Introduction to Gillespie's Algorithm in Epidemiology

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Introduction

- Infectious diseases are typically categorized as either acute or chronic.
- Acute refers to "fast" infections, where immune system will quickly counter the pathogen in a very short period and eventually remove the pathogen.
- SIR model categorizes hosts within a population as Susceptible(if previously had not been in contact with pathogen) Infected(if currently contain pathogen) and Recovered(successfully removed infection).



ODE Model

- Susceptible: $\mu N \beta SI/N \mu S$
- Infected: $\beta SI/N$ - γI - μI
- Recovered: $\gamma I \mu R$

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Initial Condition

- $\beta_0 = 1$
- $\mu_0 = 5 \times 10^{-4}$
- $\gamma_0 = 0.1$
- Initial Population: $N_0 = 5000$,
- Initial Susceptible Population: $S_0 = 500$,
- Initial Infected Population: $I_0 = 25$,
- Initial Recovered Population: $R_0 = 4475$

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Simulation:ODE Model

Here's the simulation of SIR model without Demographic Stochasticity.



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Demographic Stochasticity

- Demographic stochasticity is defined as *fluctuations in population processes that arise from the random nature of events at the level of the individual* (Keeling, Rohani,2008).
- Therefore, even though the baseline probability associated with each event is fixed, individuals experience differing fates because of different chances.
- Furthermore, the numbers of susceptible, infectious and recovered have to be an integer since people can't be split in half.

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Events In SIR Stochastic Model

- Overall:6 Events
- Birth occur at rate μN . Result: $S \rightarrow S + 1$.
- Transmission occurs at rate $\beta ir / N$. Result: $I \rightarrow I 1$ and $S \rightarrow S 1$.
- Recovery occurs at rate γI . Result: $R \rightarrow R + 1$ and $I \rightarrow I 1$.
- Death of S, I or R occurs at rate μ S, μ I, μ R. Result: I - 1 and $S \rightarrow S$ - 1, I \rightarrow I - 1. or $R \rightarrow R$ - 1.

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Gillespie's First Reaction Method

The following pseudo-code provides a slower, but often more intuitive, means of modeling demographic stochasticity;

- 1. Label all possible events E_1, \ldots, E_n .
- 2. For each event determine the rate at which it occurs, $R_1, ..., R_n$.
- 3. For each event *m* calculate the time until the next event is $\delta t_m = \frac{-1}{R_m} \log(RAND_m)$.
- 4. Find the event, p, that happens first (has the smallest δt).
- 5. The time is now updated, $t \rightarrow \delta t_p$, and event p is performed.
- 6. Return to Step 2.
- With either of these popular implementations of stochasticity, the amount of computer time needed to simulate a particular disease scenario increases linearly with the population size.
- Similarly, Simulation of a large epidemic with many cases is slower than simulating a disease close to its endemic level, as many more events occur in the same time period.

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Example

Let's do a quick example using Gillispies' first reaction method:

- 1. Possible events:
- 2. Possible rates:
 - $r_1 = 2.5, r_2 = 2.5, r_3 = 2.5$
 - $r_4 = 0.25, r_5 = 0.0125, r_6 = 2.2375$
- 3. Generate a 6×1 vector called *Rand* where $m \in \{1, 2, 3, 4, 5.6\}$, *Rand*(m):= U(0,1)
 - ▶ Rand(1) = 0.3998, Rand(2) = 0.2599, Rand(3) = 0.8001
 - ▶ Rand(4) = 0.4314, Rand(5) = 0.9106, Rand(6) = 0.1818
- 4. Calculate: $\delta t_m = \frac{-1}{R_m} \log(RAND_m)$.
 - $\delta t_1 = 0.3667 \ \delta t_2 = 0.5390 \ \delta t_3 = 0.0892$
 - $\delta t_4 = 3.3627 \ \delta t_5 = 7.4879 \ \delta t_6 = 0.7618$
 - Clearly δt_3 is the smallest
- 5. Now the time is updated to δ t_3 , and population and rates are updated:

►
$$S_1 = S_0 = 500 \ I_1 = I_0 - 1 = 24 \ R_1 = R_0 + 1 = 4476$$

 $\mathbf{6}.$ Go back to Step2 and repeat the process.

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Simulation

Here's the simulation of SIR model that includes Demographic Stochasticity.



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Simulation

Here's another simulation of SIR model that includes Demographic Stochasticity.



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