Nonequilibrium Field Theories and Stochastic Dynamics

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1 Master Equation

Although the Gillespie algorithm can generate a single random trajectory, to understand the statistical properties of the entire stochastic process, we need a more macroscopic descriptive tool. That is the Master equation. Master equation can describe how the probability of the each state in the system evolves over time. It is a deterministic differential equation.

The history of the master equation can be traced back to the early 20th century, when physicists such as Max Born and Werner Heisenberg first introduced it in the context of quantum mechanics and statistical physics. Its core idea is to transform microscopic random processes into a macroscopic description of probability evolution, thereby enabling a systematic analysis of the overall behavior of stochastic systems.

The fundamental principle of the master equation approach is probability conservation: the rate of change of the probability that a system is in a specific state at a given time is equal to the probability flow into that state minus the probability flow out of it. This "gain–loss" balance is not only applicable to physical systems but is also widely used in many fields such as chemical reactions, population dynamics in biology, and financial modeling. The Gillespie algorithm focuses on the stochastic evolution of a single trajectory, while the master equation concerns the deterministic evolution of the entire probability distribution. The two approaches complement each other and together form an essential toolkit for the analysis of stochastic processes.

1.1 From the microscopic process to macroscopic evolution

Let us return to the microscopic description of the Poisson process. We consider the probability $p(n, t + dt)$ of the system is on the state n when $t + dt$ when we derive the Gillespie algorithm. To reach this state, there are only two possible preceding paths:

- At time t, the system is already in state $n - 1$, and then within the next dt a jump occurs. The probability of this jump is vdt. Therefore, the contribution of this path is $p(n - 1, t) \cdot vdt$.
- At time t, the system is already in state n, and then within the next dt a jump dose not occur. The probability of no jump is $1 - vdt$. Therefore, the contribution of this path is $p(n, t) \cdot (1 - vdt)$.

By adding the probabilities of these two mutually exclusive cases, we obtain the expression for $P(n, t + dt)$:

$$p(n, t + dt) = p(n - 1, t) \cdot vdt + p(n, t) \cdot (1 - vdt) \tag{1}$$

Next, we rearrange this equation.

$$\frac{p(n, t + dt) - p(n, t)}{dt} = v \cdot p(n - 1, t) - v \cdot p(n, t) \tag{2}$$

1.2 Gain–Loss Interpretation

The structure of the master equation has a very clear physical meaning: it can be viewed as a balance equation for the probability flow at each state n.

$$\frac{d}{dt}p(n, t) = v \cdot p(n - 1, t) - v \cdot p(n, t) \tag{3}$$

- **Gain term:** $v \cdot p(n-1,t)$ represents the probability flux from state $n-1$ to state n. Its magnitude is equal to the probability of the source state $p(n-1,t)$ multiplied by the transition rate v.
- **Loss term:** $v \cdot p(n,t)$ represents the probability flux from state n to state $n+1$. Its magnitude is equal to the probability of the source state $p(n,t)$ multiplied by the transition rate v.

This "gain–loss" structure is a common feature of all master equations. It is essentially a continuity equation in a discrete state space, describing that the rate of change of the probability "density" equals the net difference between the probability "fluxes" flowing into and out of the state. This also ensures the conservation of total probability.

1.3 From Stochastic Trajectories to Deterministic Evolution

Here we observe a profound conceptual shift. The Gillespie algorithm simulates a single stochastic, unpredictable trajectory $n(t)$. In contrast, the master equation is a deterministic system of differential equations, whose solution $P(n,t)$ is a smooth, predictable function.

The connection between the two lies in the fact that the master equation describes the statistical behavior of an ensemble composed of infinitely many Gillespie trajectories. If we run countless Gillespie simulations and then, at a fixed time t, compile a histogram of the values of n from all simulations, the shape of this histogram will converge to the solution $P(n,t)$ of the master equation. Therefore, the master equation bridges the microscopic randomness with the deterministic evolution of macroscopic probabilities.

Later in the lecture, we also presented the matrix form of the master equation:

$$\frac{d}{dt}\vec{p}(t) = \mathbf{W}\vec{p}(t) \tag{4}$$

Here, $\vec{p}(t)$ is a column vector whose elements are $[p(0,t), p(1,t), p(2,t), \cdots, p(n,t)]$, and $\mathbf{W}$ is a transition rate matrix. This form reveals that the master equation is essentially a system of linear ordinary differential equations, paving the way for using linear algebra tools, such as eigenvalue decomposition, to solve the system dynamics.

