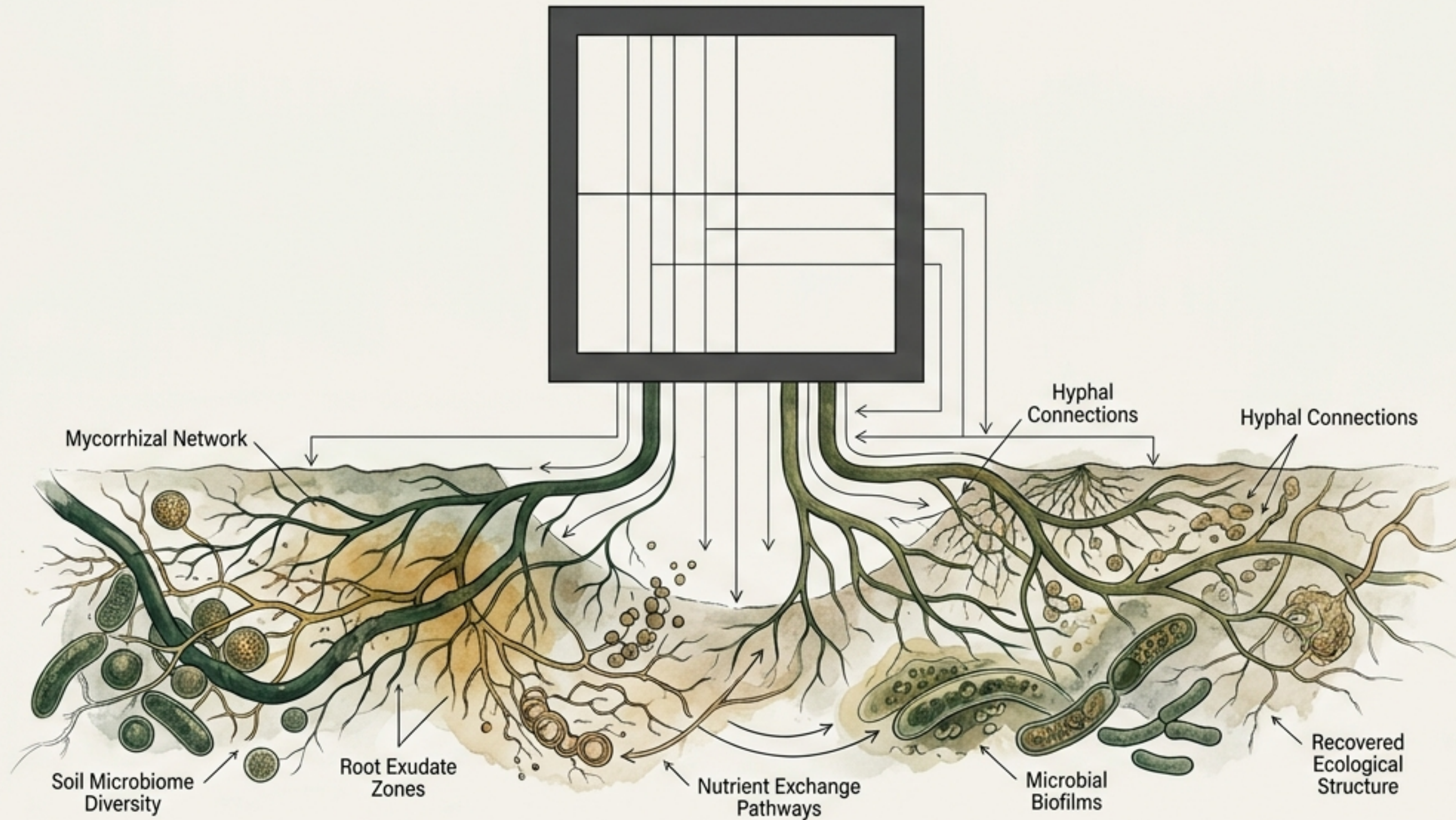


When Noise Becomes Structure

Microbiomes, Projection Failure, and the Recovery of Ecological Organization

Based on the June 2026 Flyxion analysis of *npj Science of Plants*.

A model is a projection. What happens when the discarded information holds the structure of life?



