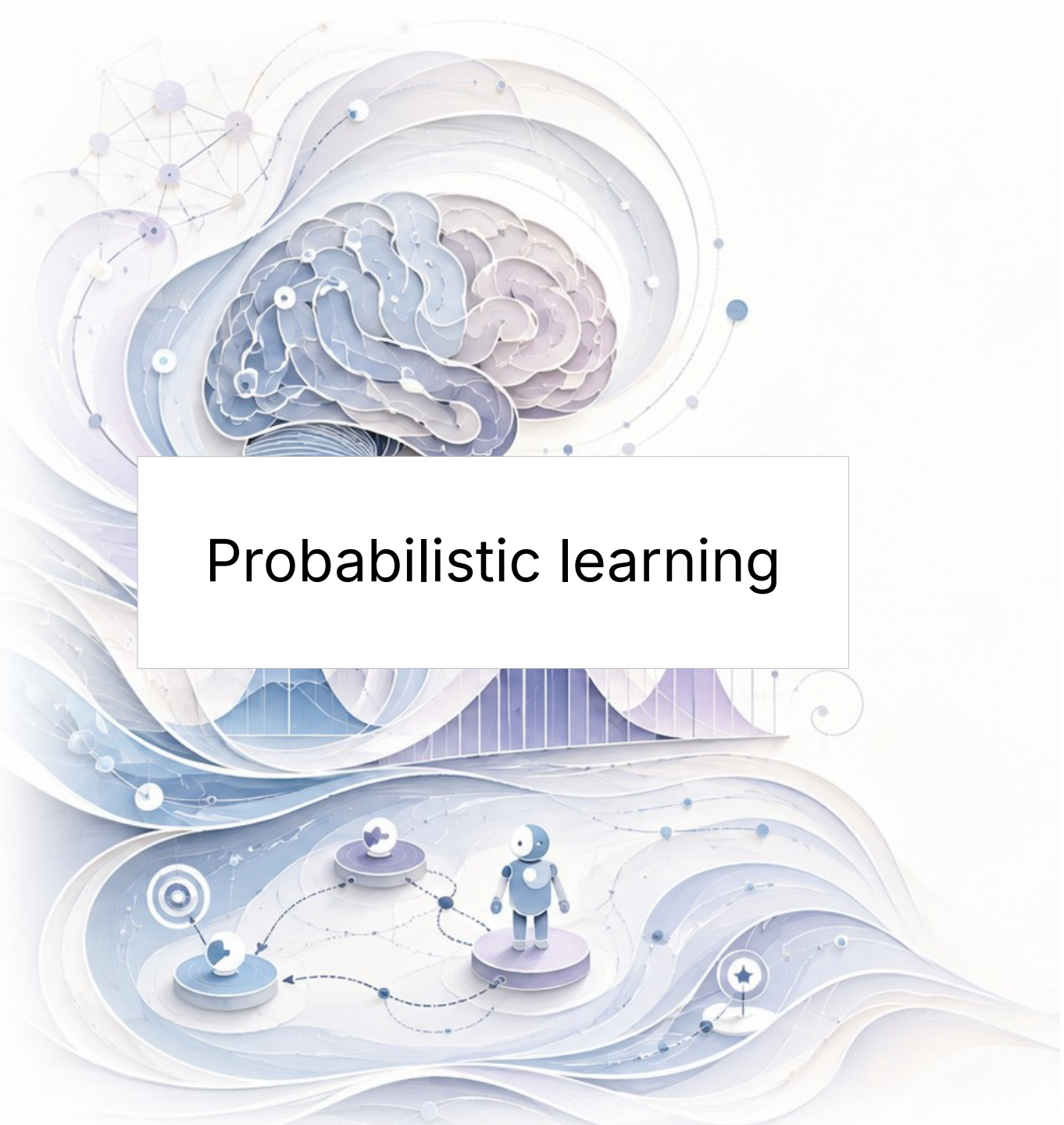
A Mathematical Unification *of* Learning & Evolution

