

# Stochastic Simulation Algorithms

SISMID 2025

# The SIR Model

$$\frac{dS}{dt} = -\beta S \frac{I}{N}$$

$$\frac{dI}{dt} = \beta S \frac{I}{N} - \gamma I$$

$$\frac{dR}{dt} = \beta S I - \gamma I$$

**Recall that:**

Rate of event is proportional to time until event

Here, rates depend on current states (number of S/I/R)

So, rates are constant ***until*** the states change

When the states change, the rates change

# The SIR Model

$$\frac{dS}{dt} = -\beta S \frac{I}{N}$$

$$\frac{dI}{dt} = \beta S \frac{I}{N} - \gamma I$$

$$\frac{dR}{dt} = \beta SI - \gamma I$$

**Recall that:**

For constant rate processes, with rate  $\theta$ , the time until the event occurs can be reasonably modeled as an exponentially distributed random variable with mean  $1/\theta$

# The SIR Model

$$\frac{dS}{dt} = -\beta S \frac{I}{N}$$

$$\frac{dI}{dt} = \beta S \frac{I}{N} - \gamma I$$

$$\frac{dR}{dt} = \beta S I + \gamma I$$

**For this simple SIR model:**

Two kinds of events can happen

1. An infection can occur, which leads to

$S \rightarrow S - 1$  and

$I \rightarrow I + 1$

This occurs at a rate  $\beta S \frac{I}{N}$

2. An infected individual recovers, which leads to

$I \rightarrow I - 1$  and

$R \rightarrow R + 1$

This occurs at a rate  $\gamma I$

# The Gillespie Algorithm

Conditional on current numbers of S, I, R and current time T

1. Take a random draws from Exponential distribution for all possible state transitions

$X$  = random draw from exponential distribution with mean  $1/(\beta S \frac{I}{N})$

$Y$  = random draw from exponential distribution with mean  $1/\gamma I$

2. Update States: IF

$X \leq Y$ , then transmission occurs first:  $S \rightarrow S - 1$ ,  $I \rightarrow I + 1$ , increment time  $T + X$

ELSE, recovery occurs first:  $I \rightarrow I - 1$ ,  $R \rightarrow R + 1$ , increment time  $T + Y$

3. Return to step 1

# Interactive session 1: Run code

Questions:

What was  $R_0$ ?

What did you notice about trajectories?

# Gillespie Algorithm

## Benefits

- Exact translation of stochastic ODE

## Costs

- Computation scales with the number of state transitions (arrows in the SIR model) AND with the population size
- For this example, must draw  $\sim 2$  random variables for every individual in the simulated population

# Tau-leaping Algorithm

$$\frac{dS}{dt} = -\beta S \frac{I}{N}$$

$$\frac{dI}{dt} = \beta S \frac{I}{N} - \gamma I$$

$$\frac{dR}{dt} = \beta SI + \gamma I$$

**Recall that:**

IF an event occurs at a constant rate  $\theta$ , THEN the number of events that will occur in a time interval  $\Delta T$  will be distributed as:

Poisson( $\theta * \Delta T$ )

i.e. number of events will increase with the rate AND the duration of the interval



# Tau-leaping Algorithm

$$\frac{dS}{dt} = -\beta S \frac{I}{N}$$

$$\frac{dI}{dt} = -\beta S \frac{I}{N} - \gamma I$$

$$\frac{dR}{dt} = -\beta SI + \gamma I$$

**So, for relatively small time steps,  $\Delta T$ :**

We can assume that the number of new infections that will occur will be distributed as:

$$\text{Poisson}(\beta S \frac{I}{N} * \Delta T)$$

And the number of recoveries that will occur will be distributed as:

$$\text{Poisson}(\gamma I * \Delta T)$$

# Tau-leaping Algorithm

Conditional on current numbers of S, I, R and time step  $\Delta T$

1. Make random draws:

New infections,  $dSI$ , are random draw from  $\text{Poisson}(\beta S \frac{I}{N} * \Delta T)$

