Persistence, Permanence, and Extinction in Infinite-Dimensional Random Dynamical Systems

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Motivation: long-term survival in ecological models

A central question in population dynamics is whether interacting species survive in the long run. Since the classical works of Lotka and Volterra, notions such as

extinction, persistence, permanence, boundedness, etc,

have become fundamental tools for describing the asymptotic behavior of biological systems. For instance,

- Permanence: populations eventually stay uniformly away from extinction and remain bounded.
- Persistence: populations survive away from the extinction state, possibly in weaker senses.

Our abstract measure-theoretic approach

Instead of studying a particular model, we consider a finite measure space $(E, \mathcal{E}, \mu)$ and a function $f : \mathbb{R} \times E \to \mathbb{R}_+$.

This framework allows us to study the logical relations among biological notions independently of the specific system.

- We compare extinction, weak persistence, strong persistence, permanence, and ultimate boundedness.
- We include versions in measure and Cesàro-average versions, i.e., "in mean" properties.
- We prove a hierarchy of implications among these notions.

The goal is to provide a common abstract layer that can simplify the analysis of concrete ecological models.

Why an abstract framework?

In concrete ecological models, the same biological idea may appear in different mathematical forms. E. g.: survival may be described through:

- pointwise behavior of trajectories;
- convergence in measure;
- time averages;
- separation from the extinction boundary.

The abstract framework allows us to compare these notions without depending on the particular equations of the model.

Same biological question, different mathematical formulations.

A hierarchy of biological notions

Extinction, persistence, permanence, and boundedness are not independent.

Some notions are stronger than others. For instance,

$$\text{permanence} \implies \text{strong persistence} \implies \text{weak persistence}.$$

Similarly, permanence also contains an upper boundedness condition:

$$\text{permanence} \implies \text{ultimate boundedness}.$$

Thus, one goal is to organize these definitions into a clear implication structure.

Pointwise notions versus notions in measure

There are two complementary ways to describe long-term survival.

- Pointwise notions: describe the behavior of $f(t, y)$ for a.e. $y \in E$.
- Notions in measure: describe the size of the subset of E where the population satisfies a given property.

Pointwise persistence gives information along almost every individual parameter or initial condition.

Persistence in measure gives information about the asymptotic size of the surviving region.

Individual trajectories versus size of the surviving set.

Why to consider persistence in mean?

A population can be very small at some times and still have a positive long-term average, justifying the use of Cesàro averages:

$$\frac{1}{t}\int_0^t f(s,y)\,ds.$$

The corresponding biological question becomes:

Does the population survive on average over long time intervals?

These notions are especially useful in non-autonomous and random models, where oscillations and temporal variability are natural.

Connecting the two parts of the talk

1st part: compares biological notions in an abstract measure-theoretic setting.

2nd part: applies the same philosophy to random dynamical systems.

Measure-theoretic framework

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logical relations among concepts

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Random dynamical systems

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geometry of attractors relative to extinction

Let $(E, \mathcal{E}, \mu)$ and $f : \mathbb{R} \times E \to \mathbb{R}_+$ be L^1_{loc} on the 1st variable and $\mathcal{E}$-measurable on the second. Then, f is said to be

- μ-extinct in measure, if

$$\lim_{t \to \infty} \mu(\{y \in E : f(t, y) > \epsilon\}) = 0, \quad \forall\, \epsilon > 0;$$

- μ-weakly-persistent in measure, if

$$\limsup_{t \to \infty} \mu(\{y \in E : f(t, y) > 0\}) = \mu(E);$$

- μ-strongly-persistent in measure, if

$$\liminf_{t \to \infty} \mu(\{y \in E : f(t, y) > 0\}) = \mu(E).$$

Other biological concepts

- μ-ultimately bounded in measure, if $\forall\ \epsilon \in (0, \mu(E))$, $\exists\ M > 0$ s.t.

$$\limsup_{t\to\infty}\{\mu(\{y \in E\colon f(t,y) > M\})\} < \epsilon;$$

- μ-permanent in measure, if $0 < m \leq M$ are s.t.

$$\begin{aligned}&\liminf_{t\to\infty}\{\mu(\{y \in E\colon f(t,y) \geq m\})\}\\ =&\liminf_{t\to\infty}\{\mu(\{y \in E\colon f(t,y) \leq M\})\} = \mu(E);\end{aligned}$$

- μ-asymptotically permanent in measure, if $\forall\ \epsilon \in (0, \mu(E))$, $\exists$ $0 < m \leq M$ s.t.