A century of quantitative genetics hid the microbiome inside the residual error

$$P = \beta_G G + \beta_E E + \beta_{GE} (G \times E) + \varepsilon$$

The Molar Variables

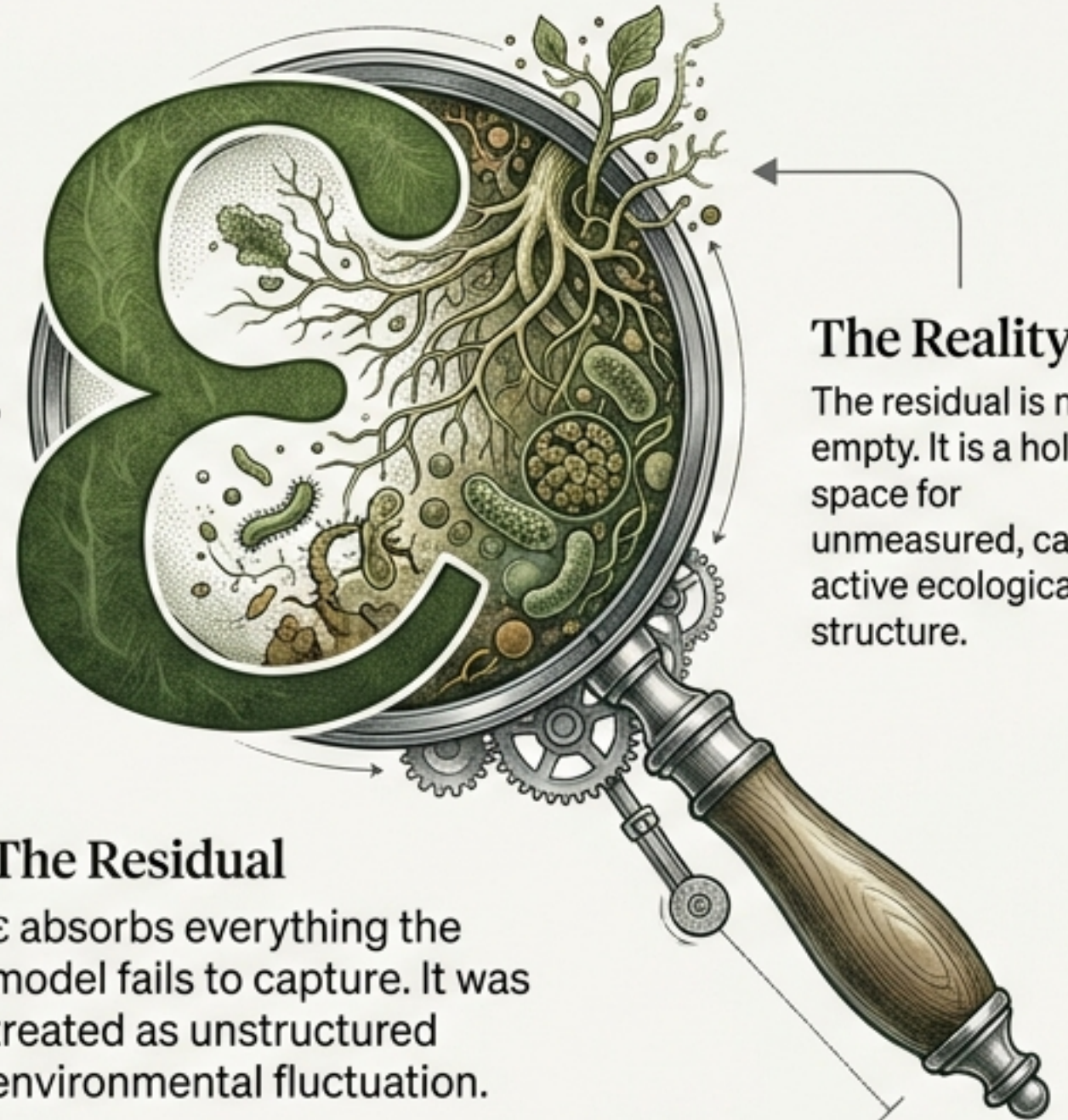
Genotype (G) and Environment (E) drove crop yields for decades.

The Residual

ε absorbs everything the model fails to capture. It was treated as unstructured environmental fluctuation.

The Reality

The residual is not empty. It is a holding space for unmeasured, causally active ecological structure.



The GEM framework extracts structured ecological information from statistical noise

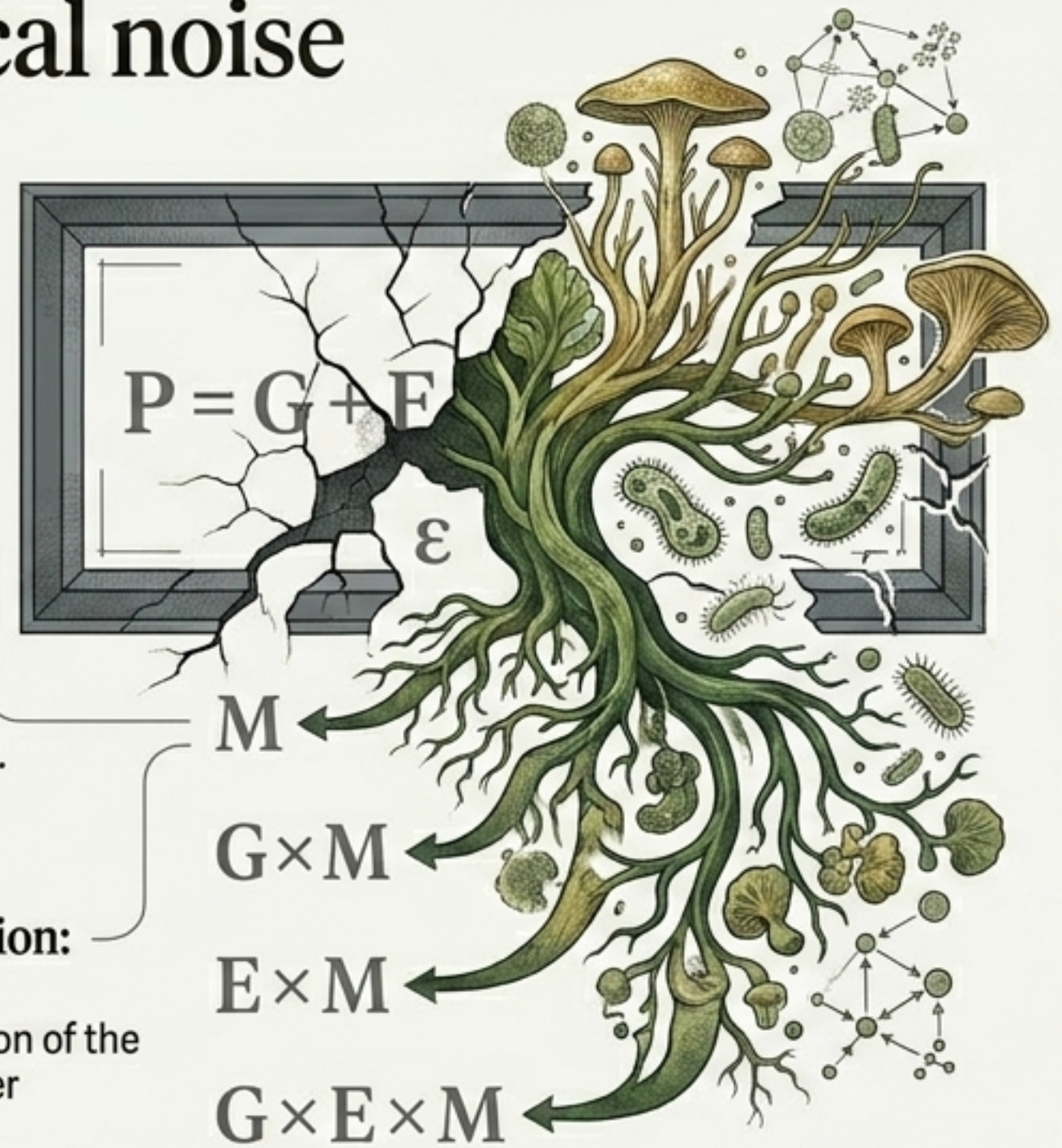
The 2026 Proposal (Araujo / Oyserman): Formally transition to GEM to reduce epistemic noise.

