inoculation (IRSSS) is the most effective strategy. The circle structure means each infected person has only two immediate neighbors. Inoculating a neighbor cuts off one of patient zero's two paths for immediate spread. This is a strategic block that maximizes the chance of containing the initial outbreak.

By comparison, Random Inoculation (e.g., ISRSS) is less effective. While the randomly chosen person is protected, patient zero still has two susceptible neighbors who can start the spread. The infection must travel farther to reach the protected individual, but the initial, rapid expansion of the disease is not blocked as effectively.

*Explain any differences you see intuitively.*

The recovered individual acts as an absorbing barrier (a "firewall"). When the pathogen transmission process attempts to cross this individual, it fails. Placing this firewall immediately adjacent to the infection source is the most efficient way to reduce the total size of the eventual outbreak.

## IMPLEMENTATION

The initialization steps are quite similar to the previous mini project #1 (the report `Mini_Project_1_Report.pdf` can be found via the following link <https://github.com/hliu030115-Cornell/5110miniProject>).

Next, create a directory for this lab, and create a python file (or more). The components (NumPy, SciPy, and Matplotlib) should be imported at the start of the python code. All the codes relating to this mini project can be found via the following link:

<https://github.com/hliu030115-Cornell/5110miniProject>

After coding, let generative AI check the grammar and logic, and run the codes. The Pass criterion should be the rightly displayed diagrams and the correct outputs.

Acknowledgement Statement: Part of his project is completed with the help from ChatGPT, which I highlighted with light blue.