2 Solving the Master equation by generating function

Although the master equation has an elegant form, it is essentially an infinite-dimensional system of coupled ordinary differential equations, and solving it directly is usually very difficult. To address this challenge, a powerful tool has been developed in mathematical physics — the generating function.

2.1 Definition and Transformation of the Generating Function

The core idea of the generating function is to perform a nonlinear summation of an infinite sequence of probabilities and encode them into a single function $G(s,t)$:

$$G(s,t) = \sum_{n=0}^{\infty} p(n,t)s^n \tag{5}$$

Here the variable s is an auxiliary variable without direct physical meaning, but it acts like a "ledger": the coefficient of s^n in $G(s,t)$ is exactly the probability $p(n,t)$ which we are interested in. The magical power of the generating function lies in its ability to transform the difference operations in the master equation (such as $p(n,t)$) into algebraic operations. We multiply both sides of the master equation by s^n, and then sum over all n:

$$\sum_{n=0}^{\infty} \frac{d}{dt}p(n,t)s^n = \sum_{n=0}^{\infty} v \cdot p(n-1,t)s^n - \sum_{n=0}^{\infty} v \cdot p(n,t)s^n \tag{6}$$

Let us handle this equation term by term:

- **Left side:** Since summation and differentiation can be interchanged, we obtain

$$\sum_{n=0}^{\infty} \frac{d}{dt} p(n,t) s^n = \frac{d}{dt} \sum_{n=0}^{\infty} p(n,t) s^n = \frac{d}{dt} G(s,t) \tag{7}$$

- **The second term in the right side:**

$$\sum_{n=0}^{\infty} v \cdot p(n,t) s^n = v \cdot \sum_{n=0}^{\infty} p(n,t) s^n = v \cdot G(s,t) \tag{8}$$

- **The first term in the right side:** This is the most crucial step. We make a change of variables, letting $m = n - 1$, thus $n = m + 1$

$$\sum_{n=0}^{\infty} v \cdot p(n-1,t) s^n = \sum_{m=0}^{\infty} v \cdot p(m,t) s^{m+1} = v \cdot s \cdot \sum_{m=0}^{\infty} p(m,t) s^m = v \cdot s \cdot G(s,t) \tag{9}$$

By combining these three terms, we have successfully transformed the infinite-dimensional system of ordinary differential equations into a single-variable partial differential equation:

$$\frac{d}{dt} G(s,t) = v \cdot s \cdot G(s,t) - v \cdot G(s,t) \tag{10}$$

2.2 Solving and Result Restoration/Reconstruction

The equation for $G(s,t)$ is a simple first-order linear ordinary differential equation (for fixed s), which we can solve directly by integration. First, we need an initial condition. Typically, we assume the system starts from state n at $t = 0$, i.e., $p(n,0) = \delta_{n,0}$. This initial condition corresponds in the generating function space to:

$$G(s,0) = \sum_{n=0}^{\infty} p(n,0) s^n = p(0,0) s^0 = 1 \tag{11}$$

Now, by solving the differential equation $\frac{dG}{G} = v(s-1)dt$ and integrating from $t = 0$ to t, we obtain:

$$\ln(G(s,t)) - \ln(G(s,0)) = v(s-1)t \rightarrow G(s,t) = \exp(v(s-1)t) \tag{12}$$

We have thus obtained the analytical expression for the generating function. The final step is how to "decode" the probability $p(n,t)$ from $G(s,t)$. According to the definition of the Taylor expansion, $p(n,t)$ is precisely the coefficient of s^n in the Taylor expansion of $G(s,t)$ at $(s = 0)$, divided by $n!$. A more intuitive approach is to directly expand $G(s,t)$:

$$G(s,t) = \sum_{n=0}^{\infty} \frac{(vt)^n}{n!} s^n e^{-vt} = \sum_{n=0}^{\infty} [e^{-vt} \frac{(vt)^n}{n!}] s^n. \tag{13}$$

By comparing this expansion term by term with the generating function definition $G(s,t) = \sum_{n=0}^{\infty} p(n,t) s^n$, we immediately obtain the solution of the master equation:

$$p(n,t) = e^{-vt} \frac{(vt)^n}{n!} \tag{14}$$

This is exactly the familiar Poisson distribution with mean $(\lambda = vt)$.