New recoveries,  $dIR$ , are random draw from  $\text{Poisson}(\gamma I * \Delta T)$

2. Update states

$$S_{\text{new}} = S - dSI$$

$$I_{\text{new}} = I + dSI - dIR$$

$$R_{\text{new}} = R + dIR$$

Update time by  $\Delta T$

3. Return to 1

# Tau-leaping Algorithm

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New recoveries, dIR, are random draw from  $\text{Poisson}(\gamma I * \Delta T)$

2. Update states

$$S_{\text{new}} = S - \text{dSI}$$

$$I_{\text{new}} = I + \text{dSI} - \text{dIR}$$

$$R_{\text{new}} = R + \text{dIR}$$

Update time by  $\Delta T$

3. Return to 1

Recall the definitions of **Incidence** and **Prevalence**,

Which of the terms at the left is the **Incidence**?

Which of the terms at the left is the **Prevalence**?

Is the number of children newly diagnosed for measles at clinic **Incidence** or **Prevalence**?

# Tau-leaping Algorithm

## Benefits

- Computation (number of random draws) is independent of population size  
(Note: while this makes a small difference in this code, it makes a **large** difference when simulating with births and deaths)

## Costs

- Inexact. Requires assumption that rate is constant over  $\Delta T$ , even though we know states are changing.

# Interactive session 2: Run code

Questions:

How well do projections of Gillespie and Tau-leaping match?

# Tau-leaping Algorithm

## Benefits

- Computation (number of random draws) is independent of population size  
(Note: while this makes a small difference in this code, it makes a **large** difference when simulating with births and deaths)

## Costs

- Did anyone get “warning” errors?

There were 50 or more warnings (use warnings() to see the first 50)

# Tau-leaping Algorithm

Conditional on current numbers of S, I, R and time step  $\Delta T$

1. Make random draws:

New infections, dSI, are random draw from  $\text{Poisson}(\beta S \frac{I}{N} * \Delta T)$

New recoveries, dIR, are random draw from  $\text{Poisson}(\gamma I * \Delta T)$

2. Update states

$$S_{\text{new}} = S - dSI$$

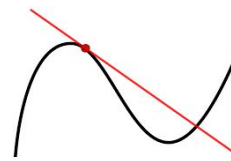
$$I_{\text{new}} = I + dSI - dIR$$

$$R_{\text{new}} = R + dIR$$

Update time by  $\Delta T$

3. Return to 1

Tangent



It is possible to make a random draw of dIR that is greater than I, which makes  $I_{\text{new}} < 0$

This can be addressed by disallowing negative outcomes in code, or using binomial draws

# Tau-leaping Algorithm

$$\frac{dS}{dt} = -\beta S \frac{I}{N}$$

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$$\frac{dR}{dt} = -\beta SI + \gamma I$$

**ALSO, for relatively small time steps,  $\Delta T$ :**

Rate in Poisson process can be translated to probability of event and modeled as a Binomial random variable.

The number of new infections that will occur will be:

$$\text{Binomial}(S, 1 - \exp(-\beta \frac{I}{N} * \Delta T))$$

And the number of recoveries that will occur will be:

$$\text{Binomial}(I, 1 - \exp(-\gamma * \Delta T))$$



# Tau-leaping Algorithm

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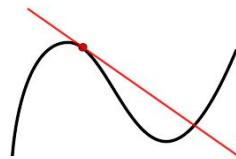
$$\text{Binomial}(I, 1 - \exp(-\gamma * \Delta T))$$

Recall that this expression turns **rate** ( $\beta S \frac{I}{N}$  or  $\gamma$ ) measured over time into **risk**, which is measured per population.

