Lecture Notes: Poisson Processes

Poisson processes are a fundamental concept in stochastic modeling, providing a rigorous mathematical framework for understanding events that occur randomly in time or space. Arrival times and counting processes such as Poisson processes find applications in a myriad of contexts, each with its own set of challenges and implications. For instance, in healthcare, modeling the arrival times of patients in an emergency room can be crucial for optimizing resource allocation and improving patient outcomes. Similarly, understanding the time intervals between bus arrivals at a specific stop can offer insights into public transportation scheduling and efficiency. In the realm of computer science, the arrival times of data packets in a network can be analyzed to optimize bandwidth and reduce latency. Businesses too can benefit; for example, modeling the arrival times of customers in a service queue, whether in a call center or a fast-food restaurant, can lead to enhanced service management. Natural events like earthquakes, floods, and forest fires also exhibit arrival times that can be modeled to better understand and predict these phenomena. In retail, the time between customer arrivals at a checkout counter can inform decisions about staffing and service speed. Social media platforms often scrutinize the timing of posts or mentions to understand user engagement or to detect trending topics. In manufacturing, arrival times of components on an assembly line can be critical for identifying bottlenecks and optimizing production. Financial markets are another fertile ground where the arrival times of buy/sell orders can shed light on market dynamics. Finally, in ecology, monitoring the arrival times of different species at a watering hole or feeding station can offer invaluable data for conservation efforts and ecological research.

Counting processes

Definition 1 (Counting Process)**.** *A counting process is a stochastic process* $\{N(t), t \geq 0\}$ *that represents the total number of events that have occurred up to time* t*. The function* $N(t)$ *satisfies the following properties:*

1. $N(0) = 0$ *(initial condition)*
2. $N(t)$ *is integer-valued for all* $t \geq 0$
3. $N(t)$ *is non-decreasing as* t *increases; that is, if* $s < t$*, then* $N(s) \leq N(t)$
4. *The function* $N(t)$ *is right-continuous, meaning that for each* t*,* $\lim_{s \to t^+} N(s) = N(t)$

In simpler terms, a counting process counts the number of times a certain event has occurred by any given time t. The count starts at zero and can only increase as time moves forward.

Consider a time interval T that we divide into n smaller intervals, each of length $\Delta t = \frac{T}{n}$. We are interested in counting the number of occurrences of a particular event within each small time interval Δt.

Initially, let's model this as a Bernoulli process. In each small time interval Δt, the event can either occur with probability p or not occur with probability $1 - p$.

$$P(\text{Event occurs in } \Delta t) = p \tag{1}$$

$$P(\text{Event does not occur in } \Delta t) = 1 - p \tag{2}$$

For large n and small Δt, we can relate p to a rate parameter λ as follows:

$$p = \lambda \Delta t \tag{3}$$

Now, let's consider the number of events X that occur in the entire interval T. The variable X is a sum of n independent Bernoulli random variables, each with success probability p. Therefore, X follows a binomial distribution:

$$X \sim \text{Binomial}(n, p) \tag{4}$$

The probability of observing exactly k events in T is given by:

$$P(X = k) = \binom{n}{k} p^k (1-p)^{(n-k)} \tag{5}$$

Substitute $p = \lambda \Delta t$ and $1 - p = 1 - \lambda \Delta t$:

$$P(X = k) = \binom{n}{k} (\lambda \Delta t)^k (1 - \lambda \Delta t)^{(n-k)} \tag{6}$$

The binomial coefficient can be expanded as:

$$\binom{n}{k} = \frac{n!}{k!(n-k)!} = \frac{n(n-1)\cdots(n-k+1)}{k!} \tag{7}$$

Substitute this into the probability mass function:

$$P(X = k) = \frac{n(n-1)\cdots(n-k+1)}{k!} (\lambda \Delta t)^k (1 - \lambda \Delta t)^{(n-k)} \tag{8}$$

The first limit becomes 1 as n gets larger and larger. The second limit turns into $\exp(-\lambda T)$ in the same way. These observations lead us to a key theorem about how the Bernoulli process evolves into a Poisson process.

Theorem 1 (Convergence from Bernoulli to Poisson)**.** *Let X be the number of events in a time interval T broken down into n smaller intervals. Each smaller interval has length $\Delta t = \frac{T}{n}$. If each interval has a Bernoulli-distributed event occurrence with probability $p = \lambda \Delta t$, then as n approaches infinity with $n \Delta t = T$ constant, the distribution of X turns into a Poisson distribution. Specifically,*

$$\lim_{n \to \infty} \binom{n}{k} p^k (1-p)^{(n-k)} = \frac{(\lambda T)^k}{k!} \exp(-\lambda T) \tag{9}$$

In this limit, X follows a Poisson distribution with parameter λT.