Aydin Mohseni

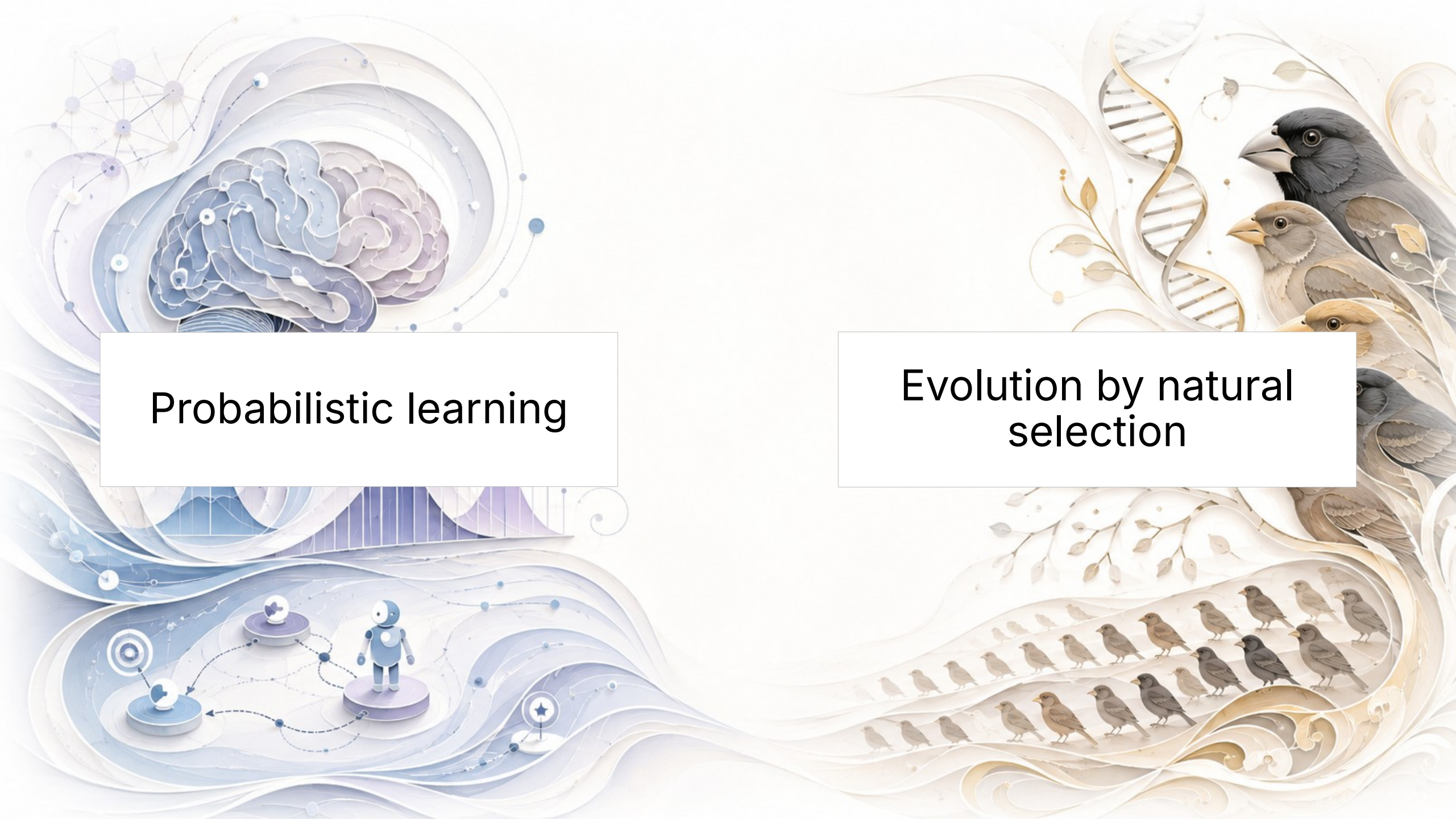
INSTITUTE FOR COMPLEX SOCIAL DYNAMICS

CONCEPTUAL FOUNDATIONS OF SAFE AI LAB

CARNEGIE MELLON UNIVERSITY

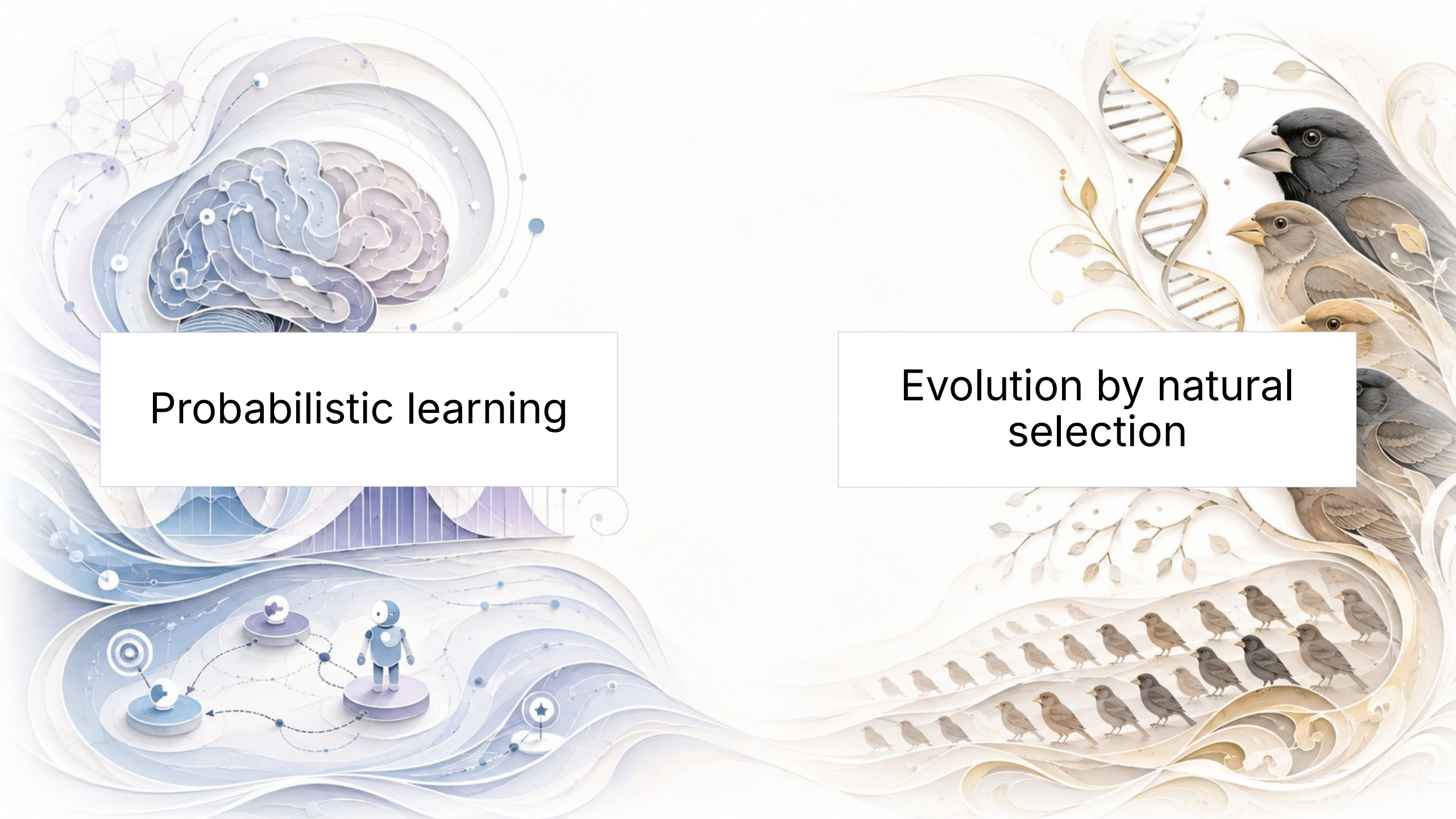


Probabilistic learning



Probabilistic learning

Evolution by natural selection



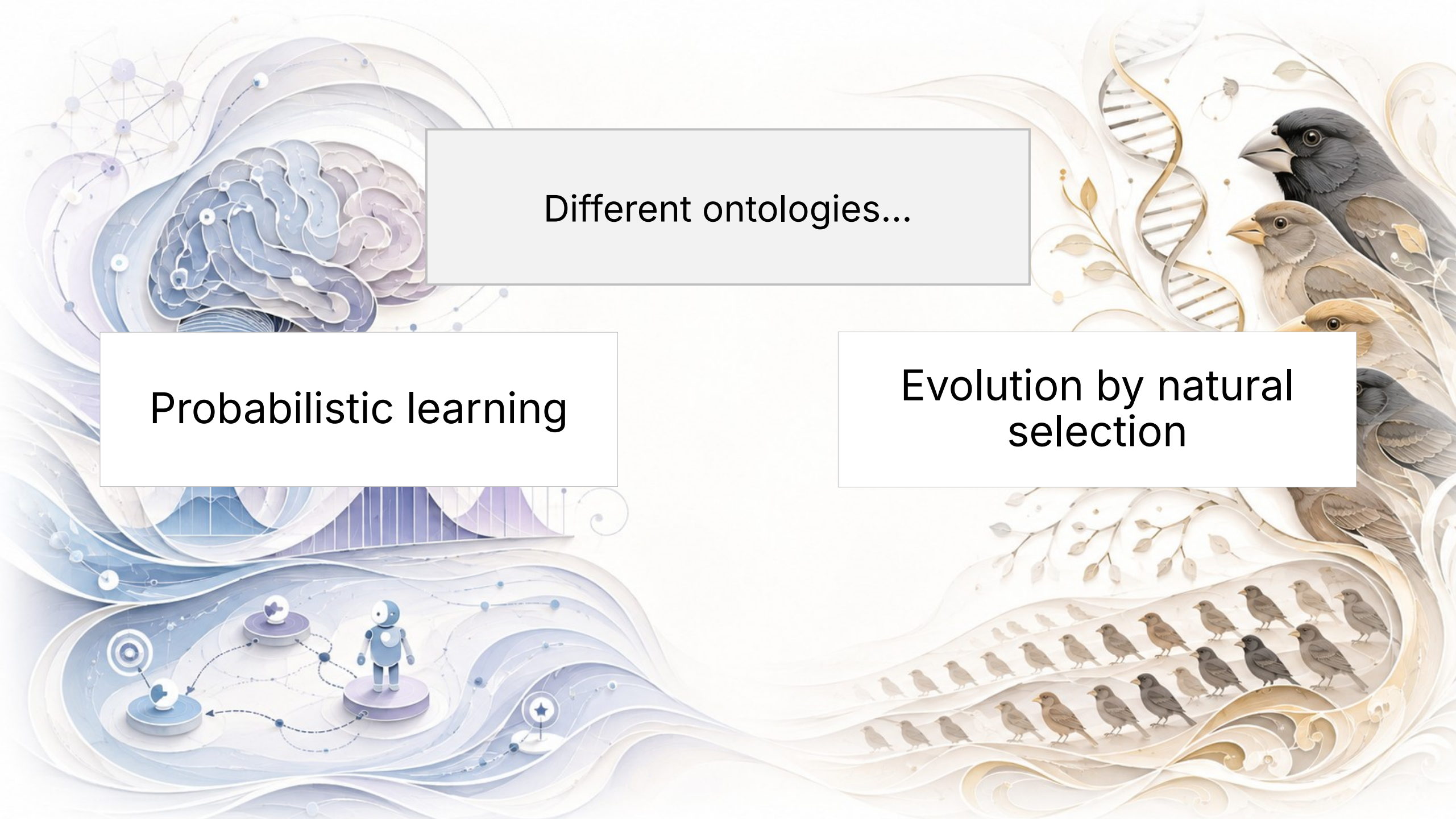
Probabilistic learning

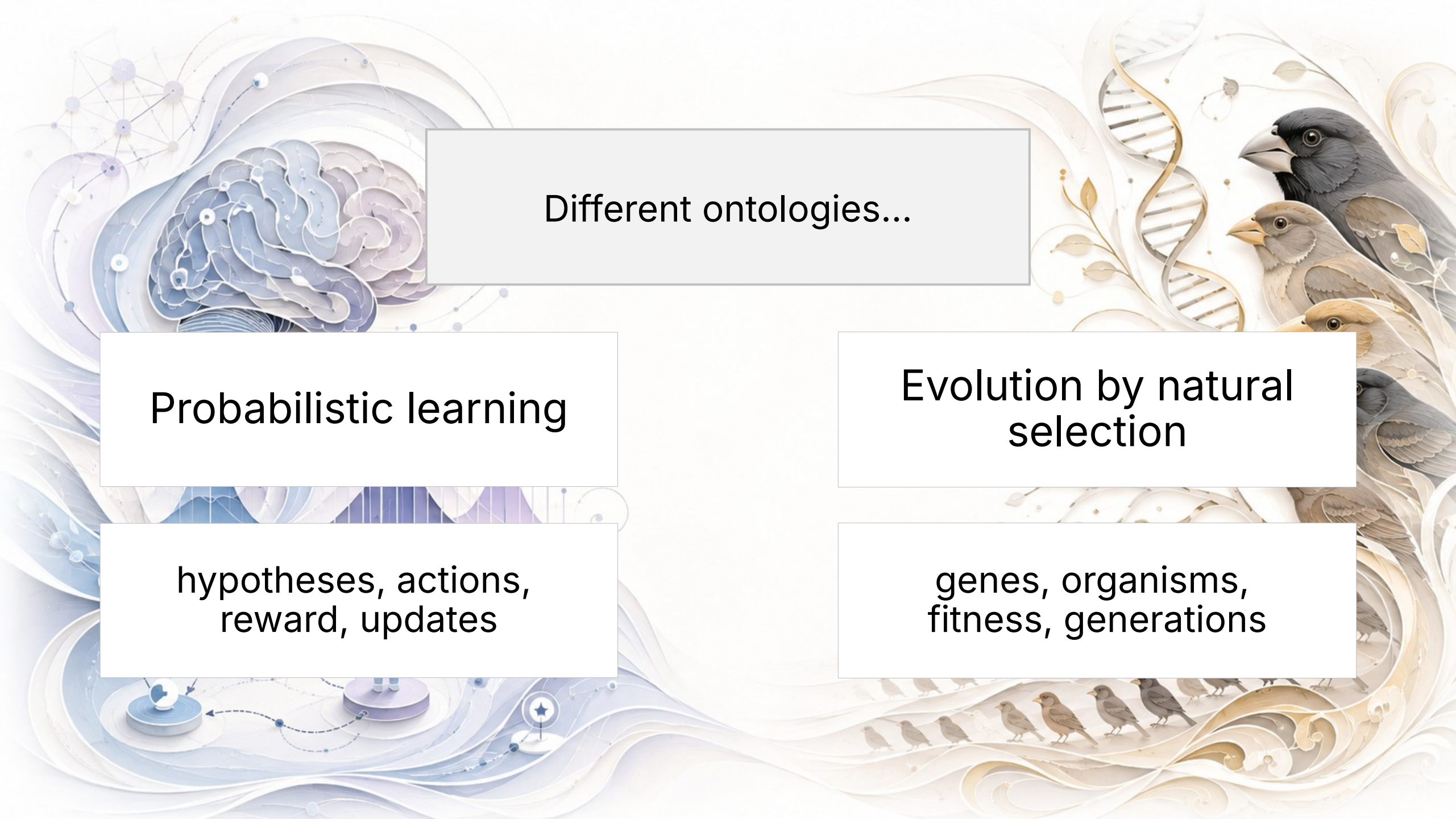
Evolution by natural selection

Different ontologies...

Probabilistic learning

Evolution by natural selection




Different ontologies...
Probabilistic learning
hypotheses, actions, reward, updates
Evolution by natural selection
genes, organisms, fitness, generations

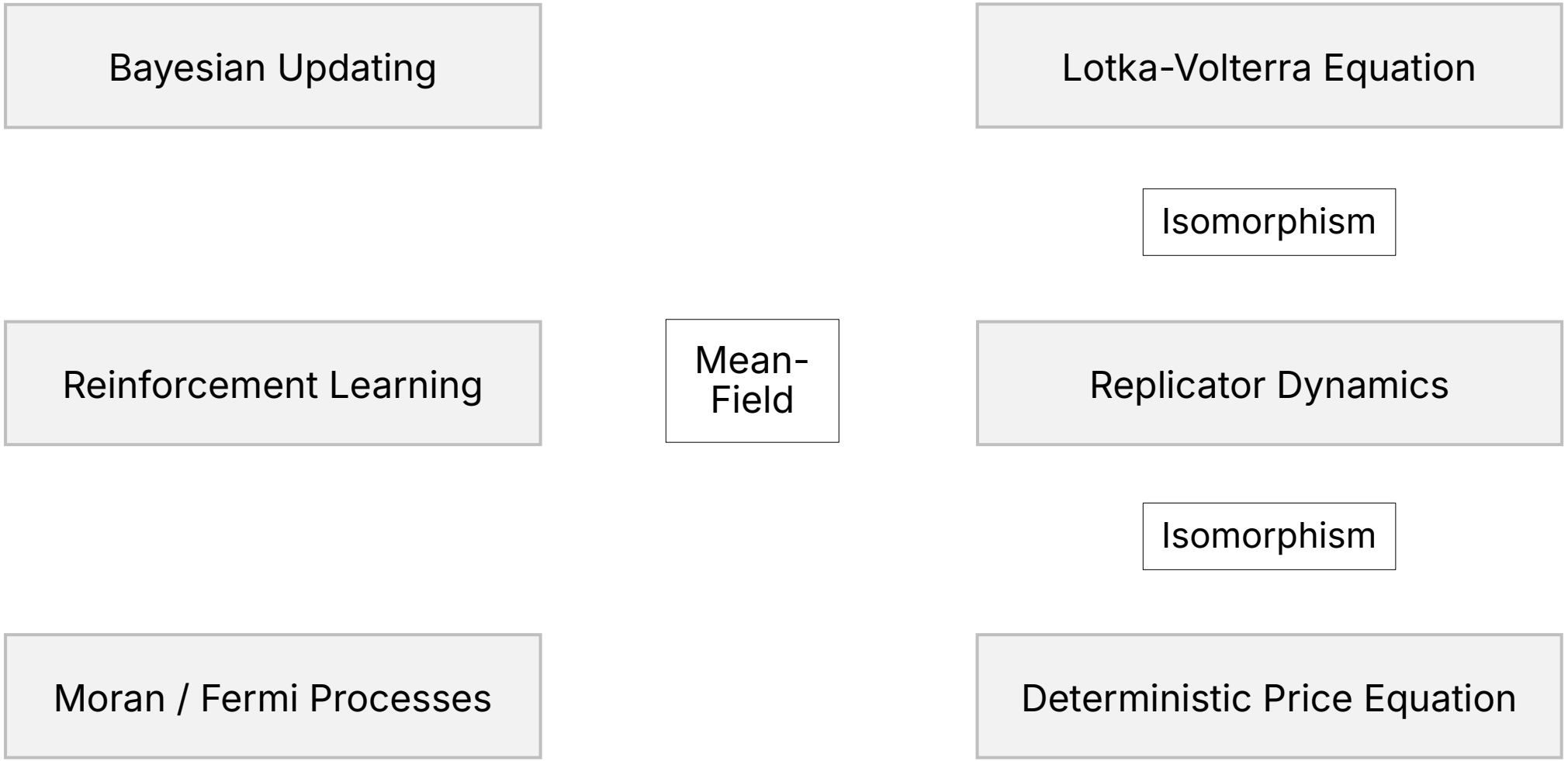
These are elegantly mathematically connected.

Probabilistic learning	Evolution by natural selection
hypotheses, actions, reward, updates	genes, organisms, fitness, generations

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Probabilistic learning	Evolution by natural selection
hypotheses, actions, reward, updates	genes, organisms, fitness, generations

In particular...


Bayesian Updating
Lotka-Volterra Equation
Isomorphism
Reinforcement Learning
Mean-Field
Replicator Dynamics
Isomorphism
Moran / Fermi Processes
Deterministic Price Equation

Bayesian Updating



Shalizi
2009
Dynamics of Bayesian Updating with Dependent Data and Misspecified Model

Reinforcement Learning



Borgers & Sarin
1997
Learning Through Reinforcement and Replicator Dynamics

Moran / Fermi Processes



Traulsen et al
2005
Coevolutionary Dynamics: From Finite to Infinite Populations

Lotka Voltera Equation



Hofbauer
1981
On the Occurrence of Limit Cycles in the Volterra–Lotka Equation

Replicator Dynamics



Page & Nowak
2002
Unifying Evolutionary Dynamics

Deterministic Price Equation

This whole story has yet to be laid out in one place...

So, let’s do that.