$$P = G + E + (G \times E) + \epsilon$$

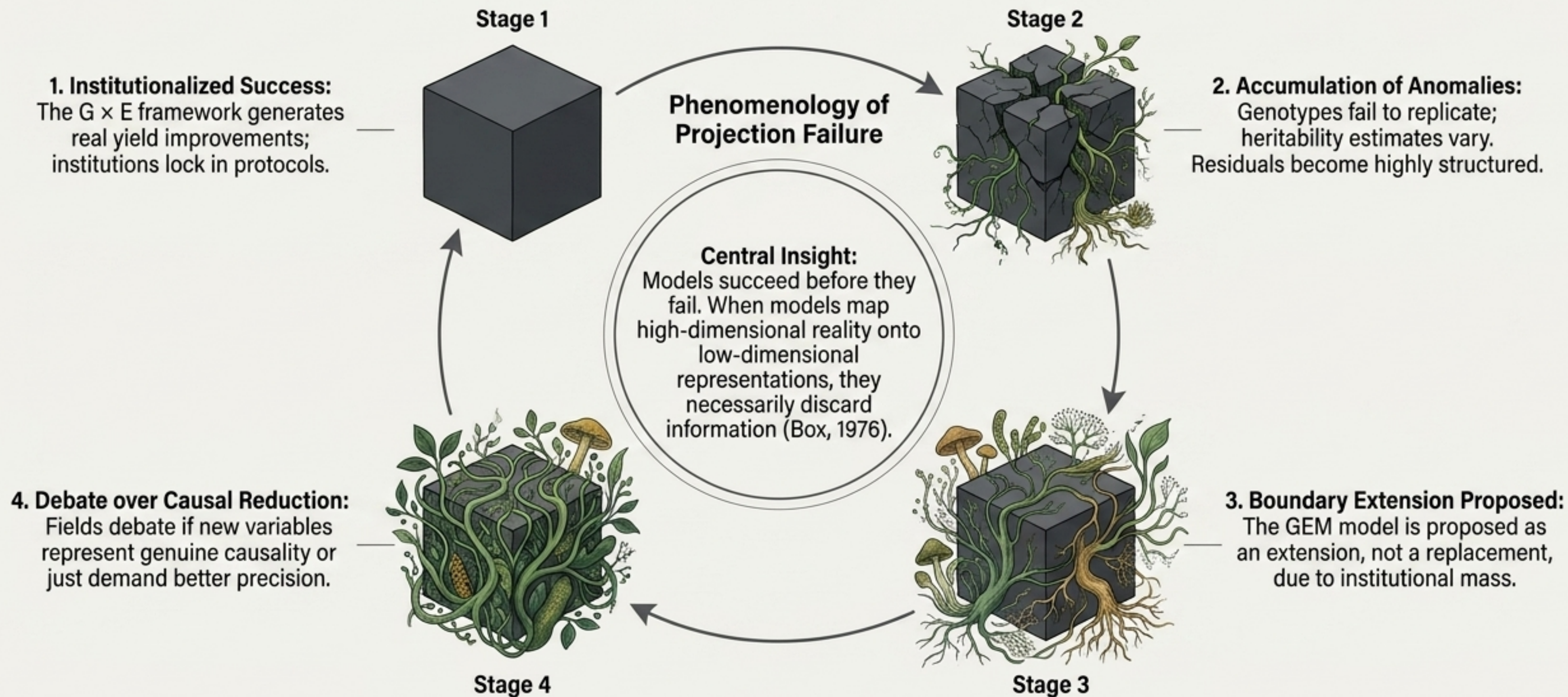
Classical Molar Model
(pre-GEM)

Microbiome (M):
No longer an environmental accident. Partially heritable, genotype-responsive, and biologically significant.

The Boundary Expansion:
This is not just adding a parameter; it is an expansion of the system boundary to recover omitted causal structure.