Poisson Processes

In the world of stochastic processes, the Poisson process holds a place of prominence for its mathematical elegance and wide-ranging applicability. It's a vital tool in various domains such as queuing theory, telecommunications, and even quantum physics. The Poisson process serves as a mathematical model for situations where events occur randomly in time or space.

Homogeneous Poisson Process

We start by introducing the most straightforward version of the Poisson process, the Homogeneous Poisson Process. In this variant, the rate at which events happen is constant over time, making it a natural extension of the Bernoulli process under limiting conditions.

Definition 2 (Homogeneous Poisson Process)**.** *Let $(N(t) : t \geq 0)$ be a counting process. $N(t)$ is said to be a Homogeneous Poisson Process with rate $\lambda > 0$ if the following conditions hold:*

1. $N(0) = 0$

2. *The increments are independent.*
3. *The number of events in any interval of length t follows a Poisson distribution with mean λt.*

The Homogeneous Poisson Process is uniquely characterized by its rate parameter λ, which tells us the average number of events per unit time. It's called 'homogeneous' because this rate is constant across time. This process provides a stochastic model for a variety of real-world phenomena where events occur continuously and independently at a constant average rate.

The concept of waiting times is crucial for understanding any stochastic process, and the Poisson process is no exception. In a Homogeneous Poisson Process, the waiting times between successive events are exponentially distributed.

Theorem 2 (Exponential Waiting Times)**.** *In a Homogeneous Poisson Process with rate λ, the time T until the first event occurs follows an exponential distribution with parameter λ, i.e.,*

$$P(T \leq t) = 1 - e^{-\lambda t}$$

This theorem can be derived from the properties of the Poisson process and provides essential insights into the behavior of the system. For example, it tells us that the process has no memory, meaning the time until the next event is independent of the past.

To prove that the waiting times are exponentially distributed in a Homogeneous Poisson Process, let's consider the probability that no event occurs in the interval $[0, t]$. According to the definition of a Homogeneous Poisson Process, the number of events $N(t)$ in any interval $[0, t]$ follows a Poisson distribution with mean λt. Therefore,

$$P(N(t) = 0) = \frac{e^{-\lambda t}(\lambda t)^0}{0!} = e^{-\lambda t} \tag{10}$$

Now, the time T until the first event occurs is greater than t if and only if no event occurs in the interval $[0, t]$. Therefore,

$$P(T > t) = P(N(t) = 0) = e^{-\lambda t} \tag{11}$$

To find the distribution of T, we can find its cumulative distribution function (CDF), which is given by $P(T \leq t)$. The CDF is the complement of $P(T > t)$:

$$P(T \leq t) = 1 - P(T > t) = 1 - e^{-\lambda t} \tag{12}$$

Differentiating both sides with respect to t gives us the probability density function (PDF) of T:

$$f_T(t) = \frac{d}{dt} P(T \leq t) = \lambda e^{-\lambda t} \tag{13}$$

This is the PDF of an exponential distribution with rate parameter λ, completing the proof.

The memoryless property is a unique feature of the exponential distribution that has significant implications for the Poisson process. In mathematical terms, the memoryless property for an exponentially distributed random variable T with rate λ is described as follows:

$$P(T > s + t \,|\, T > s) = P(T > t) \quad \text{for all } s, t \geq 0 \tag{14}$$

This equation states that the probability that we have to wait an additional t time units given that we've already waited s time units is the same as if we had not waited at all.

To prove the memoryless property, we need to show that the conditional probability $P(T > s + t \,|\, T > s)$ equals $P(T > t)$.

Starting with the definition of conditional probability:

$$\begin{aligned} P(T > s + t \,|\, T > s) &= \frac{P(T > s + t \,\text{and}\, T > s)}{P(T > s)} \\ &= \frac{P(T > s + t)}{P(T > s)} \end{aligned}$$

We've used the fact that $T > s + t$ implies $T > s$, which allows us to simplify the numerator. Now, we know that T is exponentially distributed with rate λ, so:

$$\begin{aligned} P(T > s + t \,|\, T > s) &= \frac{e^{-\lambda(s+t)}}{e^{-\lambda s}} \\ &= e^{-\lambda t} \\ &= P(T > t) \end{aligned}$$

This completes the proof of the memoryless property.