Replicator Dynamics

The simplest dynamics capturing natural selection.

$$\dot{x}_i = x_i\big[f(x_i) - \bar{f}(x)\big], \qquad \bar{f}(x) = \sum_j x_j\, f\big(x_j\big)$$

Intuition. A type grows in proportion to its excess over the population mean fitness.

Formal analogues

Domain

Domain	i	f_i	$\bar{f}(x)$
Evolution	genotype / phenotype	reproductive fitness	mean fitness
Bayesian Updating	hypothesis	likelihood	marginal probability of evidence
Reinforcement Learning	action / strategy	expected reward	average reward

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Evolution genotype / phenotype fitness mean fitness

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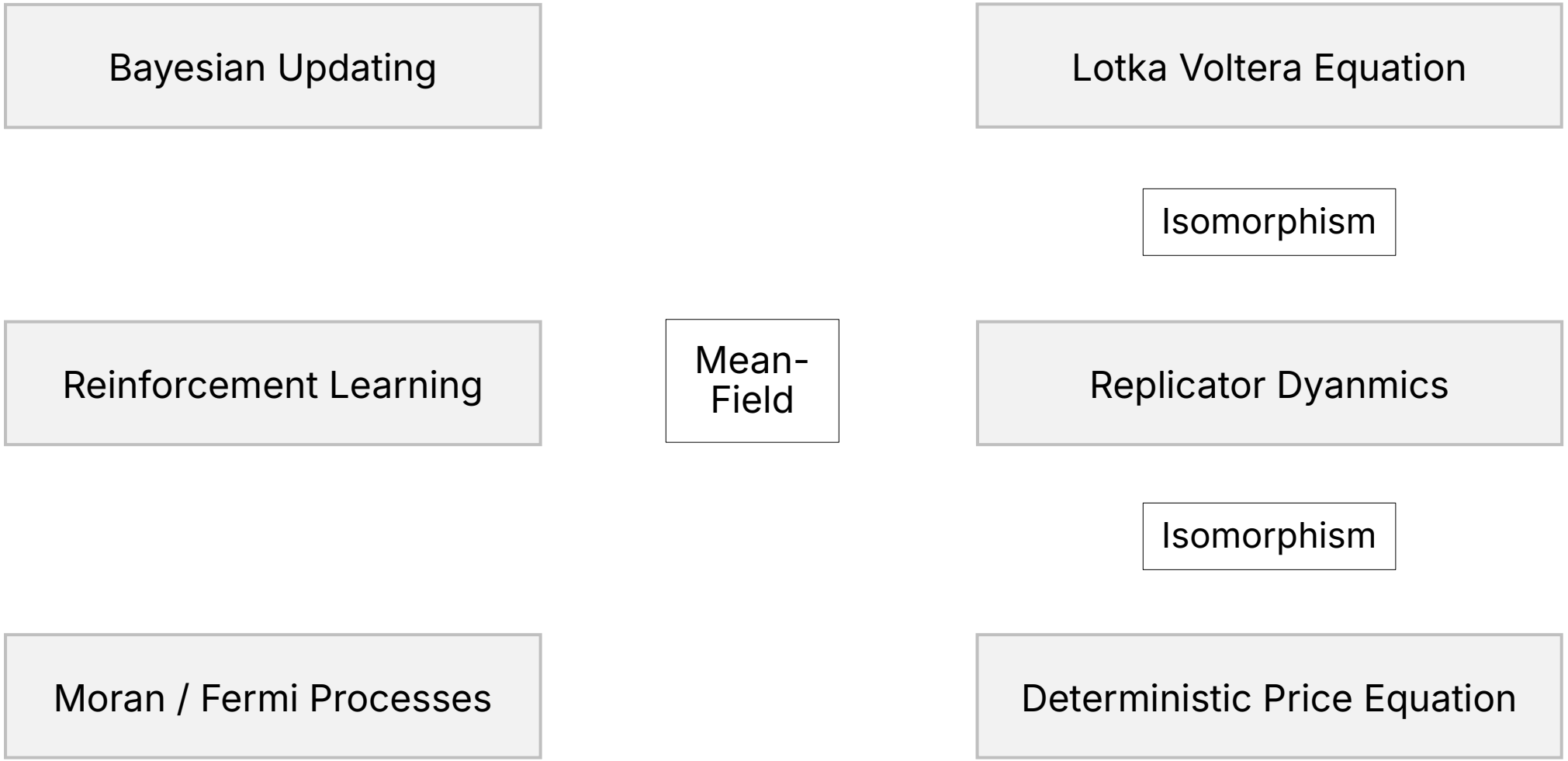
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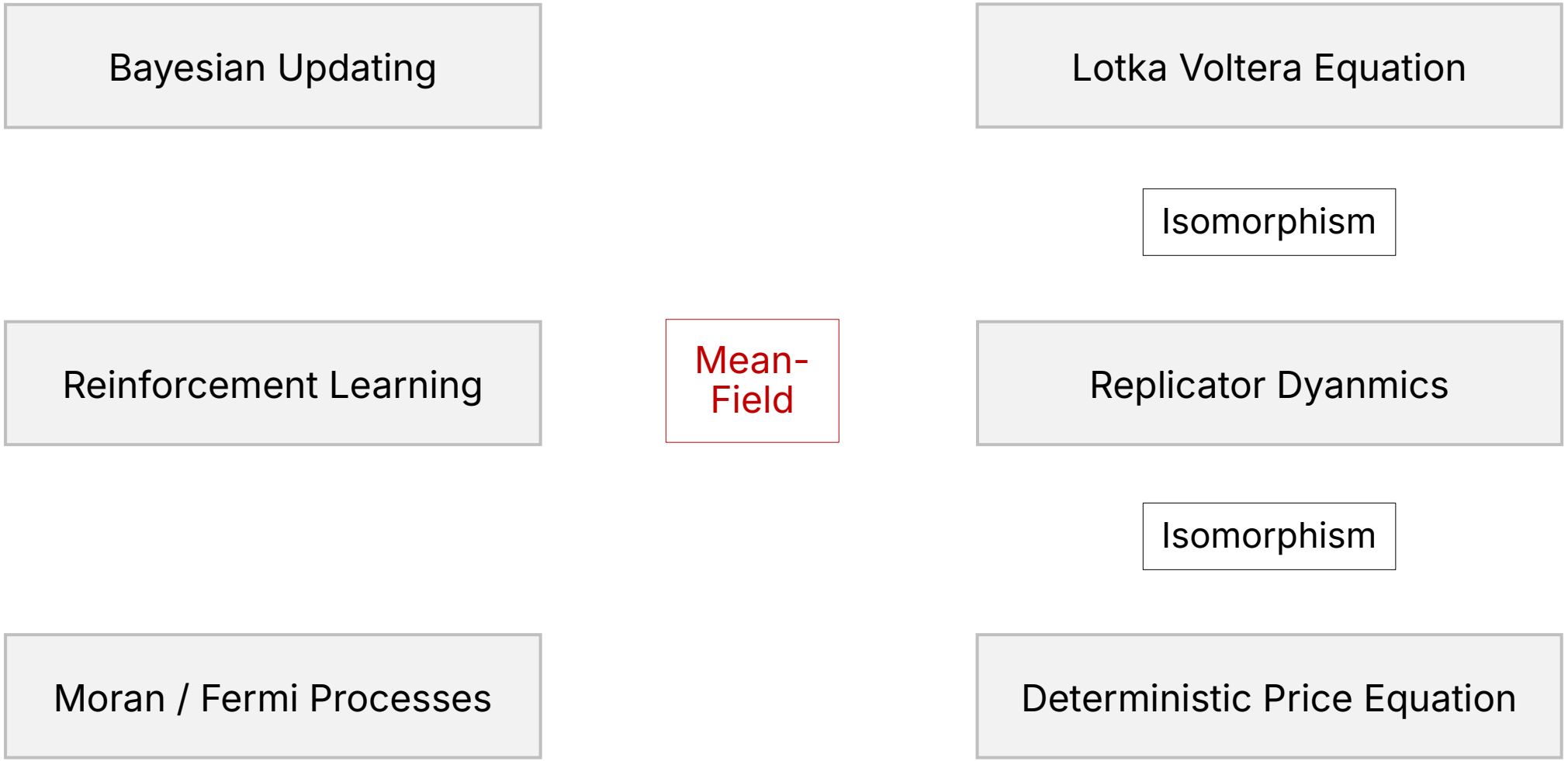
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Formal analogues

Each of our demonstrations will show a row of this table collapsing onto RD.

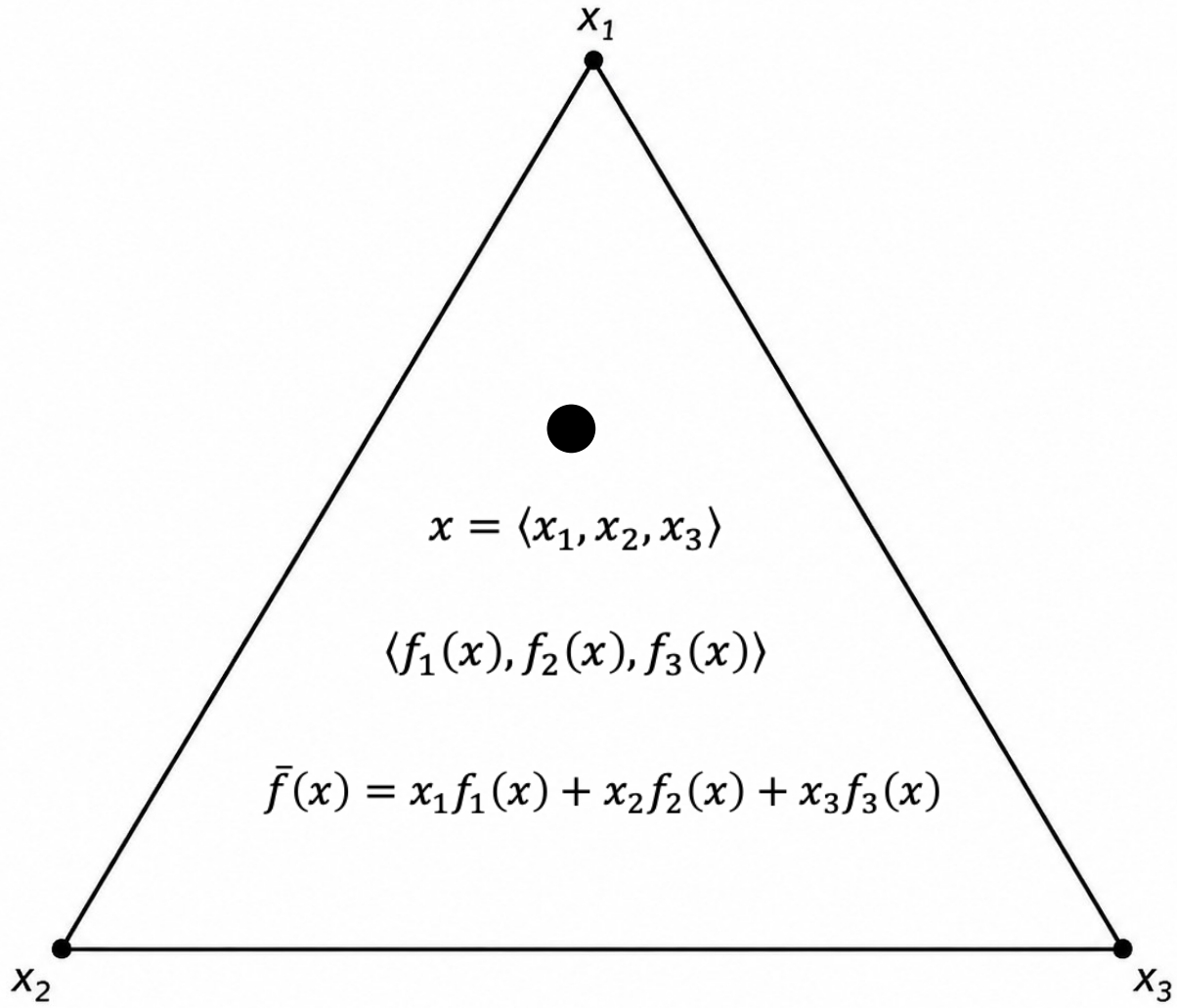
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Bayesian Updating
Lotka Voltera Equation
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Notation

- $x = \langle x_1, \ldots, x_n \rangle$ on the simplex Δ_n: share of type i
- $f_i(x)$: fitness / performance of type i
- $\bar{f}(x) = \sum_j x_j f_j(x)$: population-mean fitness / performance