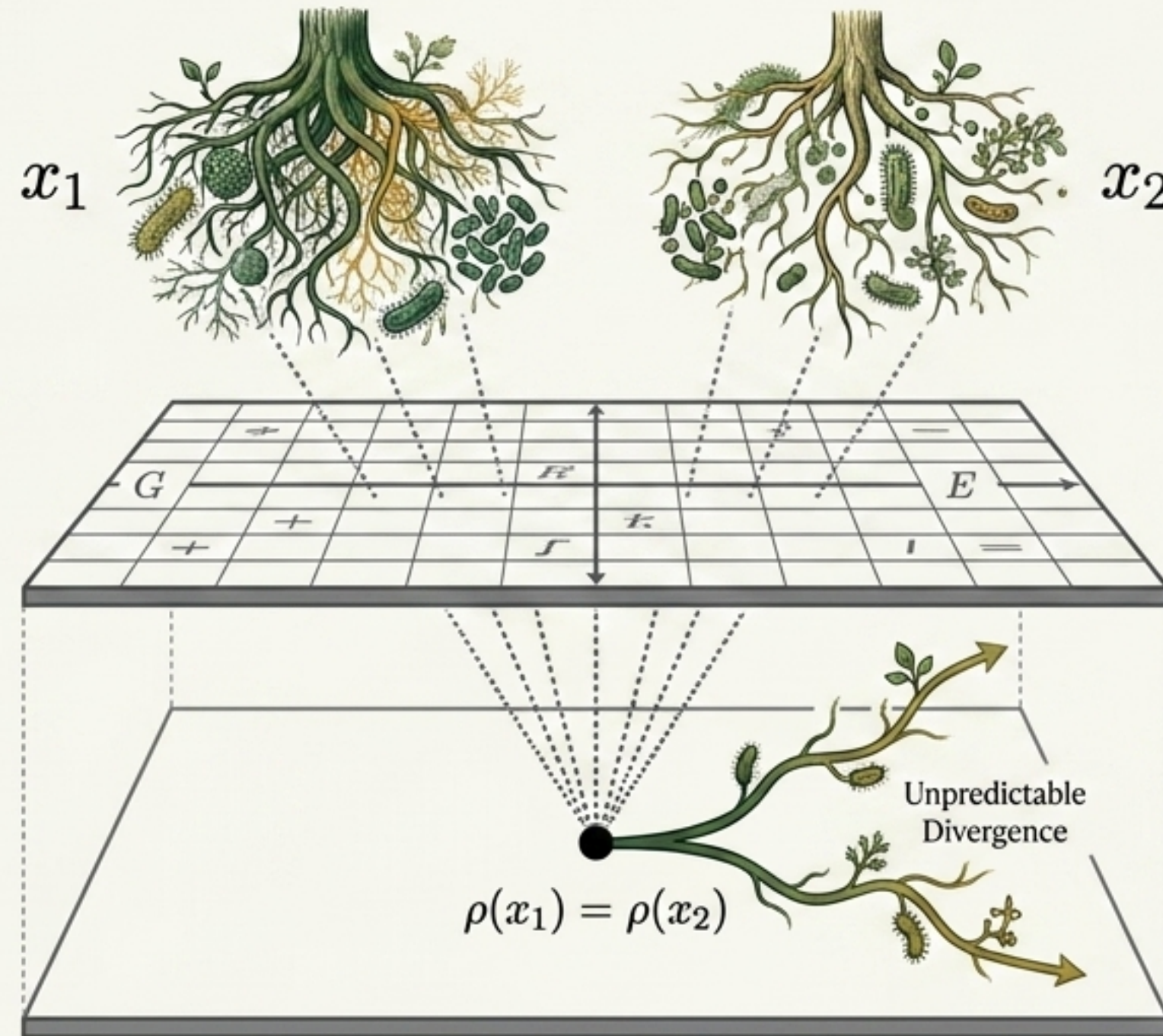


Successful models lock in boundaries that eventually force their own projection failure



The mathematics of missing variance guarantees blindness by design

The $G \times E$ Projection Filter



Fiber Collapse:

Two ecologically distinct states ($x_1 \neq x_2$) become indistinguishable under the classical projection.