Theorem 3 (Memoryless Property)**.** *The waiting times in a Homogeneous Poisson Process are memoryless, i.e., for any $s, t \geq 0$,*

$$P(T > s + t \,|\, T > s) = P(T > t)$$

Non-Homogeneous Poisson Process

The Homogeneous Poisson Process assumes a constant event rate, which may not always be suitable for modeling real-world phenomena. For example, in applications like web traffic analysis or emergency room visits, the rate of events could vary by time of day. The Non-Homogeneous Poisson Process addresses this by allowing a time-dependent rate function $\lambda(t)$.

Definition 3 (Non-Homogeneous Poisson Process)**.** *Let $(N(t) : t \geq 0)$ be a counting process. $N(t)$ is said to be a Non-Homogeneous Poisson Process if the following conditions hold:*

1. $N(0) = 0$
2. *The increments are independent.*
3. *The number of events in any time interval $[s, t]$ follows a Poisson distribution with mean $\int_s^t \lambda(u)\,du$, where $\lambda(t)$ is a rate function that can vary with time.*

In a Non-Homogeneous Poisson Process, the rate function $\lambda(t)$ captures how the event rate varies over time. This rate function must be non-negative for all t and can take on various forms such as linear, sinusoidal, or even step functions to model different kinds of time-dependence.

The Non-Homogeneous Poisson Process retains many of the mathematical properties of its homogeneous counterpart, such as the independence of increments, but it adds a layer of complexity due to the time-dependent rate function. It is widely used in fields like epidemiology to model the spread of diseases, in finance to model the occurrence of extreme events, and in telecommunications to model variable traffic loads.

Birth-Death Process

A Birth-Death process is a specific type of continuous-time Markov chain often used to model population dynamics, queuing systems, and chemical reactions.

Definition 4 (Birth-Death Process)**.** *A Birth-Death process is a continuous-time Markov chain $\{X(t) : t \geq 0\}$ characterized by birth rates λ_n and death rates μ_n depending on the current state n. The process evolves as follows:*

- *From state n, it transitions to state $n+1$ with rate λ_n.*
- *From state n, it transitions to state $n-1$ with rate μ_n.*

Birth-Death processes are widely used in ecology to model population growth and decline, in computer science to model queuing systems, and in epidemiology to model the spread of diseases.

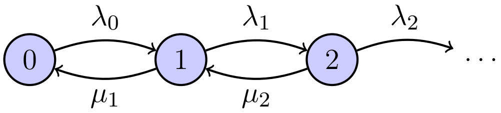


Figure 1: Diagram illustrating a Birth-Death Process

One of the important aspects of a Birth-Death process is its stationary distribution, which describes the long-term behavior of the process. The stationary distribution can often be derived using balance equations.

Stochastic Processes in Real-World Applications: An Integrated Perspective

Stochastic processes offer a powerful mathematical framework for systems evolving under uncertainty. This section provides an integrated overview of various stochastic processes, emphasizing their interconnectedness, properties, and real-world applications. We will focus on Non-Homogeneous Poisson Processes, Birth-Death Processes, and Branching Processes.

Non-Homogeneous Poisson Process: This generalizes the Homogeneous Poisson Process by allowing a time-dependent rate function $\lambda(t)$, making it apt for modeling real-world scenarios like web traffic or emergency room visits where the event rate varies.

Definition 5 (Non-Homogeneous Poisson Process)**.** *Let $(N(t) : t \geq 0)$ be a counting process. $N(t)$ is a Non-Homogeneous Poisson Process if it satisfies:*

1. $N(0) = 0$
2. *The increments are independent.*
3. *The number of events in any interval $[s, t]$ is Poisson-distributed with mean $\int_s^t \lambda(u)\,du$, where $\lambda(t)$ is a non-negative, time-dependent rate function.*

Remark: The flexibility of $\lambda(t)$ allows for modeling various time-dependent behaviors like linear, sinusoidal, or step functions. It's widely used in fields like epidemiology, finance, and telecommunications.

Conditional Waiting Times: Unlike its homogeneous counterpart, the waiting times are not exponentially distributed. Conditional distributions often involve solving integral equations.

Public Bike Availability via Birth-Death Models: In urban areas, public bike-sharing systems require effective management of bike availability. We model a single station as a Birth-Death process.

Model Assumptions:

- The station has a finite capacity of N bikes.
- The rates of returning bikes (λ) and picking up bikes (μ) can be time-dependent, potentially modeled by Non-Homogeneous Poisson Processes.