$$\liminf_{t\to\infty}\{\mu(\{y \in E\colon f(t,y) \leq M\})\} \geq \mu(E) - \epsilon \quad \text{and}$$

$$\liminf_{t\to\infty}\{\mu(\{y \in E\colon f(t,y) \geq m\})\} \geq \mu(E) - \epsilon;$$

- L-weakly-persistent in measure (L for the Lebesgue integral), if

$$\limsup_{t\to\infty}\left\{\mu\left(\left\{y\in E\colon\ \left(\frac{1}{t}\int_0^t f(s,y)ds\right)>0\right\}\right)\right\}=\mu(E);$$

- L-strongly-persistent in measure, if

$$\liminf_{t\to\infty}\left\{\mu\left(\left\{y\in E\colon\ \left(\frac{1}{t}\int_0^t f(s,y)ds\right)>0\right\}\right)\right\}=\mu(E);$$

- μ-extinct, if $\lim_{t\to\infty} f(t,y) = 0$, for almost all $y \in E$;
- μ-weakly-persistent, if $\limsup_{t\to\infty}\{f(t,y)\} > 0$, for almost all $y \in E$;
- μ-strongly-persistent, if $\liminf_{t\to\infty}\{f(t,y)\} > 0$, for almost all $y \in E$;
- μ-permanent, if there exist $C, M > 0$ s.t.

$$0 < C \leq \liminf_{t\to\infty}\{f(t,y)\} \leq \limsup_{t\to\infty}\{f(t,y)\} \leq M \ \ (\mu\text{–a.e.});$$

- μ-ultimately bounded, if there exists $M > 0$ s.t.