2.3 The Power of Generating Functions: Calculating Moments

Generating functions not only allow us to solve the master equation analytically, but they also provide a straightforward way to compute the moments of the distribution. Recall the definition:

$$G(s,t) = \sum_{n=0}^{\infty} p(n,t)s^n. \tag{15}$$

The moments of the random variable $n(t)$ can be obtained by differentiating the generating function with respect to s and then evaluating at $s = 1$:

- **Mean (first moment):**

$$\langle n(t)\rangle = \sum_{n=0}^{\infty} np(n,t) = \left.\frac{\partial G(s,t)}{\partial s}\right|_{s=1} = vt\exp\left(vt(s-1)\right)|_{s=1} = vt \tag{16}$$

- **Second moment:**

$$\langle n^2(t)\rangle = \left.\frac{\partial^2 G(s,t)}{\partial s^2}\right|_{s=1} + \langle n(t)\rangle \tag{17}$$

- **Variance:**

$$\mathrm{Var}[n(t)] = \langle n^2(t)\rangle - \langle n(t)\rangle^2 \tag{18}$$

For the Poisson generating function $G(s,t) = e^{vt(s-1)}$, we immediately get:

$$\langle n(t)\rangle = vt, \quad \mathrm{Var}[n(t)] = vt. \tag{19}$$

2.4 Summary

This lecture guided us to a deeper understanding of stochastic processes from three complementary perspectives: the Gillespie algorithm, the master equation, and the generating function. Together, they form a powerful and complete theoretical and computational framework.

- **Gillespie Algorithm**: Provides a numerical simulation perspective. It is an event-driven and exact algorithm that generates individual trajectories of stochastic processes, allowing us to directly observe how randomness manifests.
- **Master Equation**: Provides a probability evolution perspective. It is a deterministic differential equation that describes how the probabilities of the system being in different states evolve over time, capturing the statistical laws of the entire ensemble of stochastic trajectories.
- **Generating Function**: Provides an analytical solution perspective. It is a powerful mathematical tool that transforms the complex master equation (an infinite-dimensional system of differential equations) into a simple single equation, enabling the derivation of analytic probability distributions and the convenient calculation of statistical moments.

Each of these three approaches has its own focus, and together they provide a solid foundation for analyzing a wide range of stochastic phenomena—from particle motion in physics to population dynamics in biology.

3 Linear Death Process: The Basis of Stochastic Population Models

3.1 Application: An Introduction to Population Dynamics

Consider the simplest model: the Simple Death Process. This process can be expressed in a chemical reaction–like form:

$$A \to 0 \tag{20}$$

This indicates that individuals of species A die or disappear from the system at a certain rate. The key point here is the physical meaning of λ : it is the per capita death rate.

This means that if there are currently n individuals in the system, then the total death rate of the population is $n\lambda$. This is a crucial distinction: the transition rate is no longer a constant but depends on the current state n of the system. Such **state-dependent rates** are a common and important concept in stochastic modeling.

We can once again use the "Gain–Loss" logic to construct the master equation for this process. What we are interested in is the probability $p(n,t)$ that the population size is n at time t.

- Gain term (GAIN): For the system to reach state n at time t, it must have come from state $n+1$ through a single death event. When the population size is $n+1$, the total death rate is $(n+1)\lambda$. Therefore, the probability flux from state $n+1$ into state n is $(n+1)\lambda p(n+1,t)$
- Loss term (LOSS): If the system is currently in state n. it will leave this state due to a death event. In this case, the total death rate is $n\lambda$. Therefore, the probability flux out of state n is $n\lambda p(n,t)$

Combining the gain and loss terms, we obtain the master equation for the simple death process:

$$\frac{d}{dt}p(n,t) = (n+1)\lambda p(n+1,t) - n\lambda p(n,t). \tag{21}$$

The structure of this equation is similar to the master equation for the Poisson process, but the transition rate has changed from a constant λ to the state-dependent form $n\lambda$. This seemingly simple modification leads to a qualitative change in the system's dynamical behavior. This is an infinite-dimensional coupled system of ordinary differential equations (for $(n = 0, 1, 2, \dots)$), making its direct solution quite challenging.

3.2 Exact solution: reveals the binomial nature of survival

Instead of directly solving the master equation, let us start with a simpler problem and then gradually generalize.