# ODEs, Gillespie, Tau-leaping

- An implicit assumption of the standard ODE representation the SIR model, the difference equation representation, AND both the Gillespie and Tau-leaping algorithms is that the rate of recovery ( $\gamma$ ) is constant across time for each infected individual.
- This means that an individual is just as likely to recover after 1 day as after 10 days or 20 day (if they haven't already recovered)

Tangent

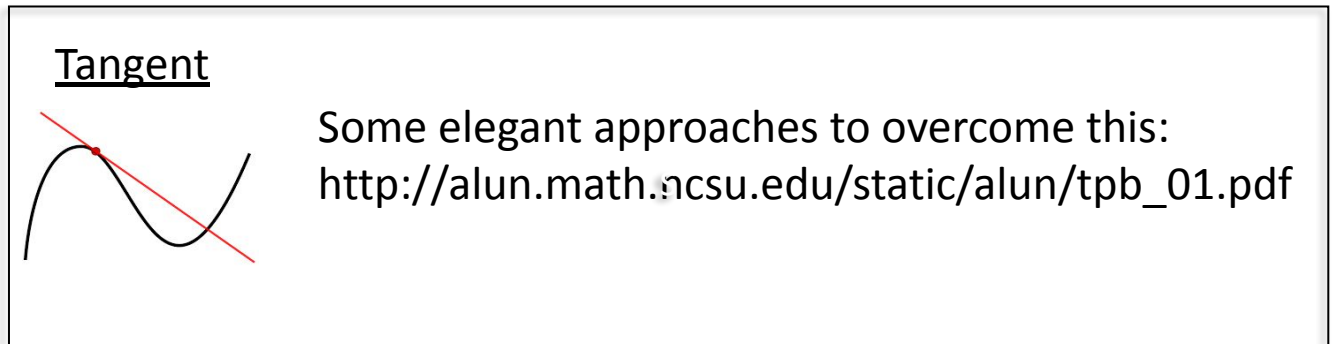


Some elegant approaches to overcome this:  
[http://alun.math.ncsu.edu/static/alun/tpb\\_01.pdf](http://alun.math.ncsu.edu/static/alun/tpb_01.pdf)

# ODEs, Gillespie, Tau-leaping

- An implicit assumption of the standard ODE representation the SIR model, the difference equation representation, AND both the Gillespie and Tau-leaping algorithms is that the rate of recovery ( $\gamma$ ) is constant across time for each infected individual.
- This means that an individual is just as likely to recover after 1 day as after 10 days or 20 day (if they haven't already recovered)

One simple approach to overcome this is to use a time step,  $\Delta T$ , that is equal to the average infectious period,  $1/\gamma$



# Chain Binomial Algorithm

If each infectious individual is expected to be infectious, for on average, a time equal to  $1/\gamma$ , then we can use a time step  $\Delta T$  that is equal to  $1/\gamma$ .

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**Why?** ... well, this means that everyone is infected for the same amount of time (Gillespie and Tau-leaping technically allow some to be infected for very short or very long times.)

# Chain Binomial Algorithm

If each infectious individual is expected to be infectious, for on average, a time equal to  $1/\gamma$ , then we can use a time step  $\Delta T$  that is equal to  $1/\gamma$ .

**Why?** ... well, this means that everyone is infected for the same amount of time (Gillespie and Tau-leaping technically allow some to be infected for very short or very long times.)

**And** ... each case recovers at the end of each time step, so the number of Is in time step  $t$  is ***BOTH*** the prevalence ***AND*** the incidence. So this more naturally matches to observed time series of incident cases.

# Chain Binomial Algorithm

Conditional on current numbers of S, I, R and time step equal to  $1/\gamma$

1.  $I_{\text{new}}$  is a binomial draw from all current susceptibles

$$I_{\text{new}} \sim \text{binomial}(S, 1 - \exp(-\beta \frac{I}{N}))$$

2.  $S_{\text{new}} = S - I_{\text{new}}$

3. Return to 1

Note that magnitude of  $\beta$  will be different than for Gillespie and Tau-leaping algorithms.

Expected value of binomial(N,p) is  $N \cdot p$ .