$$\limsup_{t\to\infty}\{f(t,y)\} \leq M \ \ (\mu\text{–a.e.});$$

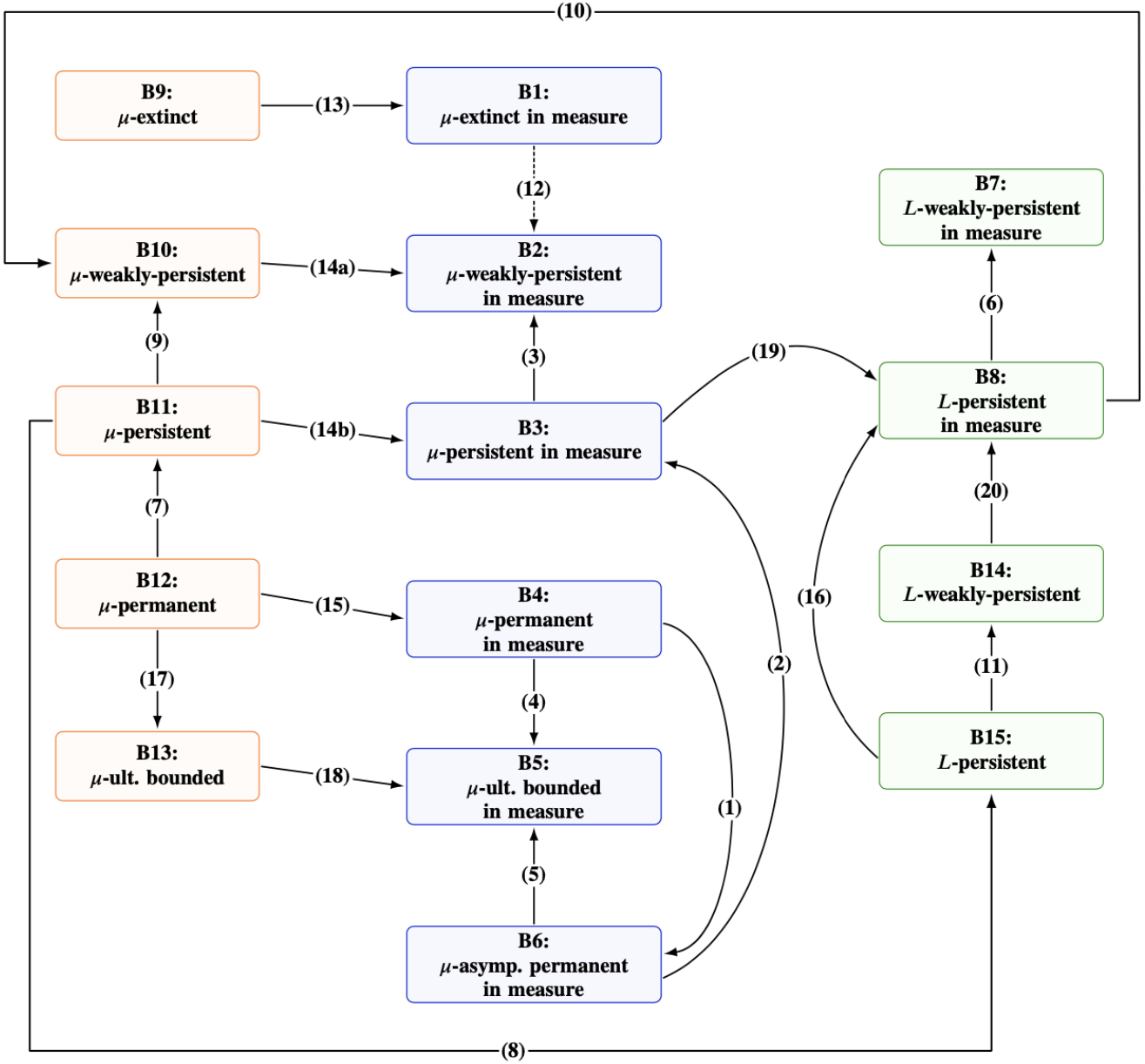
- L-weakly-persistent, if

$$\limsup_{t\to\infty}\left\{\frac{1}{t}\int_0^t f(s,y)ds\right\} > 0, \ \ (\mu\text{–a.e.});$$

- L-strongly-persistent, if

$$\liminf_{t\to\infty}\left\{\frac{1}{t}\int_0^t f(s,y)ds\right\} > 0, \ \ (\mu\text{–a.e.}).$$

Summary of the results



From population models to dynamical systems

Modern biological models include

- deterministic ODEs and PDEs,
- stochastic differential equations,
- random ordinary differential equations,
- random dynamical systems.

Typical questions are:

- Does a species become extinct?
- Do several species coexist?
- How do parameters affect long-term survival?

Most existing results answer these questions for a particular model.

Dissipative biological systems

A biological model is called dissipative if, after a sufficiently long time, all trajectories enter a bounded region of the phase space and never leave it.

Biological interpretation:

- Populations cannot grow indefinitely.
- Environmental limitations (food, space, resources, etc.) eventually bound the dynamics.
- Regardless of the initial population sizes, the long-term behavior is confined to a bounded region.

As time evolves, trajectories approach an invariant object called the

pullback random attractor.

This attractor contains all possible long-term behaviors of the system.

The attractor and the extinction set

Many biological phase spaces contain an invariant extinction set (e.g. the origin in one-species models or boundary components in multi-species models).

The existence of a pullback random attractor alone does *not* determine the biological outcome.

$$\boxed{\text{Attractor} \not\Rightarrow \text{Survival of the populations.}}$$

Instead, one must understand the geometry of the attractor relative to the extinction set.

- Is the attractor contained in the extinction set?
- Is it uniformly separated from the extinction set?
- Can different regions of the attractor exhibit different biological behaviors?

Inspired by Hale–Waltman theory, we study the structure of pullback random attractors relative to the extinction boundary.

The novelty is that biological properties are assigned to

random variables and random subsets

instead of to the whole random dynamical system. Thus,

- different regions of the same attractor may have different biological behavior;
- survival or extinction may depend on the initial data;
- the classical theory is recovered as a particular case.

Our contribution

Main results:

- representation of pullback random attractors relative to the extinction boundary;
- translation of biological notions into the language of random dynamical systems.

We consider X a metric phase space and $(\Omega, \mathcal{F}, \mathbb{P}, \theta)$ describes the random environment.

A random dynamical system is given by a cocycle $\varphi(t, \omega)x$, which represents the state at time t, starting from x, under the realization ω.

For biological models, X contains an invariant extinction boundary $\partial X_0 \subset X$.

A random set $B = \{B(\omega)\}_{\omega \in \Omega}$ represents a family of possible initial states depending on the random environment.

Formally, a quadruple $(\Omega, \mathcal{F}, \mathbb{P}, \theta)$ is a driving dynamical system if $(\Omega, \mathcal{F}, \mathbb{P})$ is a probability space and $\theta\colon \mathbb{R} \times \Omega \to \Omega$ is a map satisfying:

- $\theta_0 = \mathrm{Id}_\Omega$;
- $\theta_{t+s} = \theta_t \circ \theta_s$, for all $t, s \in \mathbb{R}$;
- the map $(t, \omega) \in \mathbb{R} \times \Omega \mapsto \theta_t \omega \in \Omega$ is $(\mathcal{B}_\mathbb{R} \times \mathcal{F}, \mathcal{F})$-measurable;
- $\mathbb{P}(\theta_t^{-1}(A)) = \mathbb{P}(A)$, $A \in \mathcal{F}$, for every $t \in \mathbb{R}$.