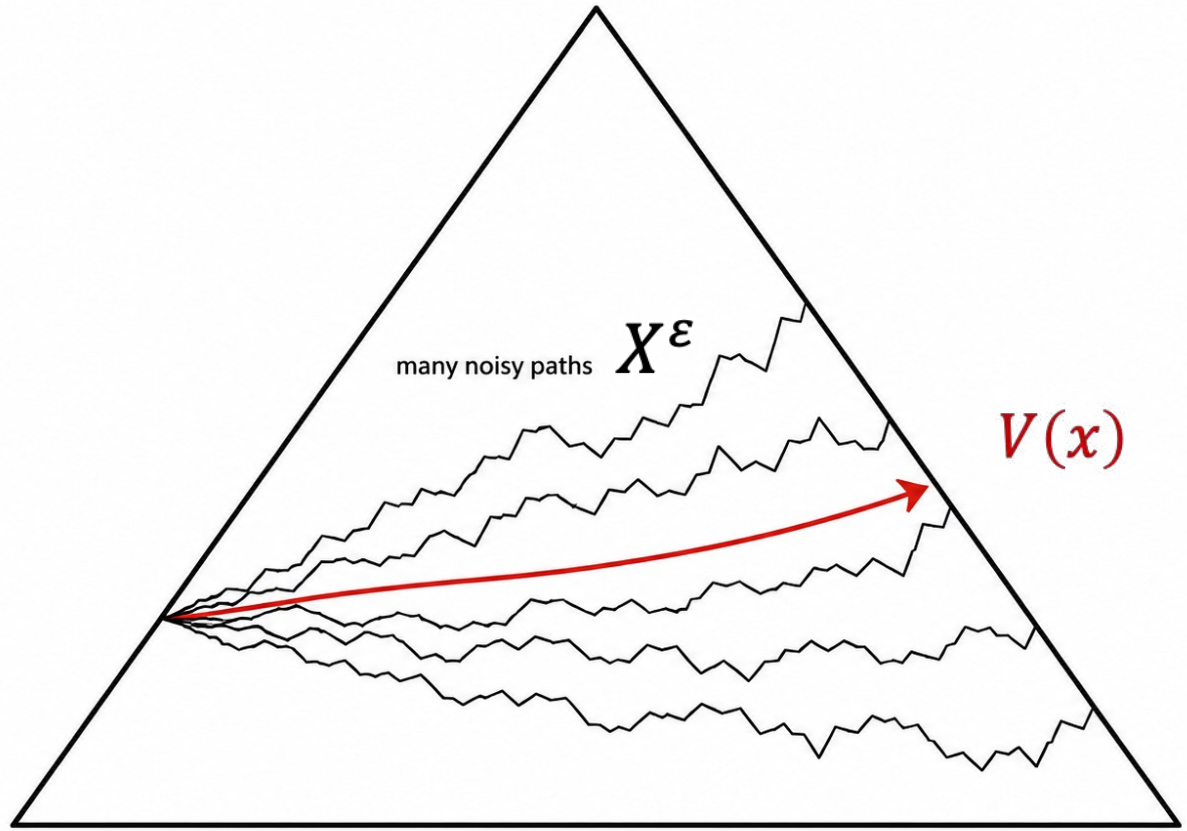


Definition. A stochastic process X^ε with scale ε is a *mean-field approximation* of $\dot{x} = V(x)$ when

$$\mathbb{E}[\Delta X^\varepsilon \mid X^\varepsilon = x] = \varepsilon V(x) + o(\varepsilon) \quad \Longrightarrow \quad X^\varepsilon \underset{\varepsilon \to 0}{\to} \dot{x} = V(x).$$

Intuition. the dynamics V describes the average behavior of X^ε

Note. Here $V(x)_i = x_i \left(f_i(x) - \bar{f}(x) \right)$ will be the replicator field.


many noisy paths X^{ε}
$V(x)$

$$\mathbb{E}[\Delta \mathrm{Bayes}] \to \mathrm{RD}$$

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arXiv: 0901.1342

Dynamics of Bayesian Updating with Dependent Data and Misspecified Models

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Pittsburgh, PA
15213-3890 USA e-mail: cshalizi@cmu.edu

Abstract: Much is now known about the consistency of Bayesian updating on infinite-dimensional parameter spaces with independent or Markovian data. Necessary conditions for consistency include the prior putting enough weight on the correct neighborhoods of the data-generating distribution; various sufficient conditions further restrict the prior in ways analogous to capacity control in frequentist nonparametrics. The asymptotics of Bayesian updating with mis-specified models or priors, or non-Markovian data, are far less well explored. Here I establish sufficient conditions for posterior convergence when all hypotheses are wrong, and the data have complex dependencies. The main dynamical assumption is the asymptotic equipartition (Shannon-McMillan-Breiman) property of information theory. This, along with Egorov's Theorem on uniform convergence, lets me build a sieve-like structure for the prior. The main statistical assumption, also a form of capacity control, concerns the compatibility of the prior and the data-generating process, controlling the fluctuations in the log-likelihood when averaged over the sieve-like sets. In addition to posterior convergence, I derive a kind of large deviations principle for the posterior measure, extending in some cases to rates of convergence, and discuss the advantages of predicting using a combination of models known to be wrong. An appendix sketches connections between these results and the replicator dynamics of evolutionary theory.

AMS 2000 subject classifications: Primary 62C10, 62G20, 62M09; secondary 60F10, 62M05, 92D15, 94A17.
Keywords and phrases: asymptotic equipartition, Bayesian consistency, Bayesian nonparametrics, Egorov's theorem, large deviations, posterior convergence, replicator dynamics, sofic systems.

1. Introduction

The problem of the convergence and frequentist consistency of Bayesian learning goes as follows. We encounter observations $X_1, X_2, \ldots$, which we would like to predict by means of a family Θ of models or hypotheses (indexed by θ). We begin with a prior probability distribution Π_0 over Θ, and update this using Bayes's rule, so that our distribution after seeing $X_1, X_2, \ldots X_t \equiv X_1^t$ is Π_t. If the observations come from a stochastic process with infinite-dimensional distribution P, when does Π_t converge P-almost surely? What is the rate of

arXiv:0911.1763v3 [math.DS] 3 May 2010

THE REPLICATOR EQUATION AS AN INFERENCE DYNAMIC

MARC HARPER

Abstract. The replicator equation is interpreted as a continuous inference equation and a formal similarity between the discrete replicator equation and Bayesian inference is described. Further connections between inference and the replicator equation are given including a discussion of information divergences, evolutionary stability, and exponential families as solutions for the replicator dynamic, using Fisher information and information geometry.

1. Introduction

To address the question of in what sense is natural selection related to information theory and statistical inference, we draw an analogy between Bayesian inference and models of natural selection available in evolutionary game theory. Exploring this requires the use of information theory which leads into the use of information geometry and the common geometric structure of information geometry and evolutionary game theory. Recognition of this framework leads to generalizations of Bayesian inference and is explored in future work.

Bayesian inference and the discrete replicator equation share a remarkable formal similarity. The continuous replicator dynamic can be analyzed using some of the same techniques used in Bayesian inference, such as by the Kullback-Liebler divergence and with exponential families. This paper describes these similarities and explains how information geometry illuminates the connection.

As a model of natural selection, the replicator dynamic models the informatic behavior of the population distribution. Emerging purely from information-theoretical constructions, the replicator requires no

Date: November 26, 2024.
2000 *Mathematics Subject Classification.* Primary: 37N25; Secondary: 91A22, 94A15.
Key words and phrases. evolutionary game theory, information geometry, information divergence, replicator equation, Bayesian inference, information geometry, Fisher information.

Bayesian updating occurs in discrete steps,
so we will use the discrete-time version of RD.

Continuous-time RD

$$\dot{x}_i = x_i\left[f_i(x) - \bar{f}(x)\right]$$

Recall. A type i grows in proportion to its excess over the population mean fitness: $\dot{x}_i \propto f(x_i) - \bar{f}(x)$.

Discrete-time RD

$$x_i^{t+1}(x) = \frac{x_i^t \, f_i(x^t)}{\bar{f}(x^t)}$$

Intuition. The population proportion x_i^{t+1} of type i in the next times step $t+1$ is its current population proportion x_i^t times the ratio of its fitness to the population mean fitness $f_i(x^t)/\bar{f}(x^t)$.

Let $\Theta = \{\theta_i\}_{i=1}^{n}$ be a finite hypothesis set with prior $P_t(\theta_i)$.

Let y_t denote the observation at time t.

Each $\theta_i \in \Theta$ assigns likelihood $P_t(y_t \mid \theta)$ to data.

Bayesian Updating

$$P_{t+1}(\theta_i) = P_t(\theta_i|y_t)$$

Intuition. Your posterior $P_{t+1}(\theta_i)$ on a hypothesis θ_i at $t+1$ on learning proposition y_t is your conditional probability $P(\theta_i|y_t)$ at t.

Bayesian Updating

$$P_{t+1}(\theta_i) = \frac{P_t(y_t|\theta_i)P_t(\theta_i)}{P_t(y_t)}$$

via Bayes' rule.

Statement. The behavior of Bayesian Updating over a hypothesis set *is* the replicator dynamics.

Hypothesis	θ_i	$\longmapsto$	i	Type
Credence	$P_t(\theta_i)$	$\longmapsto$	x_i^t	Population proportion
Likelihood	$P_t(y_t \mid \theta_i)$	$\longmapsto$	$f_i(x^t)$	Fitness
Marginal likelihood	$P_t(y_t)$	$\longmapsto$	$\bar{f}(x^t)$	Mean fitness

$$P_{t+1}(\theta_i) = \frac{P_t(y_t|\theta_i)P_t(\theta_i)}{P_t(y_t)}$$

Bayes

$$P_{t+1}(\theta_i) = \frac{P_t(y_t|\theta_i)P_t(\theta_i)}{P_t(y_t)}$$

Bayes

$$x_i^{t+1}(x) = \frac{x_i^t f_i(x^t)}{\bar{f}(x^t)}$$

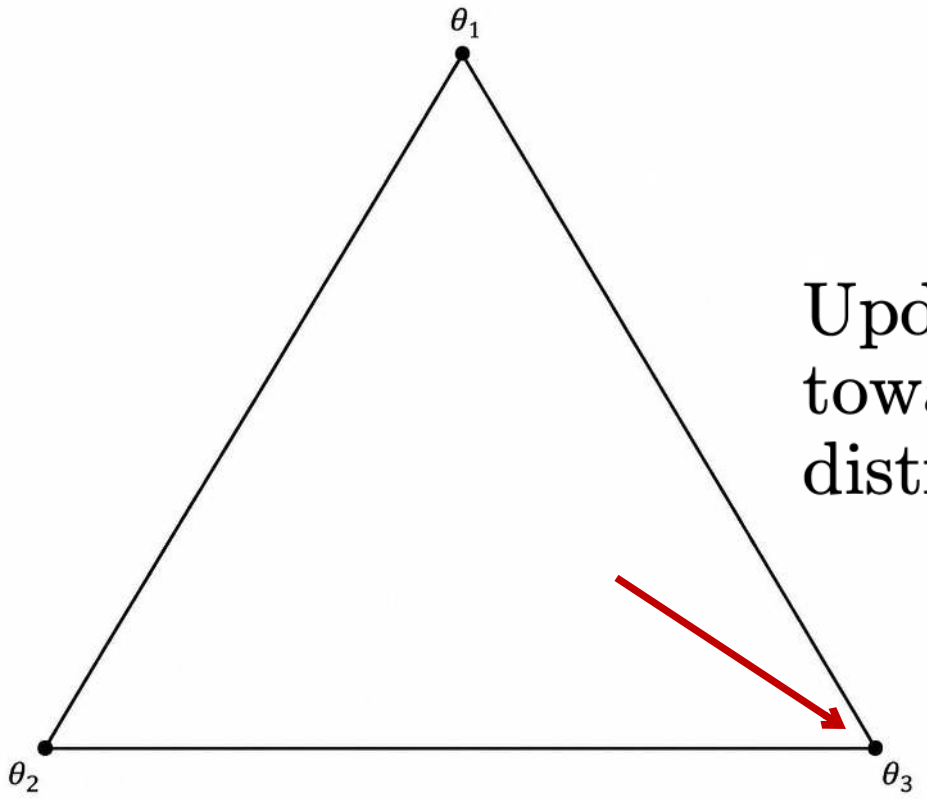
RD

N.B.: Posterior mass reweights multiplicatively by likelihood, exactly as population proportion reweights by fitness; hypotheses are types, likelihood is fitness.