The survival of the single body First, consider the case where there is only one individual initially $n_0 = 1$. What is the probability that this individual is still alive at time t? This is a classic exponential waiting-time problem. In any infinitesimal time interval dt, the probability of its death is λdt. Therefore, the probability $p(t)$ that it is still alive at time t satisfies:

$$\frac{d}{dt}p(t) = -\lambda p(t) \tag{22}$$

The solution is $p(t) = \exp(-\lambda t)$. Accordingly, the probability that it has died by time t is $q(t) = 1 - p(t) = 1 - \exp(-\lambda t)$,

Generalization to N_0 individuals Now, let us return to the case with an initial population of N_0. A core assumption of the linear death process is that the death events of each individual are independent. The death of one individual does not affect the probability of death of another. This implies that, at time t, the survival of the entire population can be viewed as N_0 independent "Bernoulli trials."

Each trial corresponds to an initial individual, and the outcome of each trial has only two possibilities:

- The individual survives until time t, with probability $p(t) = \exp(-\lambda t)$
- The individual dies until time t, with probability $q(t) = 1 - \exp(-\lambda t)$

We are interested in the probability that, out of N_0 trials, exactly N are "successes" (i.e., N individuals survive). This is precisely the definition of the binomial distribution! Therefore, we can directly write its probability distribution:

$$p(n,t) = \binom{N_0}{n}[p(t)]^N[q(t)]^{N_0-N} = \binom{N_0}{n}(e^{-\lambda t})^n(1-e^{-\lambda t})^{N_0-N}. \tag{23}$$

Once we know that the probability distribution is binomial, we can use its well-known properties to compute the mean and variance. For a binomial distribution with parameters N_0 and $p(t) = \exp(-\lambda t)$, the mean is

$$\langle n \rangle = N_0 p(t) = N_0 e^{-\lambda t}, \tag{24}$$

and the variance is

$$\mathrm{Var}(n) = N_0 p(t)(1 - p(t)) = N_0 e^{-\lambda t}(1 - e^{-\lambda t}). \tag{25}$$

Here we uncover a crucial conclusion: the mean of the stochastic process $\langle n \rangle$, exactly coincides with the deterministic mean-field solution we derived earlier! This is a beautifully general result for all linear processes. It tells us that the deterministic equation indeed captures the system's average behavior correctly.

However, the variance $\mathrm{Var}(n)$ is an entirely new quantity, arising purely from stochasticity. It quantifies the magnitude of "population noise"—that is, the extent to which actual population trajectories fluctuate around the mean due to the randomness of individual death events. This is information that the mean-field approach cannot capture at all.

3.3 Verification by computation: simulating the linear death process

We can modify the previous Gillespie algorithm to simulate this state-dependent death process. The only essential change is that, when computing the waiting time, the rate used is no longer a constant but a function of the current population size n.

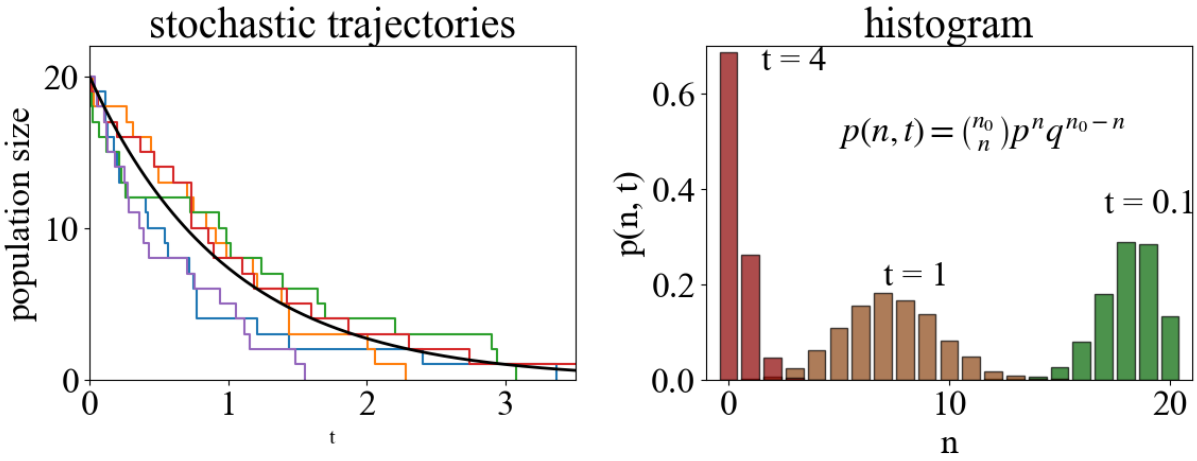

Figure 1:

Right panel (histogram): This figure shows the probability distribution of the population size at three different time points $t = 0.1, 1, 4$. The bars represent the empirical distributions obtained from tens of thousands of Gillespie simulations. As time progresses, the peak of the distribution shifts to the left (indicating a decrease in the average population) and the distribution widens (reflecting increased relative uncertainty). Eventually, at long times, most simulations end with population extinction $n = 0$. This dynamic behavior perfectly matches the binomial distribution we derived.