A random semi-dynamical system over X, with driving dynamical system θ, is a pair (φ, θ), where $\varphi\colon \mathbb{R}_+ \times \Omega \times X \to X$ is called a random cocycle over θ satisfying:

- $\varphi(0,\omega)x = x$, $\forall\ x \in X$ and $\omega \in \Omega$;
- $\varphi(t+s,\omega) = \varphi(t,\theta_s\omega) \circ \varphi(s,\omega)$, $\forall\ t,s \in \mathbb{R}_+$ and $\omega \in \Omega$;
- the map $(t,\omega,x) \in I \times \Omega \times X \mapsto \varphi(t,\omega)x \in X$ is $(\mathcal{B}_{\mathbb{R}_+} \times \mathcal{F} \times \mathcal{B}_X, \mathcal{B}_X)$-measurable;
- the map $x \in X \mapsto \varphi(t,\omega)x \in X$ is continuous, $\forall\ (t,\omega) \in \mathbb{R}_+ \times \Omega$.

Why random cocycles?

In deterministic dynamics, $x(t) = S(t)x_0$, where $S(t)$ is a semigroup.

In random environments, the evolution also depends on the realization ω:

$$x(t) = \varphi(t, \omega)x_0.$$

The cocycle identity

$$\varphi(t + s, \omega) = \varphi(t, \theta_s\omega) \circ \varphi(s, \omega)$$

expresses that, after the population has evolved for s units of time, the random environment must also be updated before the evolution continues.

The pullback limit of a random set

To describe long-term behavior, we use the pullback evolution

$$\varphi(t, \theta_{-t}\omega)B(\theta_{-t}\omega).$$

The corresponding pullback limit is denoted by $\Gamma(B, \omega)$.

Intuitively, $\Gamma(B, \omega)$ is the set of all possible limit points of trajectories starting from B.

Equivalently, $y \in \Gamma(B, \omega)$ if there exist $t_n \to \infty$ and $x_n \in B(\theta_{-t_n}\omega)$ s.t.

$$\varphi(t_n, \theta_{-t_n}\omega)x_n \longrightarrow y.$$

Recall that...

Let $\mathcal{A} = \{\mathcal{A}(\omega)\}_{\omega\in\Omega}$ and $B = \{B(\omega)\}_{\omega\in\Omega}$ be random sets. Then,

- $\mathcal{A}$ pullback attracts B, if

$$\lim_{t\to\infty} (\text{dist}_H(\varphi(t,\theta_{-t}(\omega))B(\theta_{-t}(\omega)),\mathcal{A}(\omega))) = 0, \ \ \omega \in \Omega^*;$$

- $\mathcal{A}$ pullback absorbs B, if $\exists\ T_B : \Omega \to \mathbb{R}_+$ s.t.

$$\varphi(t,\theta_{-t}(\omega))B(\theta_{-t}(\omega)) \subset \mathcal{A}(\omega), \ \ t \geq T_B(\omega), \ \ \omega \in \Omega^*.$$

A random set $\mathcal{A} = \{\mathcal{A}(\omega)\}_{\omega\in\Omega}$ is a pullback random attractor for a random semi-dynamical system (φ, θ) over X, whenever

- $\mathcal{A}$ is a random compact set,
- $\mathcal{A}$ is φ-invariant, i.e.,

$$\varphi(t,\omega)\mathcal{A}(\omega) = \mathcal{A}\left(\theta_t(\omega)\right), \quad \forall\ \omega \in \Omega^*,\ \forall\ t \geq 0;$$

- $\mathcal{A}$ pullback attracts every random bounded set $B = \{B(\omega)\}_{\omega\in\Omega}$.

The Γ-limit of a random set $B = \{B(\omega)\}_{\omega\in\Omega}$, denoted by $\Gamma(B) = \{\Gamma(B,\omega)\}_{\omega\in\Omega}$, is defined by

$$\Gamma(B,\omega) = \bigcap_{t\geq 0} \overline{\bigcup_{s\geq t} \bigcup_{x\in B} \xi_x(s,\theta_{-s}(\omega))}$$

where

- $x \in B$: choose any admissible initial population.
- $\xi_x(s,\theta_{-s}\omega)$: let this population evolve for a long time under the corresponding environmental history.
- $\cup_{x\in B}$: consider all possible initial populations.
- $\cup_{s\geq t}$: look at all sufficiently large times.
- Closure includes all limiting population states.
- $\cap_{t\geq 0}$: retain only those states that persist regardless of how far into the future we look.