Mathematical Formulation: Let $X(t)$ denote the number of available bikes at time t. The system transitions between states with time-dependent rates $\lambda_i(t)$ and $\mu_i(t)$.

Steady-State Behavior: Understanding this can offer insights into the optimal rates λ and μ for maintaining bike availability.

Birth-Death Process: This process is a general framework for systems like queues and population dynamics, finding applications in ecology, computer science, and epidemiology.

Definition 6 (Birth-Death Process)**.** *A Birth-Death process is a continuous-time Markov chain* $\{X(t) : t \geq 0\}$ *characterized by birth rates* λ_n *and death rates* μ_n *depending on the current state* n*. The process evolves as follows:*

- *From state* n*, it transitions to state* $n+1$ *with rate* λ_n*.*
- *From state* n*, it transitions to state* $n-1$ *with rate* μ_n*.*

Branching Process: These processes are specialized models used for population growth and decline.

Definition 7 (Branching Process)**.** *A Branching process is a discrete-time Markov chain* $\{Z_n : n \geq 0\}$ *where* Z_n *represents the population size at generation* n*. Each individual in generation* n *produces a random number of offspring for the next generation, typically according to some fixed probability distribution.*

Integrated Insights: Each process has unique features and applications, but they often intersect. For example, a Non-Homogeneous Poisson Process could model the time-dependent rates in a Birth-Death process for a bike-sharing system. This integrated understanding enables robust and accurate modeling of complex real-world systems.

Finally, the Branching Process is another specialized stochastic model that finds applications in fields like biology, where it can model cell division, and epidemiology, where it can represent the spread of a disease.

Definition 8 (Branching Process)**.** *A Branching process is a discrete-time Markov chain* $\{Z_n : n \geq 0\}$ *where* Z_n *represents the population size at generation* n*. Each individual in generation* n *produces a random number of offspring for the next generation, typically according to some fixed probability distribution.*

In summary, while each stochastic process has its unique features and applications, they often intersect in complex ways. For example, a Non-Homogeneous Poisson Process could be used to model the time-dependent rates in a Birth-Death process, enhancing our ability to capture the intricacies of real-world systems.

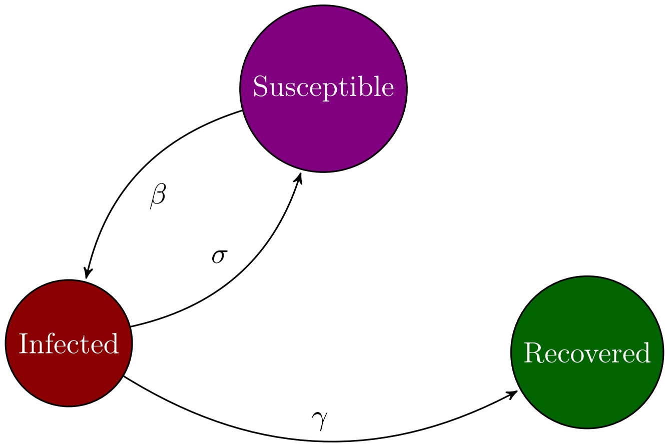
Infectious Disease Dynamics and Compartmental Models

Infectious diseases pose significant risks to public health and understanding their spread is crucial. The Susceptible-Infectious-Recovered (SIR) model is a compartmental model that offers insights into the spread of diseases in a population.

Infectious diseases are a critical concern for public health. The Susceptible-Infectious-Recovered (SIR) model, extended to include a back-transition, provides insights into disease dynamics.

The system can be described as a series of reactions that form the biochemical or epidemiological foundation for transitions between states in the SIR model. These states are denoted as Susceptible (S), Infected (I), and Recovered (R).

1. $S + I \rightarrow 2I$: A Susceptible individual (S) comes into contact with an Infected individual (I) and becomes Infected. This increases the number of Infected individuals by one while decreasing the number of Susceptible individuals by one.



2. $I \to R$: An Infected individual (I) recovers and moves to the Recovered state (R). This decreases the number of Infected individuals by one while increasing the number of Recovered individuals by one.
3. $I \to S$: An Infected individual (I) transitions back to the Susceptible state (S). This decreases the number of Infected individuals by one while increasing the number of Susceptible individuals by one.

The rate constants offer a quantitative measure for the likelihood of each reaction.