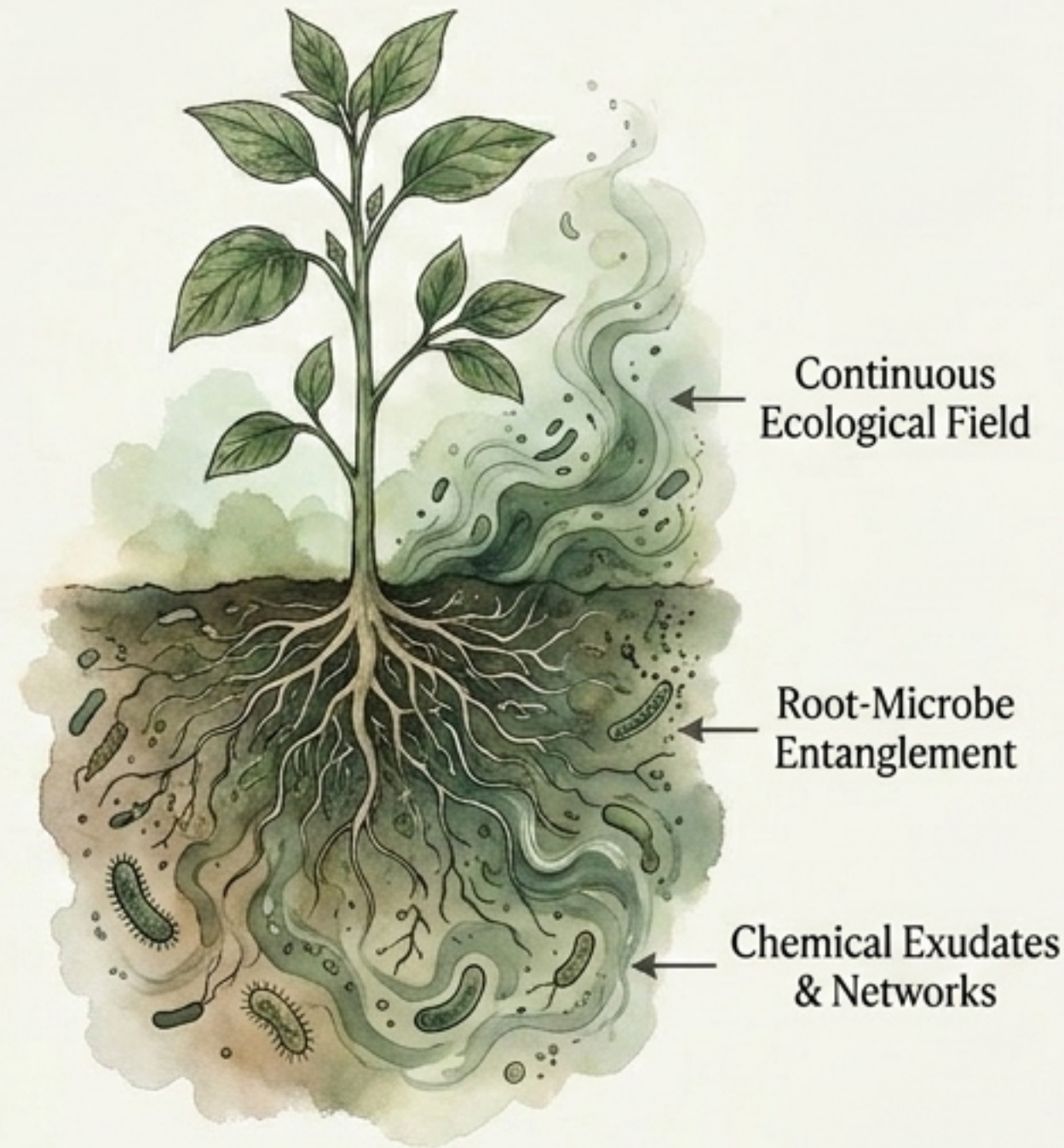
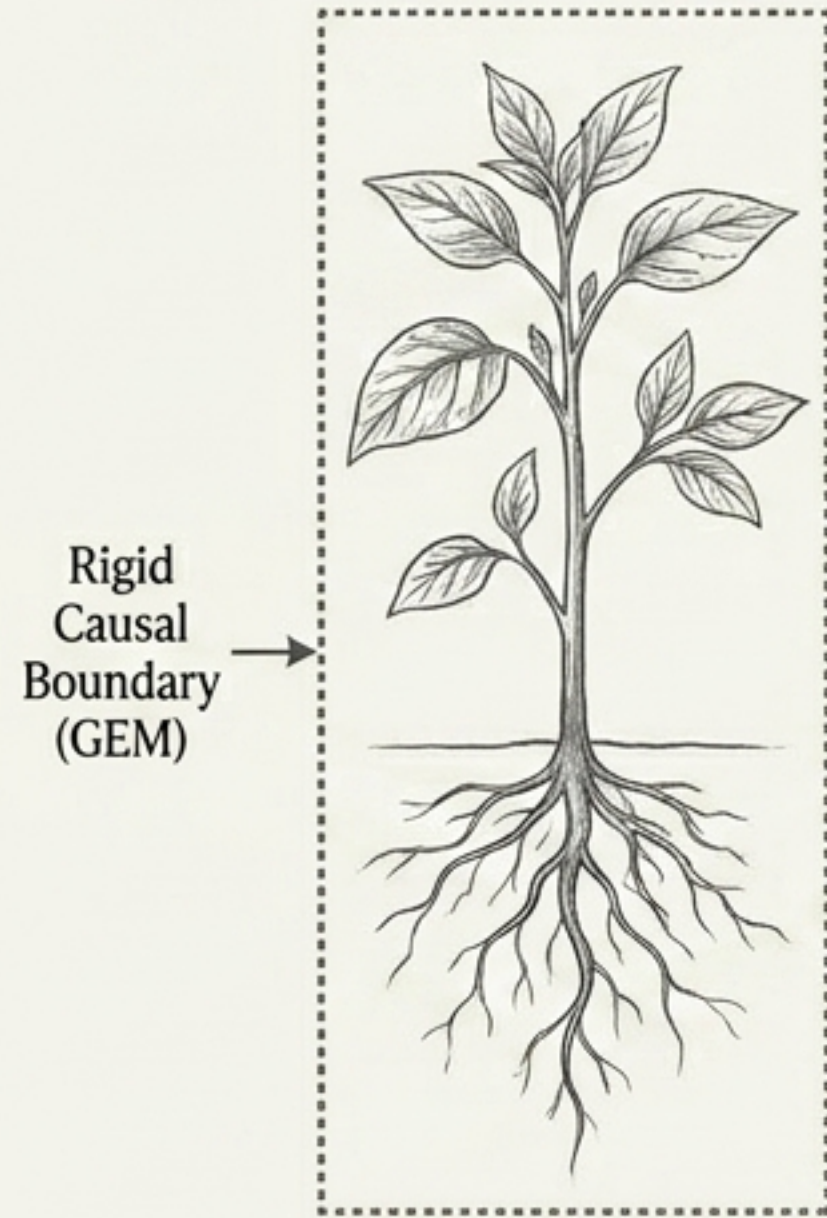
The Illusion of Noise:

Because the model collapses distinct causal structures into the same category, subsequent divergence appears as random stochastic error rather than predictable biology.