Persistence through the pullback limit

Note that $\Gamma(B, \omega)$ is the set of all asymptotically observable population states.

Persistence means that the population does not approach extinction.

Thus, for a random set B, persistence is expressed by the asymptotic separation

$$\Gamma(B, \omega) \cap \partial X_0 = \emptyset$$

meaning that $\Gamma(B)$ remains randomly bounded away from the extinction boundary.

Porposition

Let (φ, θ) satisfy the standard dissipativity and compactness assumptions, and let B be a random bounded set. Then

$$B \text{ is } \mathbb{P}\text{-persistent} \iff \Gamma(B) \text{ is strongly randomly bounded.}$$

This means that persistence of the initial random set is completely determined by the position of its pullback limit relative to extinction.

The attractor decomposes according to biology

Theorem

Suppose $\partial Y_0(\omega) \cap \Gamma(B, \omega) \neq \emptyset$, and both

$$\partial Y_0 \cap \Gamma(B) \quad \text{and} \quad \Gamma(B) \setminus \partial Y_0$$

are invariant random compact sets. Then

- $\partial Y_0 \cap \Gamma(B)$ is $\mathbb{P}$-extinct and
- $\Gamma(B) \setminus \partial Y_0$ is $\mathbb{P}$-permanent.

This means that the pullback attractor naturally splits into a biologically extinct part and a biologically permanent part.

Short summary

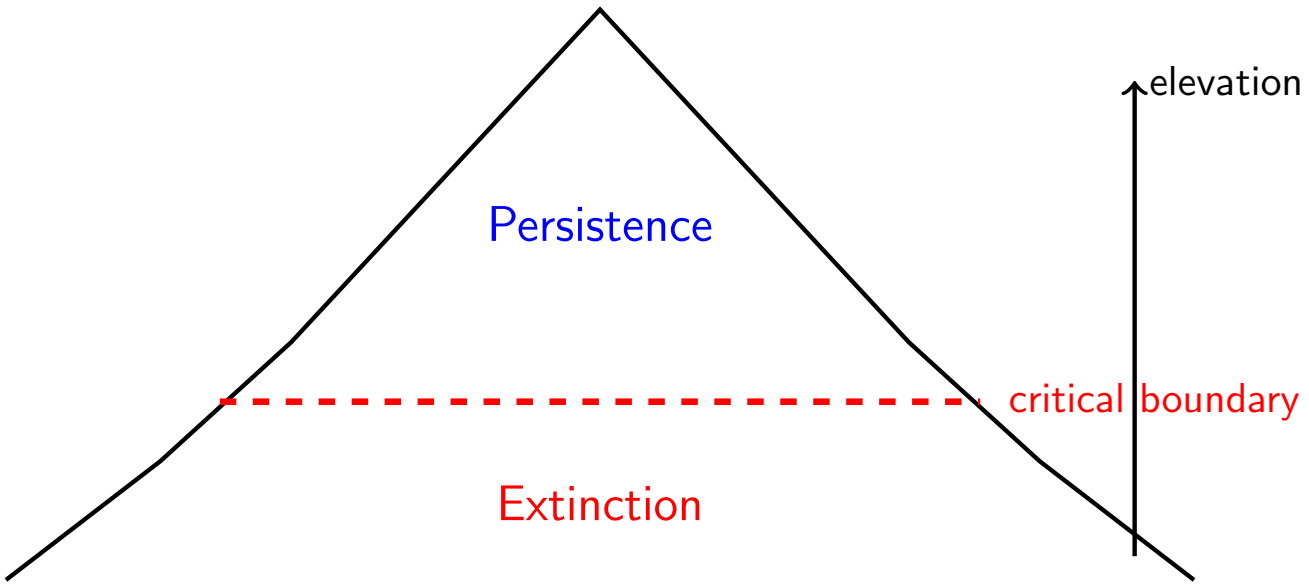
The biological behavior of a random dynamical system is described in the geometry of its pullback attractor.

- Persistence is characterized by the position of $\Gamma(B)$ relative to the extinction boundary.
- Different invariant components of the same attractor may have different biological meanings.
- The theory extends the classical Hale–Waltman approach to random dynamical systems.

The attractor is not merely a geometric object; it also carries the biological information of the system.

A geographical picture of the extinction boundary

Consider an alpine species living along an elevation gradient.



Above the threshold, environmental conditions may allow long-term survival; below it, the local population may be unable to sustain itself.

The extinction boundary separates states compatible with persistence from extinction states.

Thanks for your attention!