Bayesian updating is exactly the (discrete) replicator map with likelihood as fitness.

The marginal likelihood in log form yields KL divergence from the true distribution Q:

$$\ln(\bar{f}) \propto -\mathrm{KL}(Q \parallel \cdot)$$



Updates move P toward the true distribution.

Ascent of fitness = descent of KL divergence to the truth.

$$\mathbb{E}[\Delta \mathrm{RL}^{\alpha}] \underset{\alpha \to 0}{\to} \mathrm{RD}$$

Cross RL

The dynamic. One agent, no model of the world, learning by trial and error: it keeps a probability distribution over actions and adjusts it using only the rewards it experiences (Cross 1973).

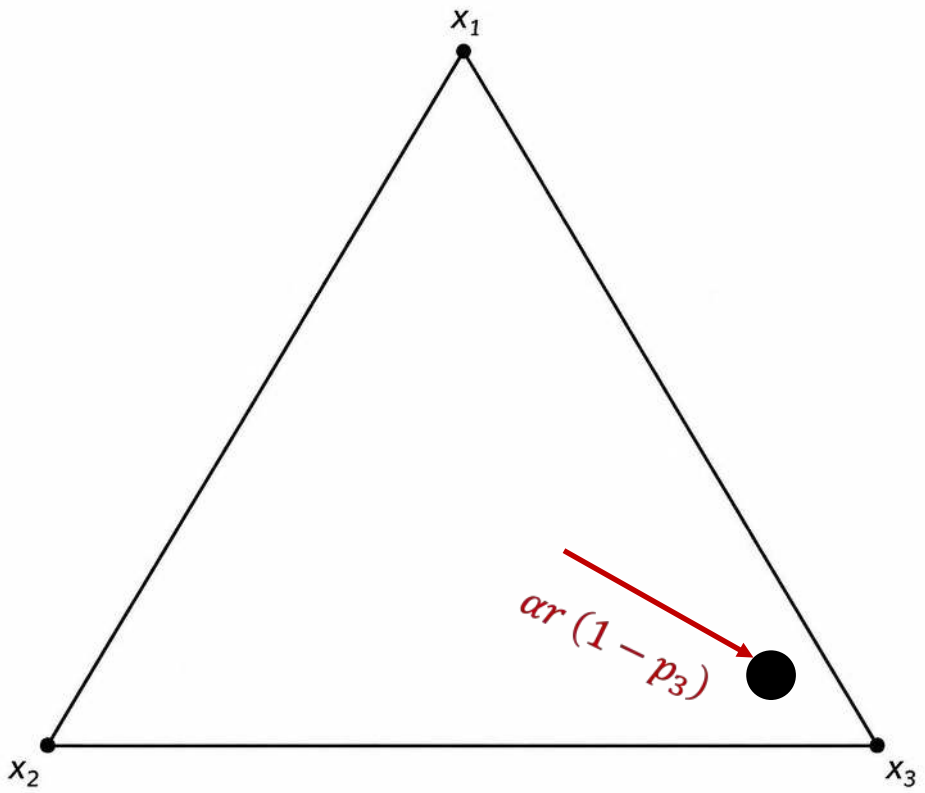
Statement. Cross reinforcement has the replicator dynamics as its mean-field limit, with reward as fitness.

Cross RL

Rule. Play action j with probability p_j;
on reward $r \in [0, 1]$, raise the chosen action and renormalize:

$$p_j \mapsto p_j + \alpha r\,(1 - p_j), \qquad p_k \mapsto p_k - \alpha r\, p_k \quad (k \neq j).$$

Intuition. What pays off gets played more; the strategy vector moves toward what works. α is the step size.


x_1
x_2
x_3
$\alpha r\ (1 - p_3)$

When you play $j \sim p$, you receive expecte reward $\mathbb{E}[r \mid j] = \pi_j$.

The update changes p_i two ways:

$$\Delta p_i = \begin{cases} +\alpha r\,(1 - p_i) & i \text{ was played} \\ -\alpha r\,p_i & \text{something else was played} \end{cases}$$

Average over which action fires and over reward:

$$\mathbb{E}[\Delta p_i \mid p] = \underbrace{\alpha\, p_i\, \pi_i (1 - p_i)}_{\text{reinforced}} - \underbrace{\alpha\, p_i \sum_{j \neq i} p_j\, \pi_j}_{\text{eroded by rivals}}$$

$$= \alpha\, p_i \left(\pi_i - \sum_j p_j\, \pi_j \right)$$

$$= \alpha\, p_i(\pi_i - \bar{\pi})$$

Rescaling time by α and letting $\alpha \to 0$ yields:

$$\dot{p}_i = p_i(\pi_i - \bar{\pi}).$$

$$\dot{p}_i = p_i[\pi_i - \bar{\pi}]$$

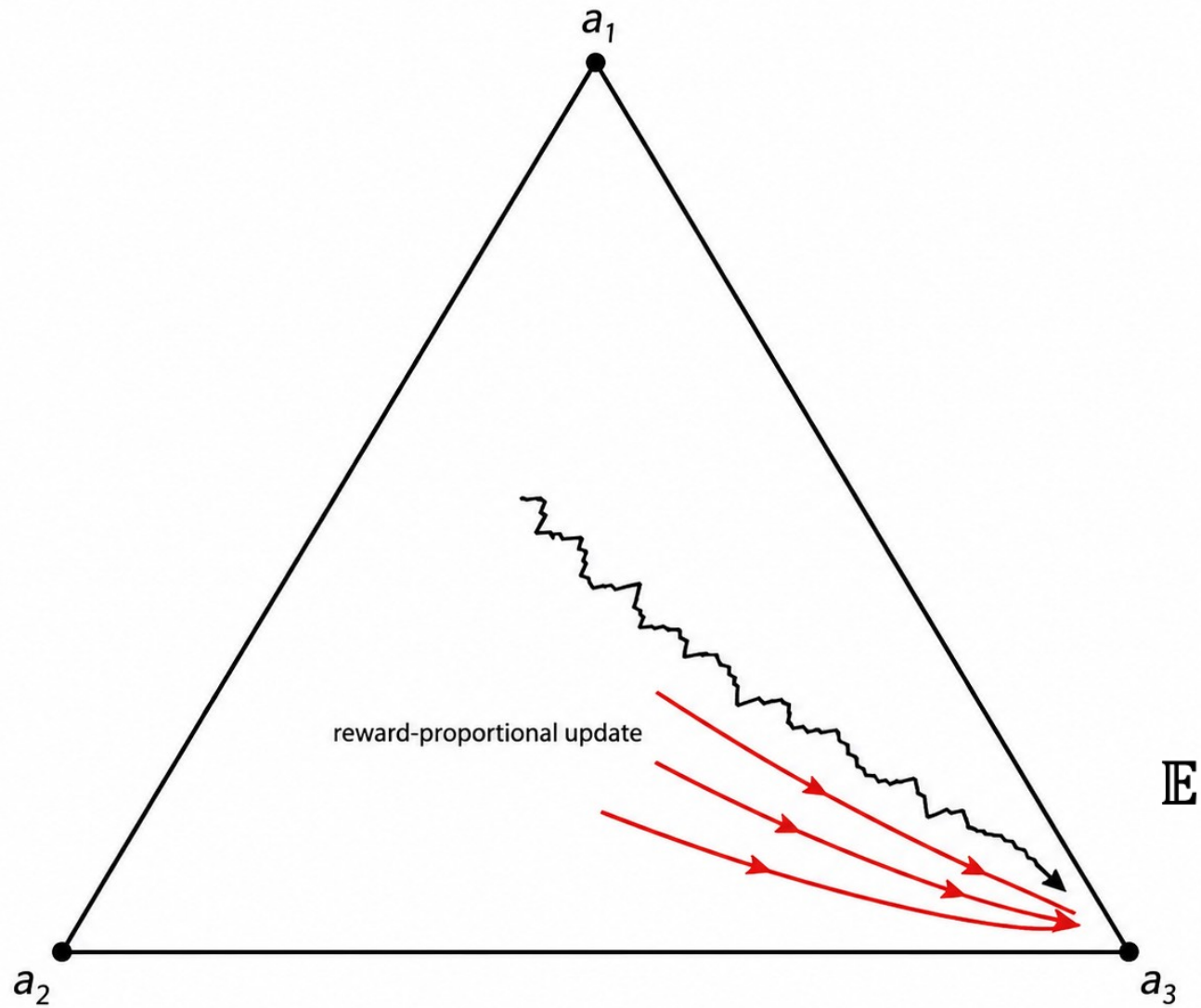
RL

$$\dot{p}_i = p_i[\pi_i - \bar{\pi}] \qquad \dot{x}_i = x_i\left[f_i(x) - \bar{f}(x)\right]$$

RL RD

The average falls out of the balance between being reinforced and being displaced. That is the replicator field.

Action	i	$\longmapsto$	i	Type
Act probability	p_{i}	$\longmapsto$	x_i^t	Population proportion
Expected reward	π_i	$\longmapsto$	$f_i(x^t)$	Fitness
Average reward	$\bar{\pi}$	$\longmapsto$	$\bar{f}(x^{\mathrm{t}})$	Mean fitness



$$\mathbb{E}[\Delta \mathrm{RL}^{\alpha}] \underset{\alpha \to 0}{\to} \mathrm{RD}$$

Moran Process

The dynamic. The canonical stochastic model of selection in a finite, fixed-size population of N competing individuals (Moran 1958).

Rule. Each step:

- One individual reproduces with probability proportional to fitness,
- One dies uniformly at random, the offspring replaces it.

Population size N stays fixed;

The composition changes one birth-and-death at a time.

Intuition. Fitter types are copied more often, so the population's makeup random-walks with a fitness bias.

Small N means noise is large;

large N means expected fitness is realized.

$$\mathbb{E}[\Delta \mathrm{MP}^{\mathbf{N}}] \underset{\mathbf{N}\to\infty}{\to} \mathrm{RD}$$

Derivation. Birth proportional to fitness and uniform death give a per-step drift

$$\mathbb{E}[\Delta x \mid x] = \frac{1}{N} \frac{x(1-x)(f_A - f_B)}{\bar{f}}.$$

Let $N \to \infty$ and :

$$\dot{x} = \frac{x(1-x)(f_A - f_B)}{\bar{f}} \xrightarrow{\text{weak selection}} x(1-x)(f_A - f_B),$$

the two-type replicator equation.

Type	i	$\longmapsto$	i	Type
Frequency of type	i/N	$\longmapsto$	x_i^t	Population proportion
Fitness	f_i	$\longmapsto$	$f_i(x^t)$	Fitness
Mean fitness	$\bar{f}$	$\longmapsto$	$\bar{f}(x^t)$	Mean fitness

Fermi Process

The dynamic. A population learning by imitating more successful strategies in proportion to their success: each individual compares payoff with a random other and imitates the more successful, stochastically (the “Fermi rule”, from the statistical-physics analogy; Traulsen–Pacheco–Nowak).

Rule. A focal individual (payoff π_f) meets a model (payoff π_m) and switches to the model's strategy with probability

$$\frac{1}{1 + e^{-\beta(\pi_m - \pi_f)}}.$$

Intuition. Copy people doing better than you, more reliably the larger the gap. β is the selection intensity, a temperature / rationality dial: $\beta \to 0$ is random copying, $\beta \to \infty$ is always-copy-the-better.

$$\mathbb{E}[\Delta \mathrm{FP}^{\varepsilon}] \underset{\varepsilon \to 0}{\to} \mathrm{RD}$$

Statement. The copying process converges to the replicator, up to a rescaling of time.