The organism is an artifact of the projection, not the primary causal unit

Molar Organism

Holobiont



The False Assumption:

The GEM model assumes the plant possesses a microbiome, just as it possesses a root system.

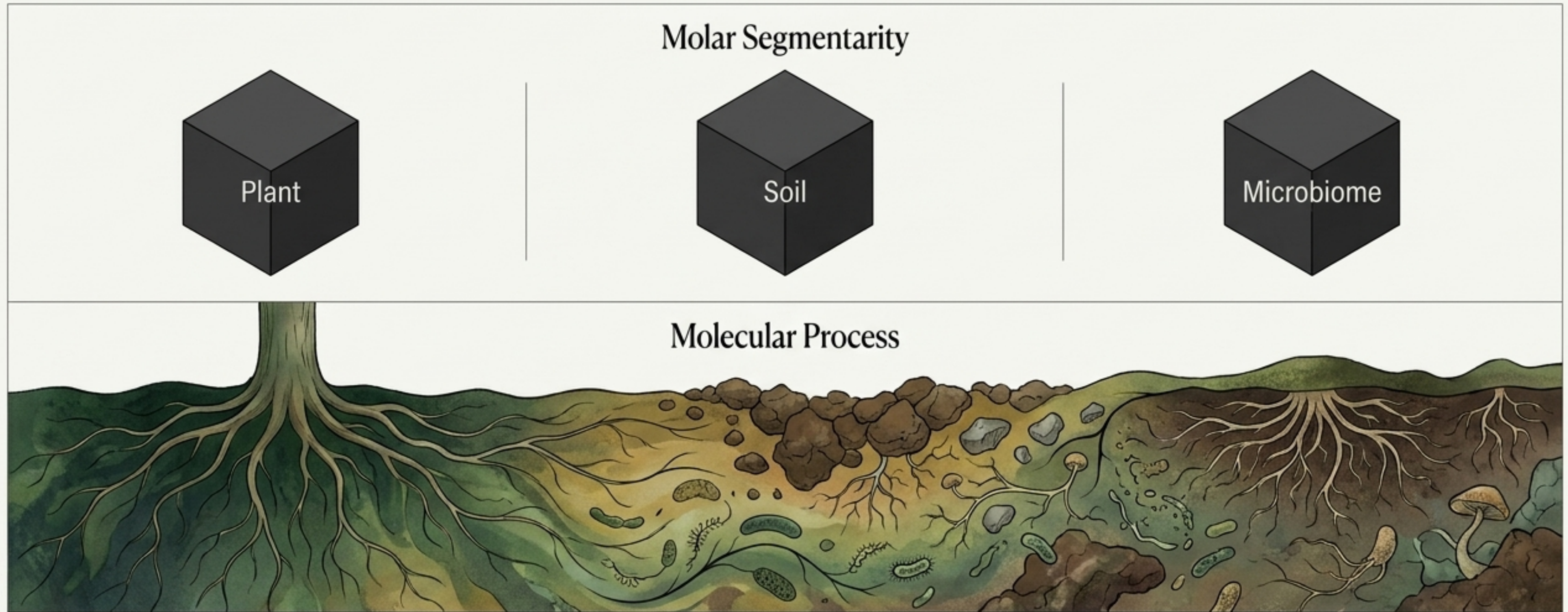
The Reciprocal Entanglement:

Root architectures genetically recruit specific microbes. The plant is partly constituted by the microbiome; the microbiome is partly constituted by the plant.

The Metaorganism:

The causal boundary isn't a clean line—it's a continuous ecological field.

Molar segments artificially divide continuous molecular processes



Molar Units (The Cuts):

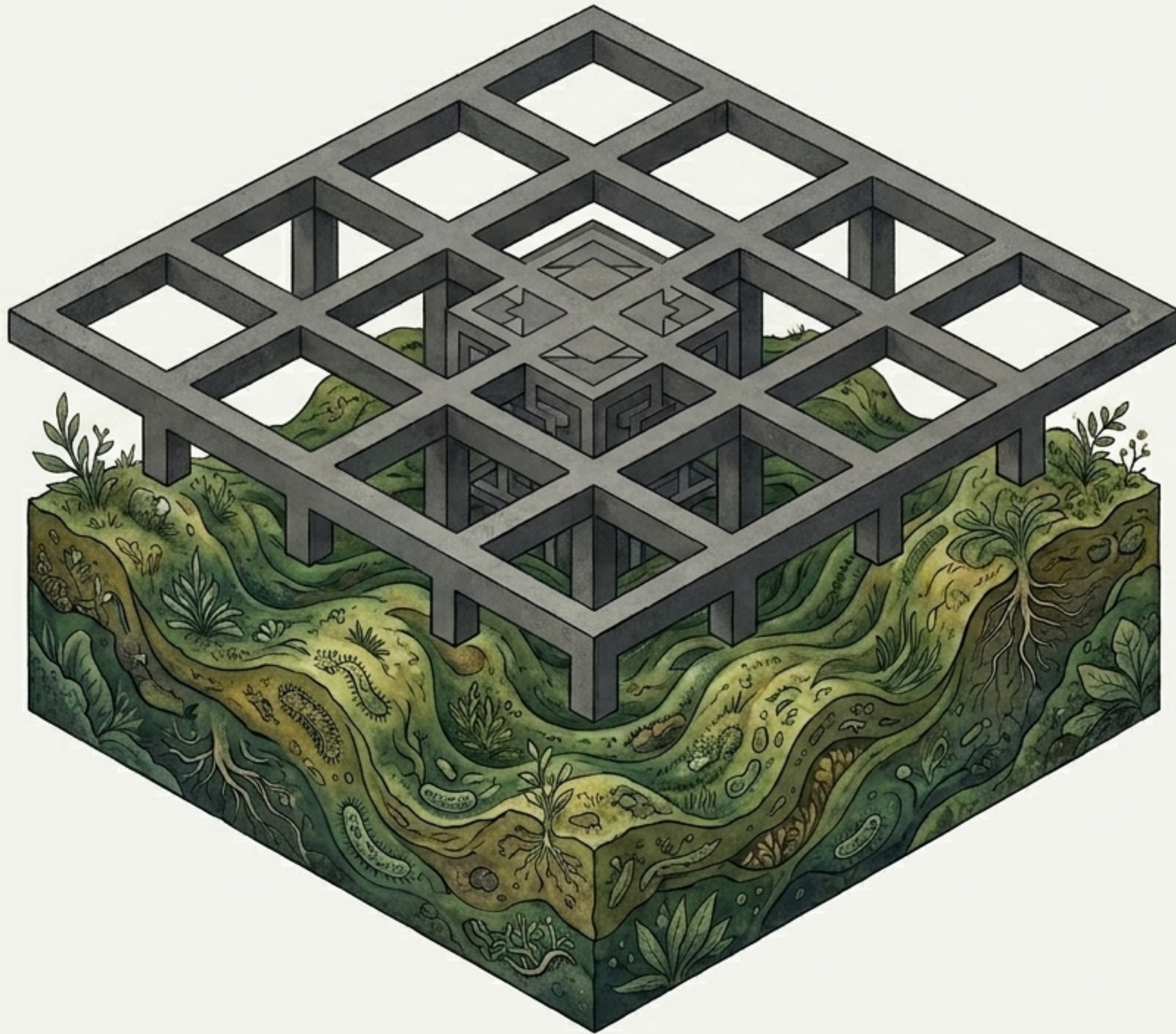
Organisms, species, and environments are artificial, institutionally recognized divisions designed for scientific tractability.