Left panel (stochastic trajectories): This figure shows three independent simulation trajectories (colored step lines). Each trajectory represents a possible history. The smooth black curve corresponds to the deterministic solution $n(t) = n_0 \exp(-\lambda t)$, i.e., the mean of the stochastic process. This figure intuitively illustrates the key feature of stochastic processes: individual realizations (trajectories) are random and discrete, but the average over many realizations converges to the deterministic mean-field solution.

4 Lotka–Volterra Process: Simulating Predator–Prey Interactions

After mastering the simplest single-species model, we now move on to a more complex and intriguing system: an ecosystem consisting of two interacting species—predators and prey. This is the well-known Lotka–Volterra model. We will see that nonlinear interactions between species give rise to dynamics far richer and more surprising than those of linear processes.

The Lotka–Volterra equations are a set of coupled nonlinear differential equations that describe the dynamics of predator–prey ecosystems. This model originated in the early 20th century out of the needs of ecological research. It was independently proposed by Alfred Lotka and Vito Volterra to explain the periodic fluctuations in predator and prey populations observed in nature.

4.1 Building an Ecosystem: The Basic Stochastic Process

We difine two kinds of species in the system:

- A: Predator
- B: Prey

The dynamics of this ecosystem are governed by four fundamental (or elementary) stochastic processes:

1. **Predator Death:** Predators may die due to natural causes. This is a linear death process, similar to the one we analyzed before.
$$A \xrightarrow{\lambda} \tag{26}$$
2. **Prey Birth:** Prey reproduce by themselves. Assuming sufficient resources, this is also a linear birth process.
$$B \xrightarrow{\beta} B + B \tag{27}$$
3. **Predation:** This is the core interaction of the model. When a predator A encounters a prey B, the prey is consumed, and at the same time a new predator is produced.
$$A + B \xrightarrow{\gamma_p} A + A \tag{28}$$
4. **Prey Competition:** When the prey population is too large, individuals compete for limited resources (e.g., food, space), leading to the death of one prey.
$$B + B \xrightarrow{\gamma_c} B \tag{29}$$

4.2 Quantifying Change: Propensity Functions

To simulate this system with the Gillespie algorithm or to derive its mean-field equations, we need to translate the symbolic reactions into mathematical rate expressions, namely the propensity functions. A propensity function a_μ represents the probability that reaction μ occurs within a unit time interval.

Assume the current system state is (N_A, N_B), where N_A is the number of predators and N_B is the number of prey.

- Predator death ($a_1 = \lambda N_A$): The total rate is proportional to the predator population N_A, just like in the linear death process.
- Prey birth ($a_2 = \lambda N_B$): The total rate is proportional to the prey population N_B.
- Predation ($a_3 = \gamma_p N_A N_B$): The total rate is proportional to the product ($N_A N_B$). This quadratic term is the key to the model. It arises from the law of mass action, which assumes that in a well-mixed system, the frequency of encounters between two different types of individuals is proportional to the product of their abundances.
- Prey competition ($a_4 = \gamma_c N_B(N_B - 1)$): Competition requires two prey individuals. Among N_B prey, the number of distinct pairs is $\binom{N_B}{2} = \frac{N_B(N_B-1)}{2}$. Therefore, the total rate is proportional to this. In Professor Frey's lecture notes, the rate constant is defined as (γ_c), which absorbs the factor $\frac{1}{2}$, so the propensity is written as $a_4 = \gamma_c N_B(N_B - 1)$. When N_B is large, this is approximately proportional to N_B^2.

4.3 Mean-Field Approximation: Coupled Rate Equations

Similar to the linear death process, we can derive deterministic equations describing the average behavior of the system by neglecting stochastic fluctuations. We introduce continuous variables $a(t)$ and $b(t)$, representing the population densities of predators and prey, respectively.

Predator density $a(t)$:

- Decreases due to natural death, with rate $-\lambda a$.
- Increases due to predation of prey, with rate $+\gamma_p ab$.

Combining these, we obtain: $\frac{d}{dt}a(t) = (-\lambda + \gamma_p b)\, a$.