Derivation. The net rate at which Areplaces Bminus the reverse is the difference of two Fermi factors, which is a hyperbolic tangent:

$$\phi(\Delta\pi) - \phi(-\Delta\pi) = \tanh\left(\frac{\beta}{2}\,\Delta\pi\right), \qquad \Delta\pi = \pi_A - \pi_B,$$

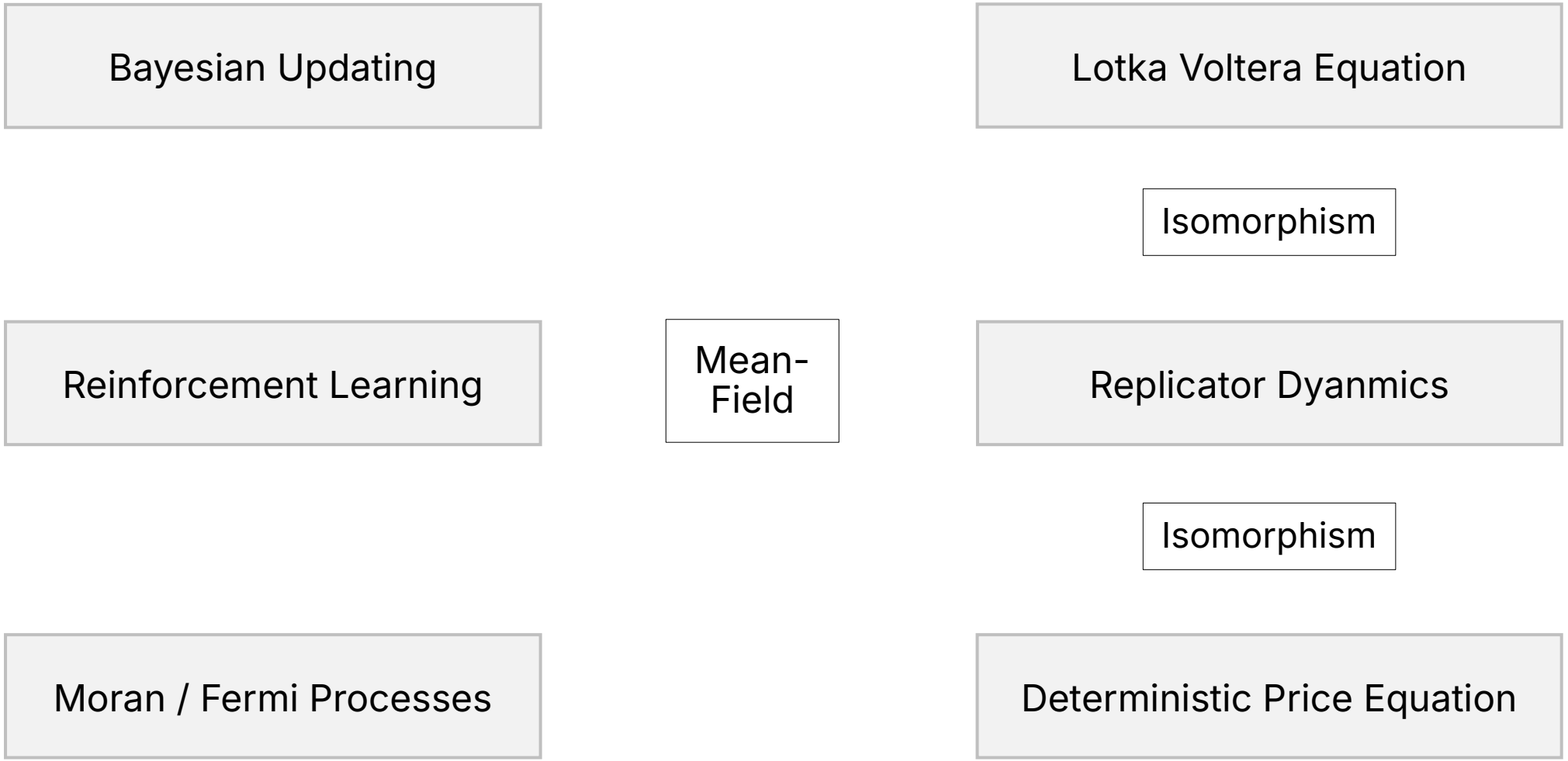
so $\dot{x} = x(1-x)\tanh\left(\frac{\beta}{2}\Delta\pi\right)$.

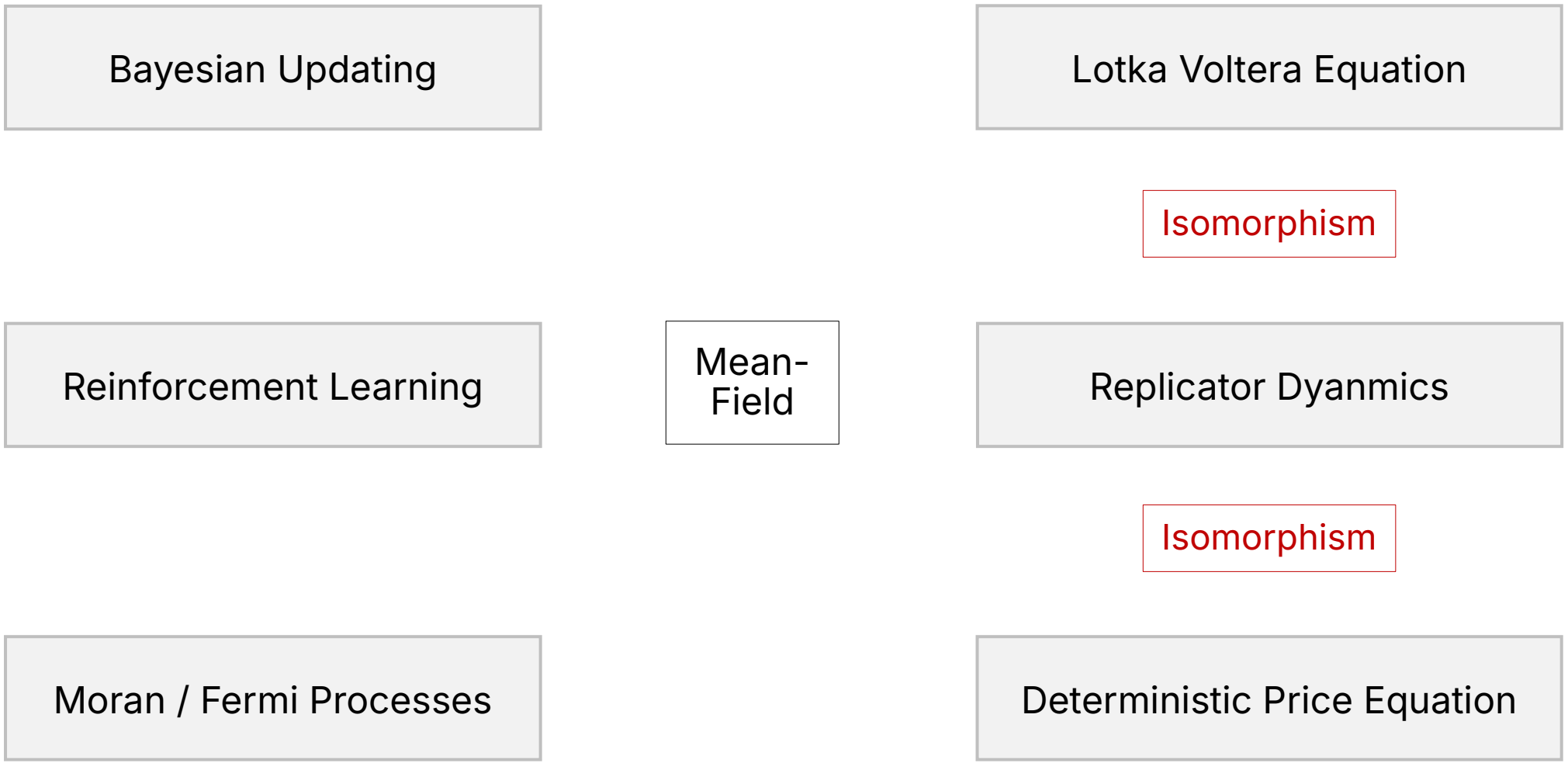
Weak selection ($\beta \to 0$) straightens the tanh:

$$\dot{x} \approx \frac{\beta}{2}\, x(1-x)\,\Delta\pi,$$

the replicator up to the time change $t \mapsto (\beta/2)t$.

Strategy	i	$\longmapsto$	i	Type
Frequency	x_i	$\longmapsto$	x_i^t	Population proportion
Payoff	π_i	$\longmapsto$	$f_i(x^t)$	Fitness
Mean payoff	$\bar{\pi}$	$\longmapsto$	$\bar{f}(x^t)$	Mean fitness

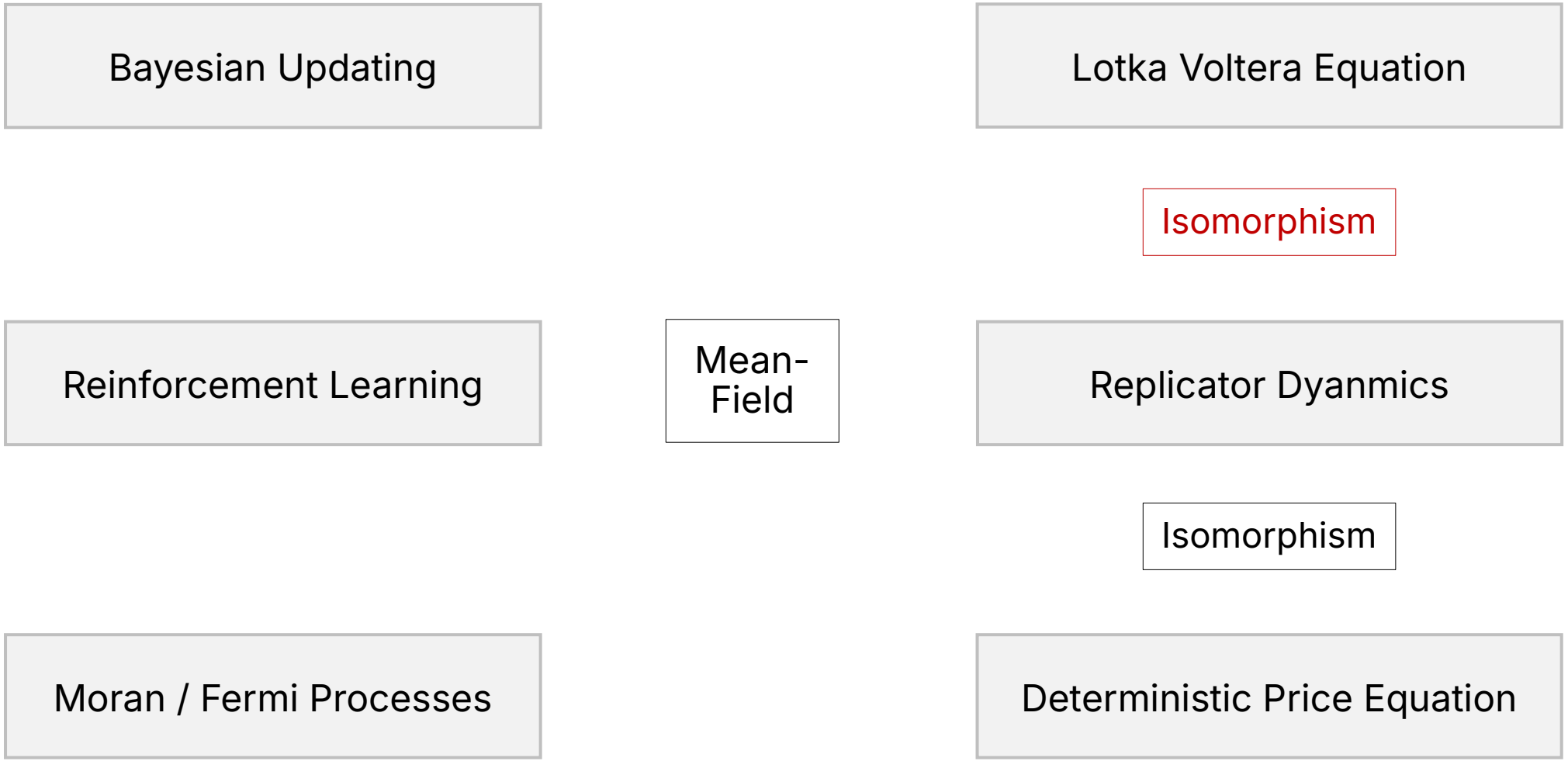

Bayesian Updating
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Definition. Two flows V and W on state spaces $\mathcal{X}$ and $\mathcal{Y}$ are isomorphic when there exists a mapping $\Phi: \mathcal{X} \to \mathcal{Y}$ that is one-to-one and onto, both ways differentiable, and—up to positive monotone time transforms—carries every solution of $\dot{x} = V(x)$ onto a solution of $\dot{y} = W(y)$:

$$\Phi: V(x) \overset{\cong}{\to} W(y).$$

Intuition. These are the same flow up to fixed points, orbits, and stability.