Molecular Processes (The Flows):

The primary flows, forces, and connections that actually produce the molar forms (Bogard, 1998).

The Error:

Breeding programs select at the molar level, underestimating how much the individual is constituted by external molecular processes.



Rigid statistical frameworks overcode the natural ecological terrain

The Trap of Overcoding:

When rigid systems impose their categorical boundaries as if they were the natural boundaries of the phenomena themselves.

Institutional Inertia:

Field trial protocols, statistical software, and funding structures actively reconstitute the bounded organism as the only tractable unit of selection.

“The model does not merely simplify the phenomena. It produces those units as the natural objects of inquiry.”

Phenotypes are not single outcomes, but basins of admissible trajectories

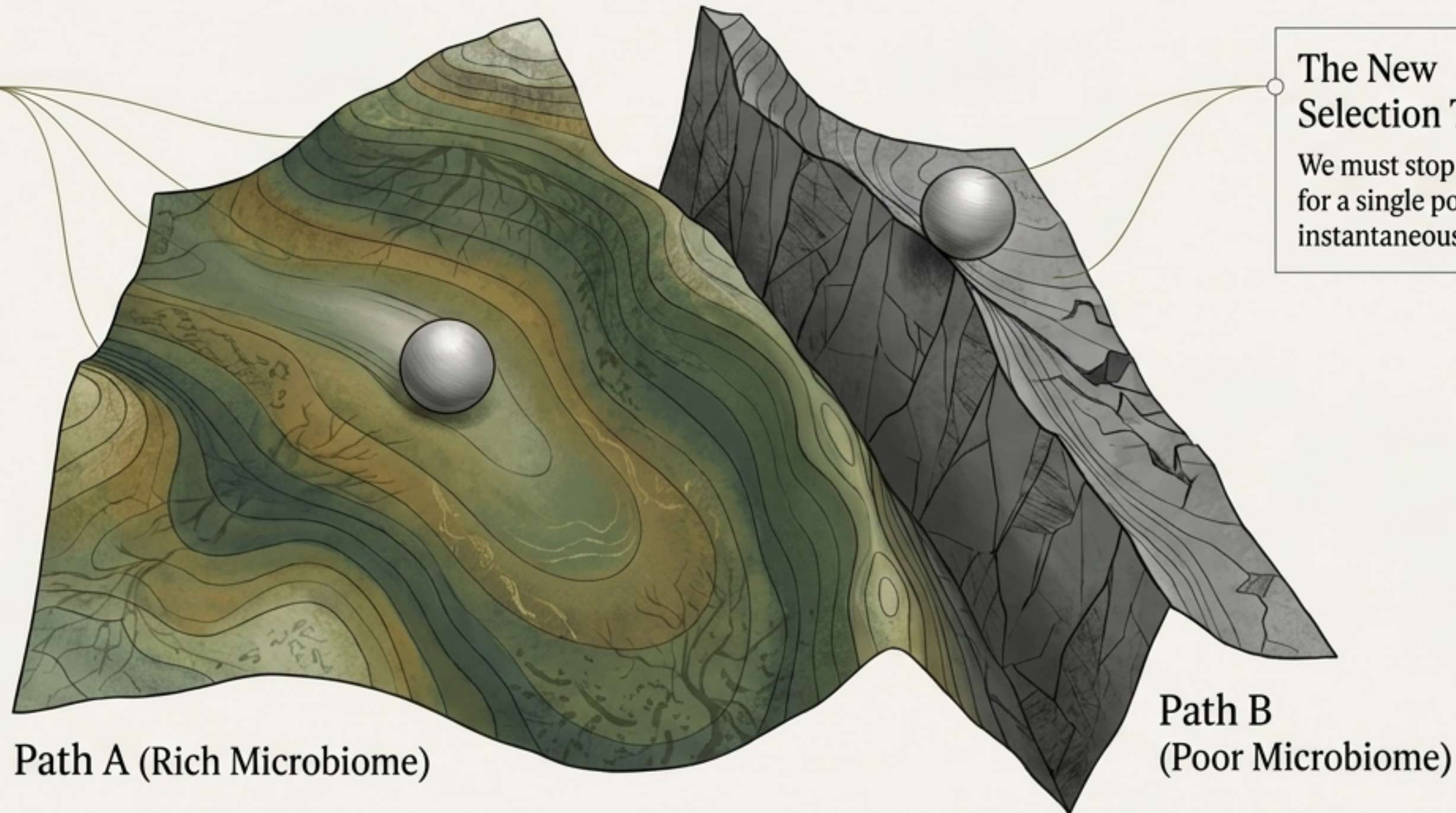
The Trajectory Basin: $A(x_0) = \{x(t) \in X : x(t) \text{ remains viable under constraints}\}$