Prey density $b(t)$:

- Increases due to self-reproduction, with rate $+\mu b$.
- Decreases due to predation, with rate $-\gamma_p ab$.
- Decreases due to internal competition, with rate $-\gamma_c b^2$ (here we useb^2 as the continuous approximation of $b(b-1)$).

Combining these, we obtain: $\frac{d}{dt}b(t) = (\mu - \gamma_p a - \gamma_c b)\, b$.

These coupled nonlinear differential equations are the deterministic Lotka–Volterra equations.

4.4 Dynamics in Phase Space: Fixed Points and Phase Portraits

The long-term behavior of the deterministic equations can be understood by analyzing their flow in the phase space (a, b). We are interested in the fixed points, that is, the points where the population densities no longer change ($\partial_t a = 0$ and $\partial_t b = 0$).

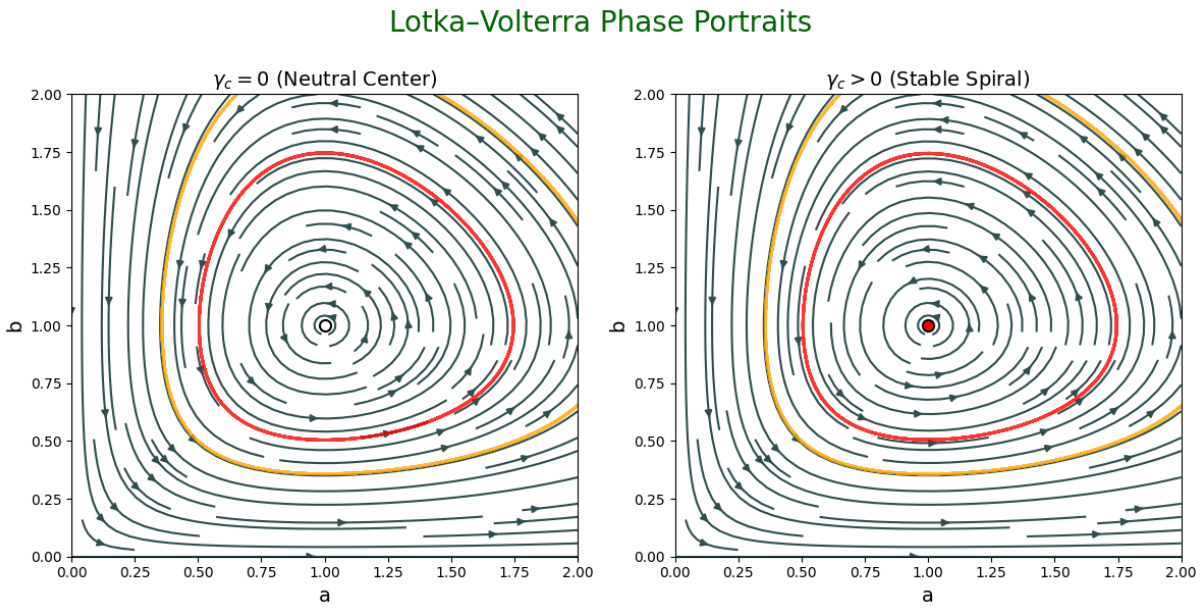

Figure 2:

Left panel ((a)): This figure clearly illustrates a neutrally stable center. The streamlines form closed loops around the central fixed point (white circle). The two trajectories we plotted (orange and dark orange) follow these closed orbits, neither approaching nor moving away from the center. This represents persistent periodic oscillations in the predator and prey populations.

Right panel ((b)): This figure shows a stable spiral point. The streamlines now all point toward the central fixed point (red circle). The trajectory we plotted (red) demonstrates population numbers oscillating while gradually decaying, eventually settling into a stable coexistence state.

4.5 Full Stochastic Simulation: The Power of the Gillespie Algorithm

The deterministic model provides us with a blueprint of the system's average behavior, but the real story is hidden in the randomness. We will now use the Gillespie algorithm to simulate the full stochastic Lotka–Volterra process.