- β: The rate constant for the first reaction. It represents the probability of a Susceptible individual becoming Infected upon contact with an Infected individual.
- γ: The rate constant for the second reaction. It represents the probability of an Infected individual recovering and moving to the Recovered state.
- σ: The rate constant for the third reaction. It represents the probability of an Infected individual transitioning back to the Susceptible state.

Rate laws are mathematical expressions that describe how fast a reaction proceeds, accounting for the current number of individuals in the involved states.

- $\beta \cdot [S] \cdot [I]$: The rate at which Susceptible individuals become Infected is proportional to the number of Susceptible individuals ($[S]$) and the number of Infected individuals ($[I]$) at any given time. The rate constant β scales this interaction.
- $\gamma \cdot [I]$: The rate at which Infected individuals recover is proportional to the number of Infected individuals ($[I]$) at any given time. The rate constant γ scales this rate.
- $\sigma \cdot [I]$: The rate at which Infected individuals transition back to the Susceptible state is proportional to the number of Infected individuals ($[I]$) at any given time. The rate constant σ scales this rate.

The exponential distribution is often used to model the time between events in a Poisson process. The probability density function (pdf) of the exponential distribution with rate λ is given by:

with rate parameter:

$$f(t; \lambda) = \lambda e^{-\lambda t} \quad \text{for } t \geq 0$$

$\lambda = \beta \cdot [S] \cdot [I] + \gamma \cdot [I]$

Theorem 4. *Let λ be the total rate of all possible reactions. Given that a reaction will occur next, the conditional probability that it is specifically reaction j is:*

$$P(\textit{Reaction } j \mid \textit{A reaction occurs}) = \frac{\textit{Rate Law of Reaction } j}{\lambda}$$

Note: The denominator, λ, serves as a normalizing constant ensuring the probabilities sum to 1 across all reactions.

In our SIR model, the waiting times for transitions between states are also exponentially distributed. The rates λ correspond to the rate constants β and γ.

Theorem 5 (Sum of Exponentials)**.** *The waiting time T for the next event in a system with multiple exponential processes (each with rate λ_i) is exponentially distributed with rate $\Lambda = \sum_i \lambda_i$.*

Proof:

Let's consider two events, one with rate λ_1 and another with rate λ_2. The combined rate is $\Lambda = \lambda_1 + \lambda_2$.

$$P(T > t) = P(\text{No event in } [0, t]) = e^{-\Lambda t}$$

Thus, the waiting time T for the next event has an exponential distribution with rate Λ.

Discussion: In our model, the next transition event for an Infected individual can be either recovery or back to susceptibility. The total rate Λ for such an individual is $\beta+\gamma$, and the waiting time for the next transition event would be exponentially distributed with this combined rate.

Once the waiting time T has been determined, the specific transition that occurs next is chosen based on a multinomial distribution.

Definition 9 (Multinomial Distribution)**.** *The multinomial distribution is a generalization of the binomial distribution for more than two categories (events). If an experiment can result in n different outcomes, and each outcome i has a probability p_i, then the multinomial distribution describes the probability of observing a specific set of counts among the n categories.*

Theorem 6 (Multinomial Transition)**.** *Given a waiting time T for the next event, the probability of transitioning to state i among n states is $p_i = \frac{\lambda_i}{\Lambda}$, where $\Lambda = \sum_{j=1}^{n} \lambda_j$.*

In the context of the SIR model, once the waiting time for the next event has been determined, the specific transition that occurs (either $S \to I$, $I \to R$, or $I \to S$) is decided by a multinomial distribution with probabilities proportional to the rate constants (β and γ).

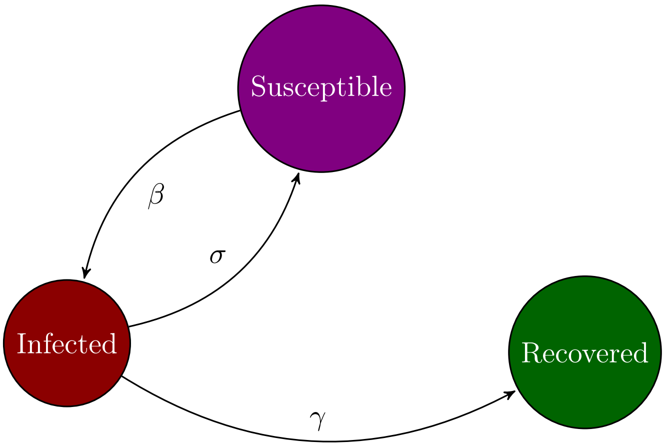
Infectious Disease Dynamics and Compartmental Models

The threat of infectious diseases is ever-present and poses substantial challenges to public health systems globally. Understanding and predicting the dynamics of disease spread are paramount. The Susceptible-Infectious-Recovered (SIR) model, a compartmental model, provides a framework to study these dynamics, especially when extended to include a back-transition possibility.