Bayesian Updating
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Lotka–Volterra Equations

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ON THE OCCURRENCE OF LIMIT CYCLES IN THE VOLTERRA–LOTKA EQUATION

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(*Received* 7 *July* 1980; *revised* 14 *November* 1980)

Key words: Volterra–Lotka equation, limit cycles, Hopf bifurcations.

1. INTRODUCTION

The paper deals with the following problem: For which dimension n do limit cycles occur in the classical Volterra–Lotka differential equation

$$\dot{x}_i = x_i\left(a_{i0} + \sum_{j=1}^{n} a_{ij}x_j\right), \quad i = 1, \ldots, n \tag{1.1}$$

defined on $\mathbb{R}^n_+ = \{x = (x_1, \ldots, x_n) \in \mathbb{R}^n: x_i \geqslant 0 \text{ for all } i\}$.

It is a classical result (see [1, p. 213] or [2, p. 300]) that for $n = 2$ isolated periodic orbits are not possible. We will show that Hopf bifurcations and hence stable limit cycles occur for dimensions $n \geqslant 3$.

This will be done by showing in Section 2 that (1.1) is equivalent to a certain differential equation on the simplex S_{n+1}, the "replicator equation"

$$\dot{y}_i = y_i\left(\sum_j a_{ij}y_j - \sum_{k,l} a_{kl}y_k y_l\right), \quad i = 0, 1, \ldots, n \tag{1.2}$$

which arises in such different fields as population genetics ($a_{ij} = a_{ji}$ in the Fisher–Wright–Haldane model), prebiotic evolution [3] and game dynamics [12, 14]. For this equation Hopf bifurcations were found for $n \geqslant 3$ in [5], whereas Zeeman [14] disproved occurrence of Hopf bifurcations for $n = 2$. His paper was the starting point for this investigation.

In dimensions $n \geqslant 3$ there are only few results on (1.1), apart from the special case $a_{ij} = -a_{ji}$, which allows a constant of motion and was treated already extensively by Volterra [13]. For the case $a_{ij} = a_{ji}$, MacArthur [6] has found a global Lyapunov function. Rescigno's paper [9] deals with the three-dimensional case. His discussion is confined to a classification of parameter values for which at least one of the 8 equilibrium points is stable. But, as observed by May and Leonard [8], unlike the two dimensional case there remain a lot of combinations of the interaction coefficients a_{ij} where all fixed points are unstable. In particular, May and Leonard study the equation

$$\begin{aligned} \dot{x}_1 &= x_1(1 - x_1 - \alpha x_2 - \beta x_3), \\ \dot{x}_2 &= x_2(1 - \beta x_1 - x_2 - \alpha x_3), \\ \dot{x}_3 &= x_3(1 - \alpha x_1 - \beta x_2 - x_3), \end{aligned} \tag{1.3}$$

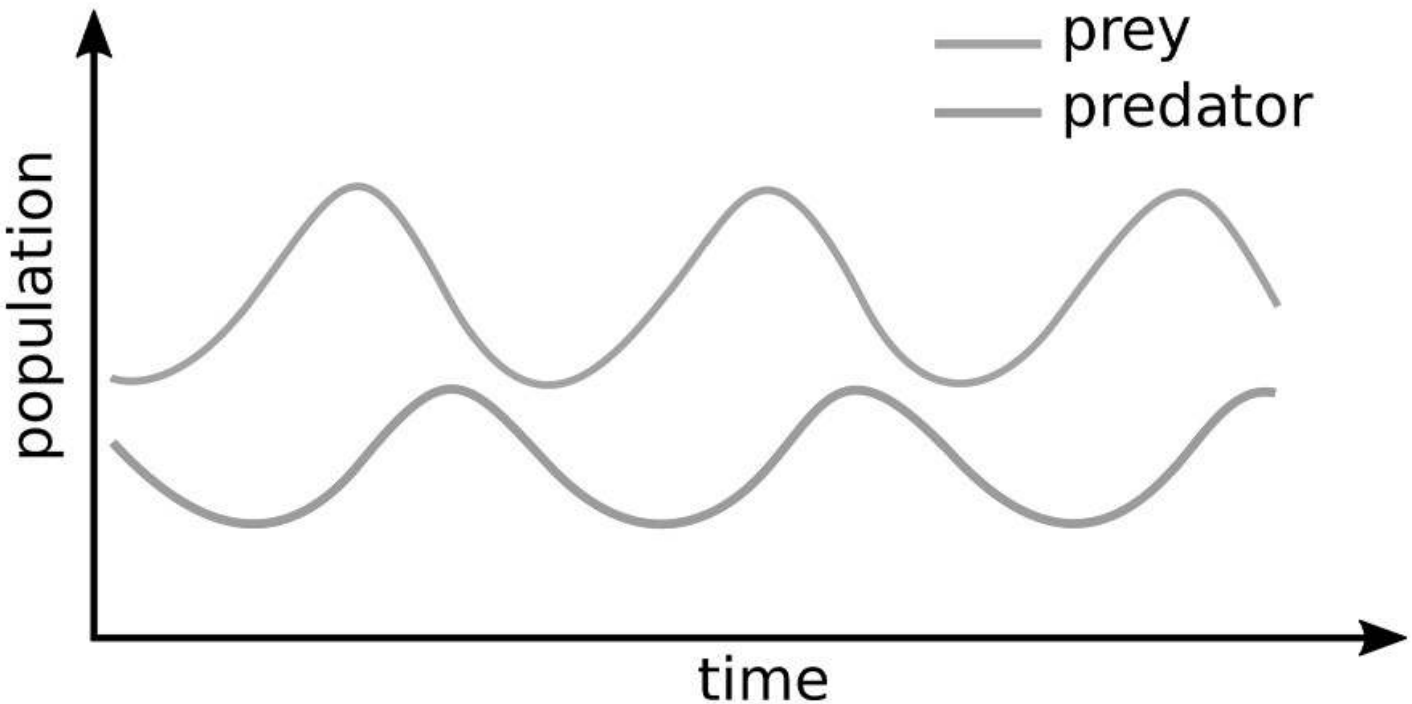
The dynamic. The founding deterministic model of population ecology: the abundances of interacting species growing and shrinking through their interactions (Lotka 1925, Volterra 1926).

Rule.

$$\dot{y}_i = y_i \left(r_i + \sum_j b_{ij}\ y_j \right)$$

- Intrinsic per-capita growth r_i;
- Interaction coefficients b_{ij} (predation, competition, mutualism).

Intuition. Each population changes at a per-capita rate set by its own baseline plus how the others help or hurt it. The state space is the open orthant, unbounded, with no simplex constraint.


prey
predator
population
time

Lotka–Volterra Equations ≅ RD

Statement. The replicator equation on Δ_n (n types) is the *same flow* as generalized Lotka–Volterra on $\mathbb{R}^{n-1}_{>0}$ ($n-1$ species).

Derivation.

The isomorphism map is Φ: $y_i = x_i / x_n$
(share of i relative to a reference type).

Differentiate its log:

$$\frac{\dot{y}_i}{y_i} = \frac{\dot{x}_i}{x_i} - \frac{\dot{x}_n}{x_n} = (f_i - \bar{f}) - (f_n - \bar{f}) = \underbrace{f_i - f_n}_{\bar{f} \text{ cancels}} .$$

With linear fitness $f_i = (Ax)_i$ and $x_k = y_k x_n$:

$$\dot{y}_i = x_n\, y_i \left((r_i + \sum\nolimits_j b_{ij}\, y_j) \right),$$

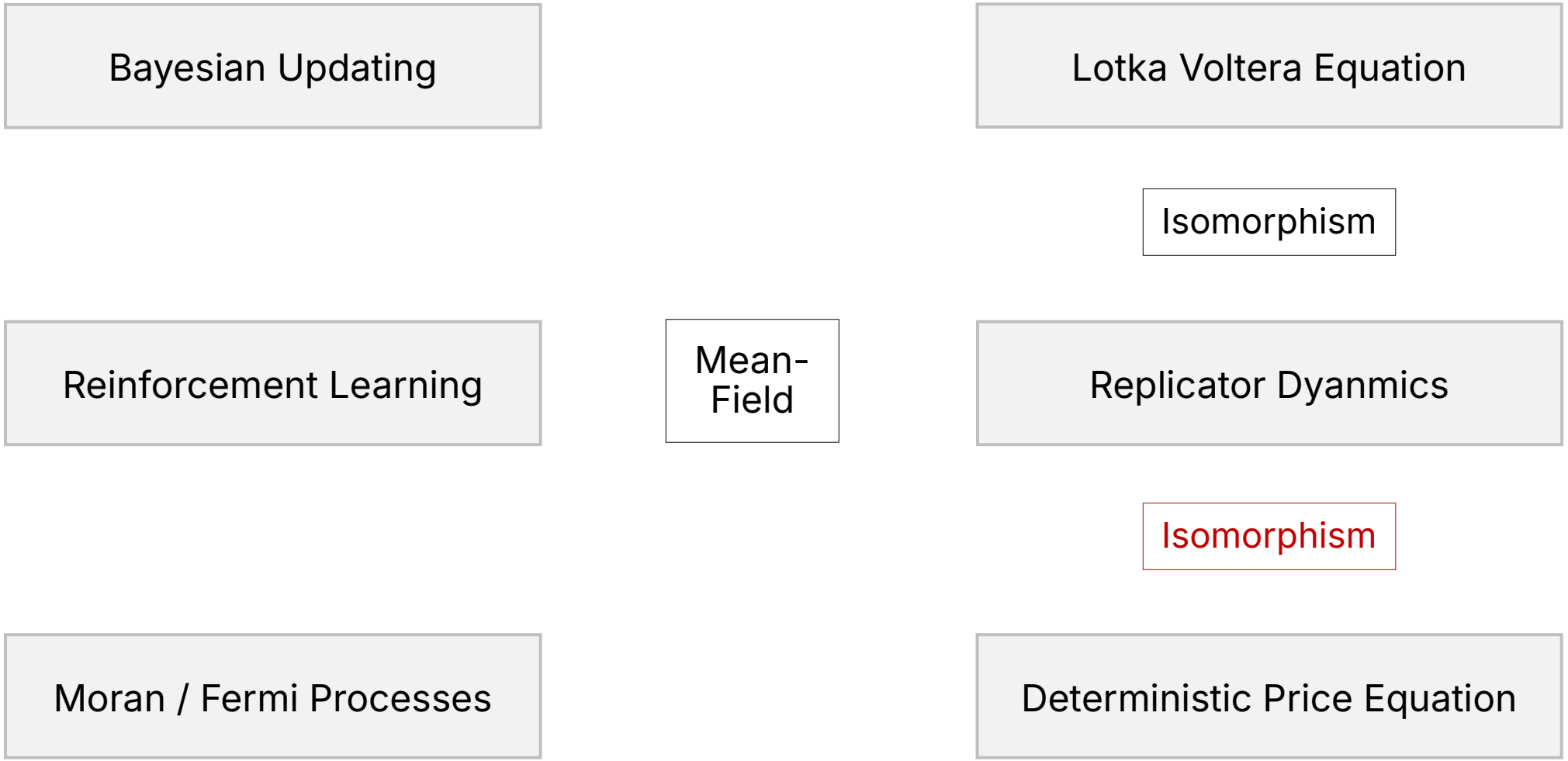
$$r_i = a_{in} - a_{nn},$$

$$b_{ij} = a_{ij} - a_{nj}.$$

The factor $x_n > 0$is shared by every equation,
so absorb it into time, $d\tau = x_n\, dt$:

$$\frac{dy_i}{d\tau} = y_i(r_i + \sum_j b_{ij}\, y_j) \qquad \text{(Lotka–Volterra).}$$

Strategy	i	$\longmapsto$	i	Type
Relative abundance	y_i	$\longmapsto$	x_i^t	Population proportion
Per-capita growth	$r_i + \sum_j b_{ij} y_i$	$\longmapsto$	$f_i(x^t)$	Fitness
No counterpart	$d\tau = x_n \, dt$	$\longmapsto$	$\bar{f}(x^t)$	Mean fitness


Bayesian Updating
Lotka Voltera Equation
Isomorphism
Reinforcement Learning
Mean-Field
Replicator Dyanmics
Isomorphism
Moran / Fermi Processes
Deterministic Price Equation

Price Equation

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Unifying Evolutionary Dynamics

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Darwinian evolution is based on three fundamental principles, reproduction, mutation and selection, which describe how populations change over time and how new forms evolve out of old ones. There are numerous mathematical descriptions of the resulting evolutionary dynamics. In this paper, we show that apparently very different formulations are part of a single unified framework. At the center of this framework is the equivalence between the replicator–mutator equation and the Price equation. From these equations, we obtain as special cases adaptive dynamics, evolutionary game dynamics, the Lotka–Volterra equation of ecology and the quasispecies equation of molecular evolution.
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Introduction

In 1906, W. F. R. Weldon, who invented the field of biometrics, noted that Darwinian evolution was essentially a mathematical theory that could only be tested using mathematical and statistical techniques. The founding fathers of evolutionary genetics, Fisher, Haldane and Wright used mathematical models to generate a synthesis between Mendelian genetics and Darwinian evolution. Kimura's theory of neutral evolution, Hamilton's kin selection and Maynard Smith's evolutionary game theory are all based on mathematical descriptions of evolutionary dynamics. Concepts like fitness and natural selection are best defined in terms of mathematical equations. The perspective of this paper is to show that apparently very different descriptions of evolutionary dynamics are part of a single unified framework (Fig. 1). We concentrate on deterministic dynamics, which represent the core of evolutionary theory. We do not consider stochastic, spatial or individual-based approaches, which are mathematically more diverse and hence less amenable to any attempt of unification. Obviously, stochastic approaches that include finite population size effects are always more realistic, but usually the basic understanding of a system can be derived by considering deterministic dynamics; stochastic extensions often work in a predictable way.