1. **Initialization**: At time $t = 0$, set the state (N_A, N_B).
2. **Compute all propensities**: Based on the current state (N_A, N_B), compute the propensities for all four reactions $\alpha_1, \alpha_2, \alpha_3, \alpha_4$.
3. **Compute total reaction rate**: Sum the propensities to get the total rate $\alpha_{\text{tot}} = \sum_{\mu=1}^{4} \alpha_\mu$.
4. **Determine the waiting time**: Generate the waiting time for the next event $\tau = -\frac{1}{\alpha_{\text{tot}}} \ln(\xi_1)$, where ξ_1 is a uniform random number on $[0, 1)$.
5. **Select the event that occurs**: This is the critical step. We need to determine which specific event occurs based on the relative probability of each reaction $\alpha_\mu/\alpha_{\text{tot}}$. This can be achieved through a **"roulette wheel" selection scheme**: Generate a second uniform random number $\xi_2 \in [0, 1)$, and then select the reaction μ that satisfies

$$\sum_{\nu=1}^{\mu-1} \alpha_\nu < \xi_2 \alpha_{\text{tot}} \leq \sum_{\nu=1}^{\mu} \alpha_\nu$$

6. **Execute the event**: According to the selected reaction type, update the system state based on the state change.
7. **Update time**: Advance the current time: $t \leftarrow t + \tau$.
8. **Repeat**: Return to Step 2 and continue the simulation until the preset total simulation time is reached.

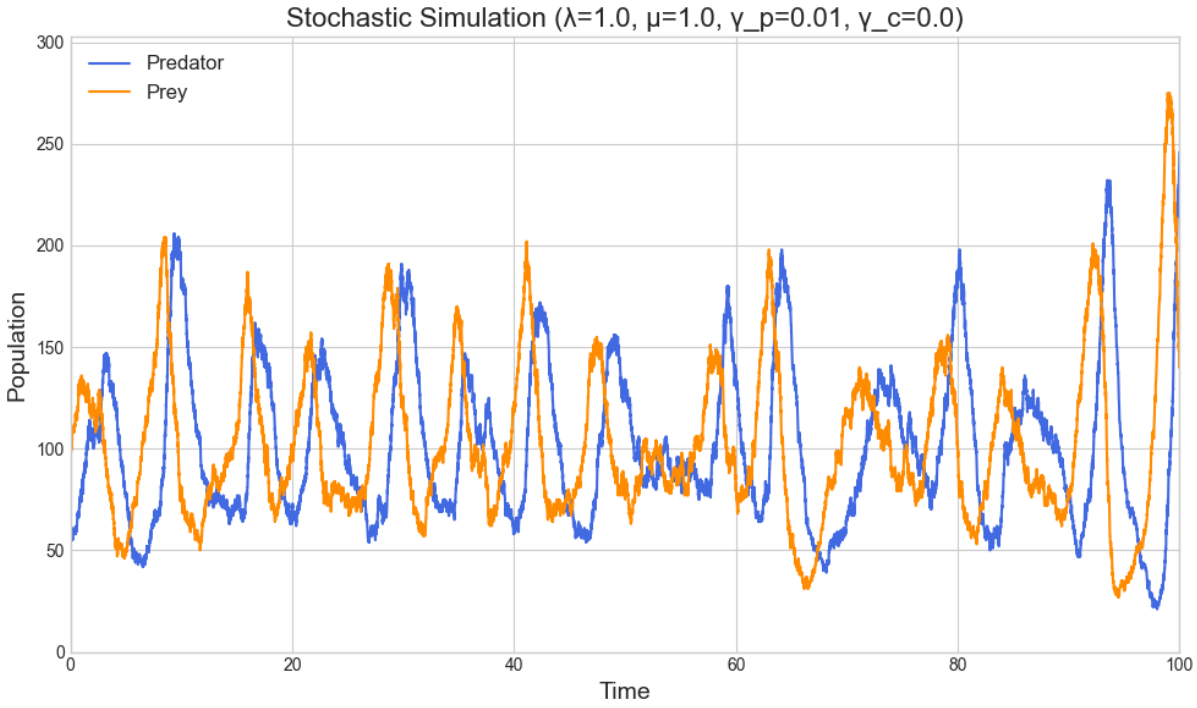

Figure 3:

This figure shows the result of a typical stochastic simulation **without prey competition** ($\gamma_c = 0$). We can observe clear **predator-prey oscillations**: The prey population (orange line) increases first, followed by an increase in the predator population (blue line) due to the abundance of food. The rise in predators then causes the prey population to drop, and subsequently, the predator population declines due to food scarcity, completing a cycle. However, unlike the perfect periodicity of the deterministic model, the **amplitude and period of the oscillations here vary randomly**.