Here, the expected value of  $I_{\text{new}}$  is when  $I=1$  and  $S=N$  is

$$E[I_{\text{new}}] = S * 1 - \exp(-\beta \frac{I}{N}) \cong \beta * S * \frac{I}{N}$$

$$= N * 1 - \exp(-\beta \frac{1}{N}) = N * 1 - \exp(-\frac{\beta}{N})$$

$$\cong N * \frac{\beta}{N}$$

$$\cong \beta \rightarrow \beta = R_0$$

# Chain Binomial Algorithm

Conditional on current numbers of S, I, R and time step equal to  $1/\gamma$

1.  $I_{\text{new}}$  is a binomial draw from all current susceptibles

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Note that magnitude of  $\beta$  will be different than for Gillespie and Tau-leaping algorithms.

Expected value of binomial(N,p) is  $N \cdot p$ .

Here, the expected value of  $I_{\text{new}}$  when  $I=1$  and  $S=N$  is

$$\begin{aligned} E[I_{\text{new}}] &= S * 1 - \exp(-\beta \frac{I}{N}) \cong \beta * S * \frac{I}{N} \\ &= N * 1 - \exp(-\beta \frac{1}{N}) = N * 1 - \exp(-\frac{\beta}{N}) \\ &\cong N * \frac{\beta}{N} \\ &\cong \beta \rightarrow \beta = R_0 \end{aligned}$$



# Chain Binomial Algorithm

## Benefits

- Computation (number of random draws) is independent of population size
- Only need 1 random draw per time step
- Natural translation to methods for inference ...

## Costs

- Inexact. Requires assumption that rate is constant over  $\Delta T$ , even though we know states are changing.

# Interactive session 3: Run code

Questions:

How well do projections of Chain Binomial match Gillespie and Tau-leaping?

# Chain Binomial Algorithm

## Benefits

- Computation (number of random draws) is independent of population size
- Randomness is limited only to the infection
- Individuals all remain infectious for the same amount time

## Costs

- Inexact. Requires assumption that rates are constant over the entire epidemic

# Chain Binomial Algorithm

Conditional on current numbers of S, I, R and time step equal to  $1/\gamma$

1.  $I_{\text{new}}$  is a binomial draw from all current susceptibles

$$I_{\text{new}} \sim \text{binomial}(S, 1 - \exp(-\beta \frac{I}{N}))$$

2.  $S_{\text{new}} = S - I_{\text{new}}$

3. Return to 1

Note that magnitude of  $\beta$  will be different than for Gillespie and Tau-leaping algorithms.

Expected value of binomial(N,p) is  $N \cdot p$ .

Here, the expected value of  $I_{\text{new}}$  is when  $I=1$  and  $S=N$  is

$$E[I_{\text{new}}] = S * 1 - \exp(-\beta \frac{I}{N}) \cong \frac{\beta}{N} * S * I = \beta * S * I$$

$$= N * 1 - \exp(-\beta \frac{1}{N}) = N * 1 - \exp(-\frac{\beta}{N})$$

$$\beta \text{ is } \sim R_0$$

$$\cong \beta \rightarrow \beta = R_0$$

# Chain Binomial Algorithm – with births

Conditional on current numbers of S, I, R and time step equal to  $1/\gamma$

1.  $I_{\text{new}}$  is a binomial draw from all current susceptibles

$$I_{\text{new}} \sim \text{binomial}(S, 1 - \exp(-\beta \frac{I}{N}))$$

2.  $S_{\text{new}} = B + S - I_{\text{new}}$

Note that magnitude of  $\beta$  will be different than for Gillespie and Tau-leaping algorithms.

3. Return to 1

Expected value of binomial(N,p) is  $N \cdot p$ .

Here, the expected value of  $I_{\text{new}}$  is when  $I=1$  and  $S=N$  is

$$E[I_{\text{new}}] = S * 1 - \exp(-\beta \frac{I}{N}) \cong \frac{\beta}{N} * S * I = \beta * S * I$$

B = birth in each time step

$$\begin{aligned} &= N * 1 - \exp(-\beta \frac{1}{N}) = N * 1 - \exp(-\frac{\beta}{N}) \\ &\cong N * \frac{\beta}{N} \\ &\cong \beta \rightarrow \beta = R_0 \end{aligned}$$