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The Quasispecies Equation

Let us start with the quasispecies equation of molecular evolution (Eigen & Schuster, 1977; Eigen *et al.*, 1989). The variable x_i denotes the relative abundance of a genetic sequence, i, in a population. The fitness, f_i, of this sequence is

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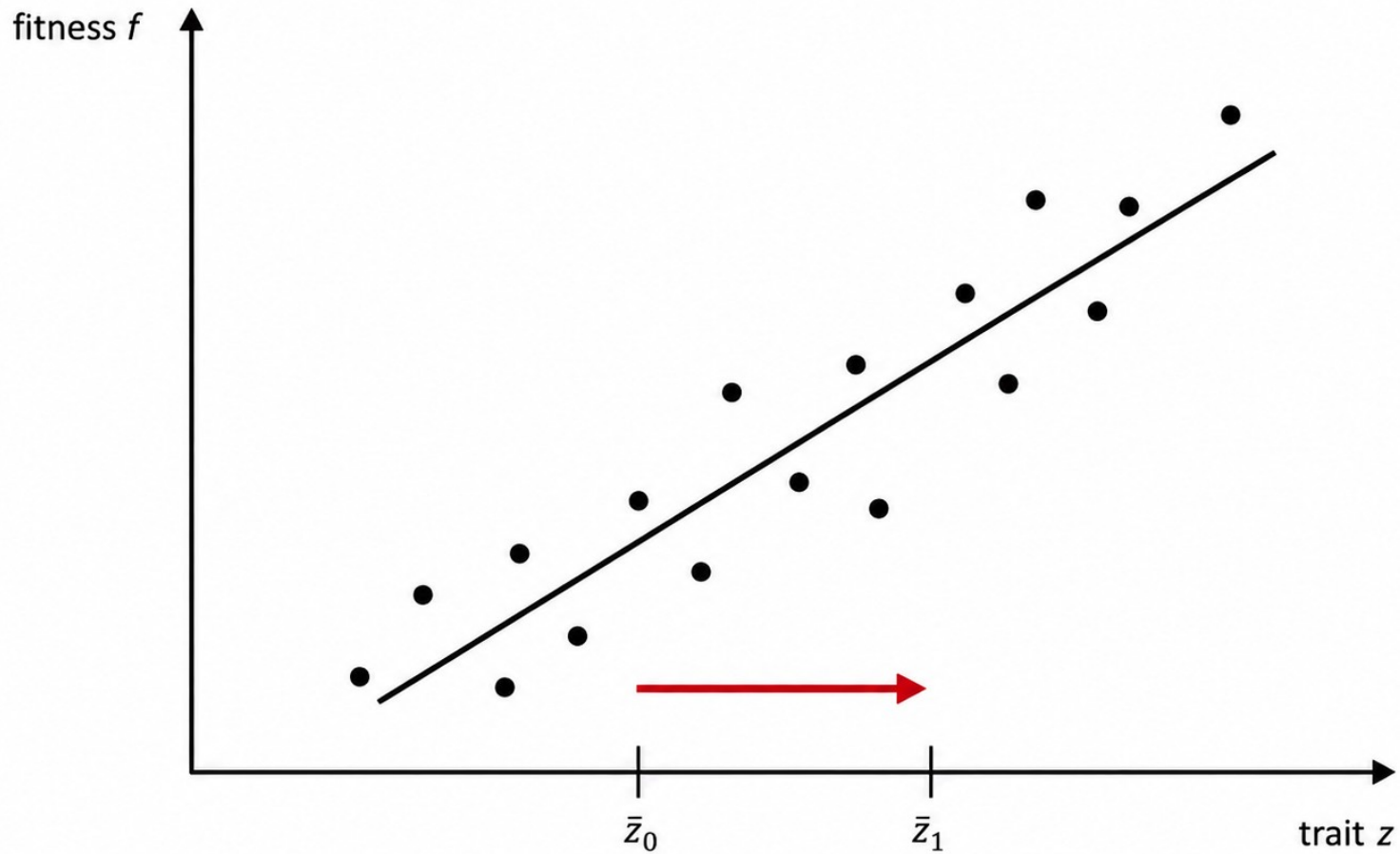
The dynamic. An exact accounting identity for how the mean of any trait changes under selection; substrate-neutral, it applies to genes, strategies, or firms (Price 1970).

Rule (continuous form).

$$\dot{\bar{z}} = \underbrace{\mathrm{Cov}_x(f, z)}_{\text{selection}} + \underbrace{\mathbb{E}_x[\dot{z}]}_{\text{transmission}}$$

The mean trait moves by its covariance with fitness, plus any change in the trait values themselves.

Intuition. Whatever correlates with success rises. With no transmission bias, only the covariance term acts.



selection = Cov(f, z)

(no transmission bias)

Price Equation $\cong$ RD

Statement. The replicator dynamics is the Price equation with no transmission bias.

Derivation. Track any trait mean $\bar{z} = \sum_i x_i z_i$ under RD:

$$\dot{\bar{z}} = \sum_i \dot{x}_i \; z_i = \sum_i x_i \left(f_i - \bar{f}\right) z_i = \mathrm{Cov}_x(f, z).$$

Take the trait to be "is type i" ($z = e_i$) and you recover

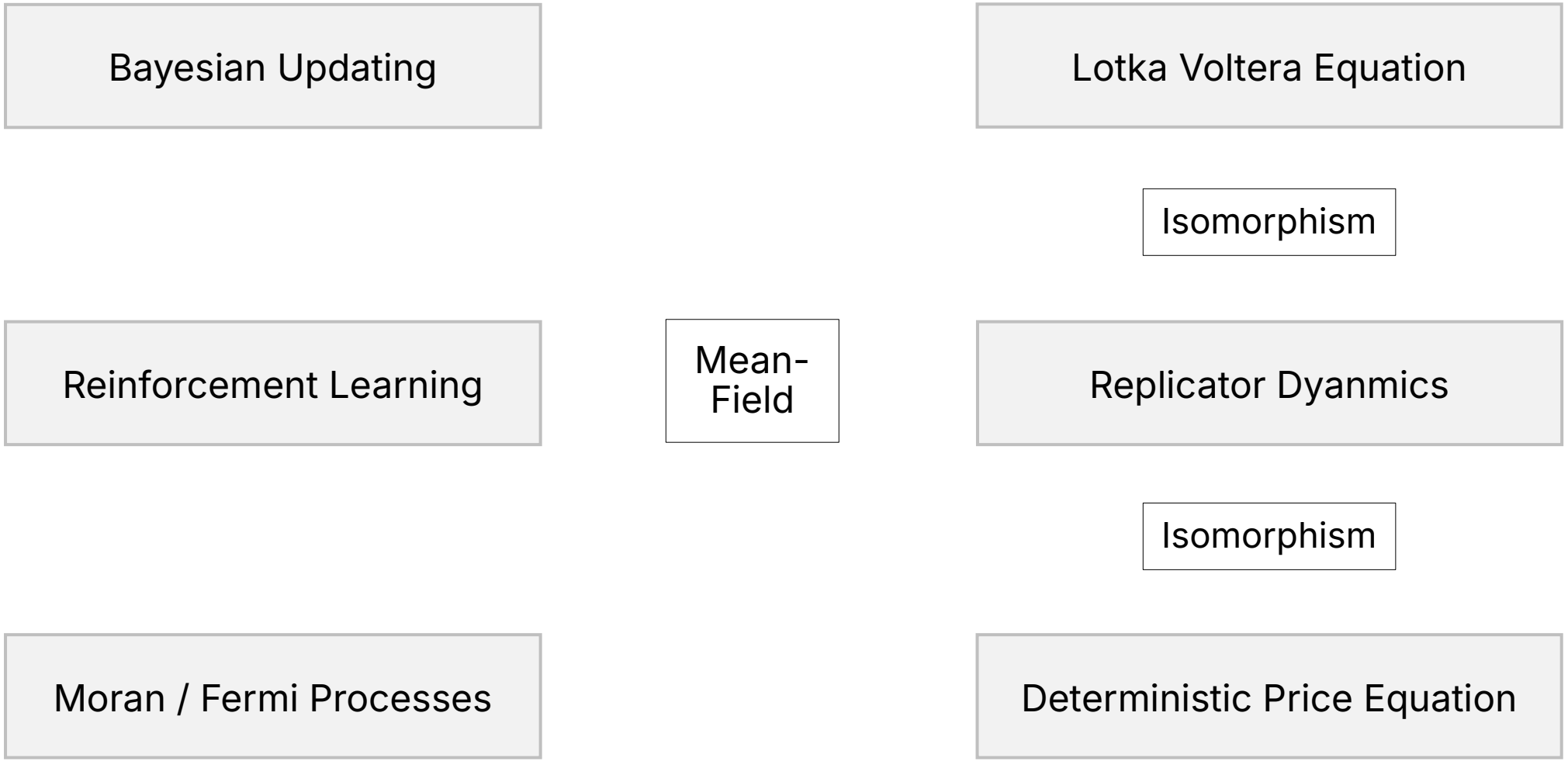
$$\dot{x}_i = x_i\left(f_i - \bar{f}\right).$$

Take $z = f$ and you get Fisher's fundamental theorem,

$$\dot{\bar{f}} = \mathrm{Var}_x(f) \geq 0.$$

Type	i	$\longmapsto$	i	Type
Frequency	w_i	$\longmapsto$	x_i^t	Population proportion
Fitness i	f_i	$\longmapsto$	$f_i(x^t)$	Fitness
Mean fitness	$\bar{f}$	$\longmapsto$	$\bar{f}(x^t)$	Mean fitness

Upshots


Bayesian Updating
Lotka Voltera Equation
Isomorphism
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Replicator Dyanmics
Isomorphism
Moran / Fermi Processes
Deterministic Price Equation

The shared logical core:

Every member has an expected flow satisfying:

$$\dot{z}_i = z_i g_i(z) \quad \Leftrightarrow \quad \frac{d}{dt} \log z_i = g_i(z)$$

- **Multiplicative form.** Growth is per-capita; extinction faces $\{z_i = 0\}$ are invariant; selection redistributes but never creates types.
- **Aggregate coupling.** g_i depends on the population only through the aggregate state z (mean-field), not on structure or identity.

What is not in the family:

Break multiplicativity

- Add innovation → replicator–**mutator**
- Non-selection law → **best response**, Q-learning

Break aggregate coupling

- Add structure → games on **graphs**
- (Noise, not a violation) → genetic **drift**
- **Spectrum:** weak selection → replicator → best response.

Upshots

What we don’t get from this connection:

- Mean-field preserves average behavior; not variance.
- Isomorphism preserves trajectories; not interpretations.

What we do get:

- “Training selects for high reward” and “selection favors high fitness” can be formally related, so learning and natural selection inherit shared formalisms;
- We can transfer of theorems across evolution, learning, and inference;
- The reason why RL, EGT, and Bayesian methods keep rediscovering each other.

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