At the heart of the model are several reactions, which represent the transitions between the states in the SIR model. These reactions are defined as:

1. $S + I \to 2I$: A Susceptible individual encounters an Infected one and becomes Infected.
2. $I \to R$: An Infected individual recovers, transitioning to the Recovered state.
3. $I \to S$: Occasionally, an Infected individual may revert to being Susceptible.

The dynamics are influenced by rate constants, which quantify the probability of each reaction:



- β: The likelihood of a Susceptible individual getting infected upon contact with an Infected individual.
- γ: The probability of an Infected individual recovering.
- σ: The chance of an Infected individual becoming Susceptible again.

The rate laws connect the microscopic interactions to the macroscopic evolution:

- $\beta \cdot [S] \cdot [I]$: The rate at which Susceptible individuals get infected.
- $\gamma \cdot [I]$: The rate of recovery.
- $\sigma \cdot [I]$: The rate of reverting from Infected to Susceptible.

The exponential distribution, commonly used to model time intervals in a Poisson process, is defined by:

$$f(t; \lambda) = \lambda e^{-\lambda t} \quad \text{for } t \geq 0$$

with the rate parameter λ given by:

$$\lambda = \beta \cdot [S] \cdot [I] + \gamma \cdot [I]$$

Our primary theorem highlights the conditional probability of specific reactions:

Theorem 7. *Let λ represent the overall rate of all potential reactions. Given an imminent reaction, the conditional probability of that reaction being specifically reaction j is:*

$$P(\textit{Reaction } j \mid \textit{A reaction will occur}) = \frac{\textit{Rate Law of Reaction } j}{\lambda}$$

In the context of the SIR model, the exponential distribution governs the waiting times for transitions. The rates, λ, correspond to the constants β and γ.

Theorem 8 (Sum of Exponentials)**.** *The waiting time, T, in a system with multiple exponential processes is exponentially distributed with rate:*

$$\Lambda = \sum_i \lambda_i$$

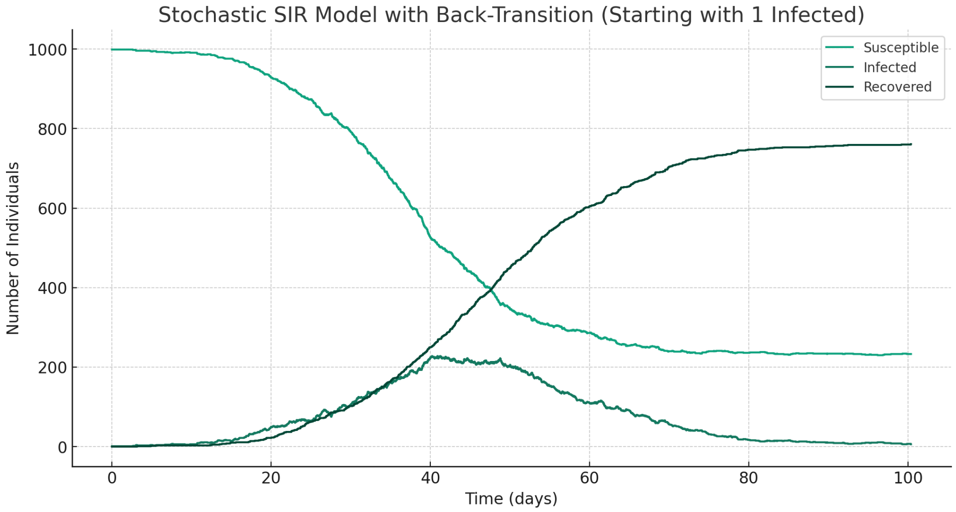


Figure 2: SIR model's time evolution, showing fluctuations in the number of individuals across different states.

This theorem emphasizes that in our model, transitions can lead to either recovery or a return to susceptibility. The combined rate, Λ, is the sum of the individual rates.

The Gillespie algorithm provides a numerical perspective on the SIR model's dynamics. The initial setup consists of 999 Susceptible individuals, 1 Infected individual, and no Recovered individuals, with rate constants set at $\beta = 0.3$, $\gamma = 0.1$, and $\sigma = 0.05$.

This simulation reaffirms our theoretical expectations, highlighting the stochastic nature of disease dynamics.