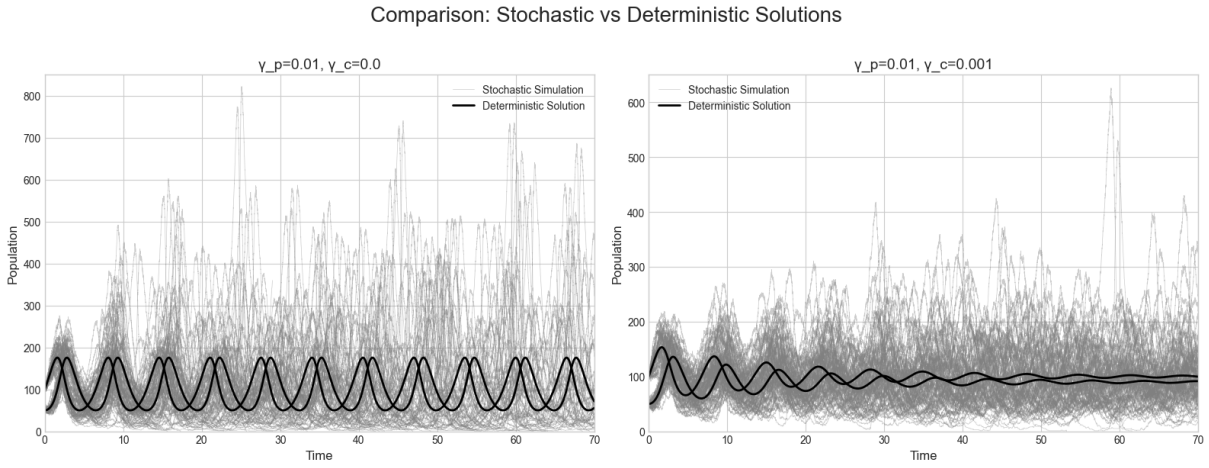

Figure 4:

The left sub-figure: The deterministic solution (thick black line) is a perfect, stable, periodic orbit. However, the behavior of the stochastic simulation (thin gray line) is fundamentally different. The amplitude of the stochastic trajectory's oscillations tends to continuously increase, exhibiting progressively higher peaks and lower troughs. Why is this? The deterministic system is conservative and is "imprisoned" on a single orbit determined by the initial conditions. In contrast, stochastic events (birth, death) act like random "kicks" to the system, allowing it to randomly walk between different orbits. Since there is no force to pull it back to a specific orbit, this random walk causes the oscillation amplitude to diffuse, greatly increasing the risk of one species' population reaching zero (i.e., extinction). In this scenario, **intrinsic noise acts to destroy stability.

The Right sub-figure: With the introduction of prey competition, the deterministic solution (thick black line) exhibits damped oscillations, eventually stabilizing at a single fixed point. The ecosystem reaches a static equilibrium. However, the stochastic simulation (thin gray line) tells a different story once again. The trajectory is indeed attracted to the vicinity of the fixed point, but it does not stop there. Instead, it continues to fluctuate randomly around the fixed point. Here, the deterministic dynamics act like a "**restoring force**", constantly trying to pull the system back to the equilibrium point; while the stochastic events act like a continuous "**driving force**", constantly kicking the system away from the equilibrium point. The dynamic balance achieved between these two forces allows the system to sustain continuous, noisy oscillations. In this case, intrinsic noise acts to maintain dynamics and prevent the system from "dying".

5 Summary

1. **Deterministic models capture average behavior**: For linear processes, or non-linear processes with extremely large population sizes (mean-field), the deterministic (average field) equations provide a good description of the system's average dynamics. For example, the mean value of a linear death process is exactly the same as the deterministic solution.

2. **Stochastic models reveal the nature of fluctuations**: Stochastic models not only provide the average behavior but also accurately quantify the fluctuations around the average (variance or the entire probability distribution). These **"demographic noise"** features are invisible in the deterministic world, yet they are an unavoidable, core component in real biological systems.

3. **The role of noise is subtly dependent on the system**: By contrasting the Lotka-Volterra model with and without competition, we arrive at a profound conclusion: Noise is not always an "annoying" random perturbation. Its role is intimately linked to the system's own deterministic dynamical structure.

    - In a **conservative system with neutrally stable orbits** (e.g., $\gamma_c = 0$), noise is **destructive**. It amplifies oscillations and drives the system toward extinction.
    - In a **dissipative system with a stable attractor** (e.g., $\gamma_c > 0$), noise is **constructive**. It counters the deterministic attraction, maintains continuous dynamic oscillations, and prevents the system from settling into a dead equilibrium.

References