The Role of the Microbiome:

Microbes modify the topology of the basin—enlarging it via nutrient access and pathogen suppression, increasing the accessibility of viable futures.

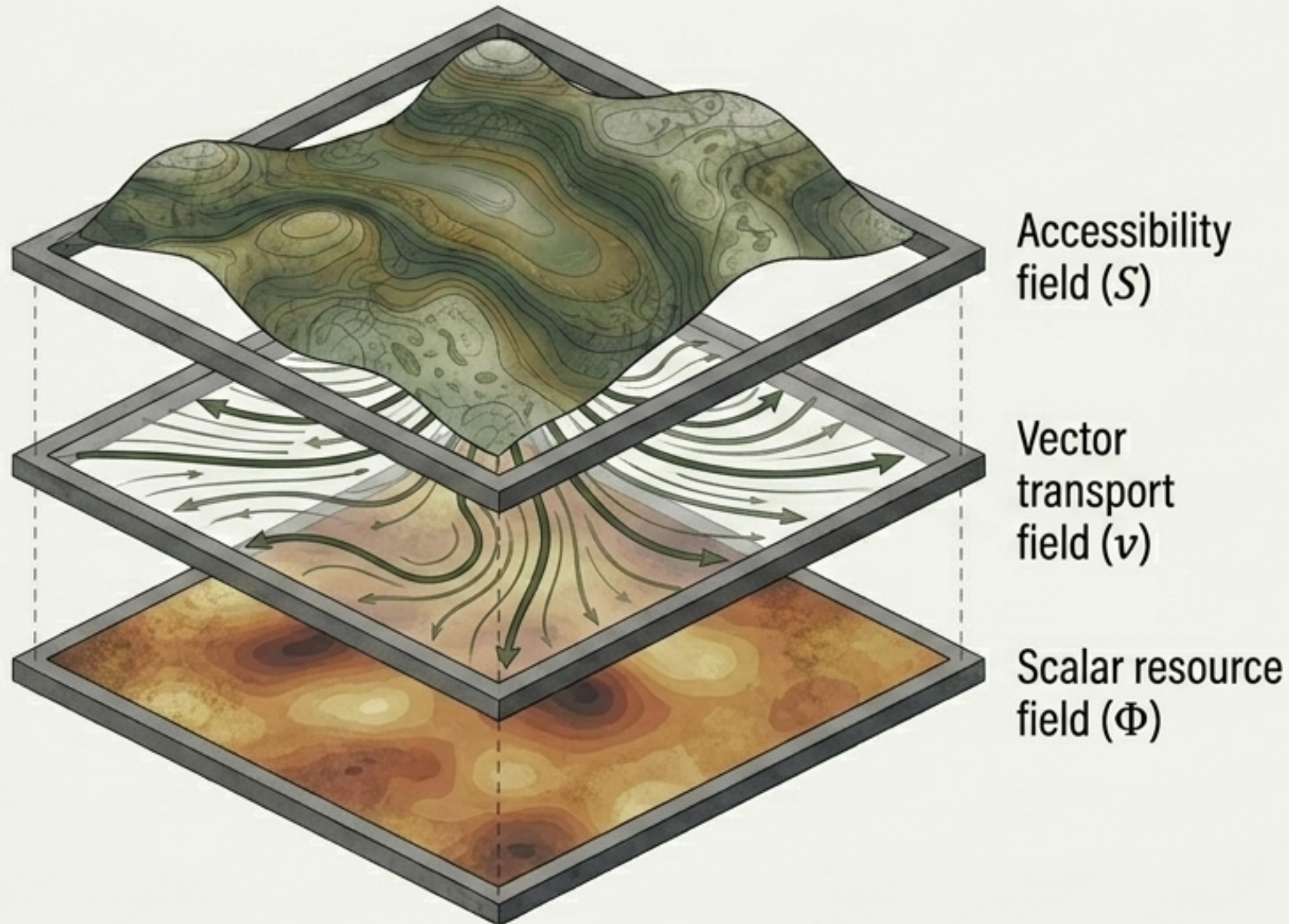
The New Selection Target:

We must stop selecting for a single point of instantaneous yield.



The RSVP framework replaces additive equations with coupled dynamic fields

Relativistic Scalar-Vector Plenum (RSVP): $P = \prod[\Phi(x, t), v(x, t), S(x, t)]$



Beyond Variables:

Genotype (G), Environment (E), and Microbiome (M) are no longer independent additive variables. They are dynamic constraints on the evolution of a coupled field.

Simultaneity:

The microbiome alters resources, redirects flows, and changes future accessibility all at once.

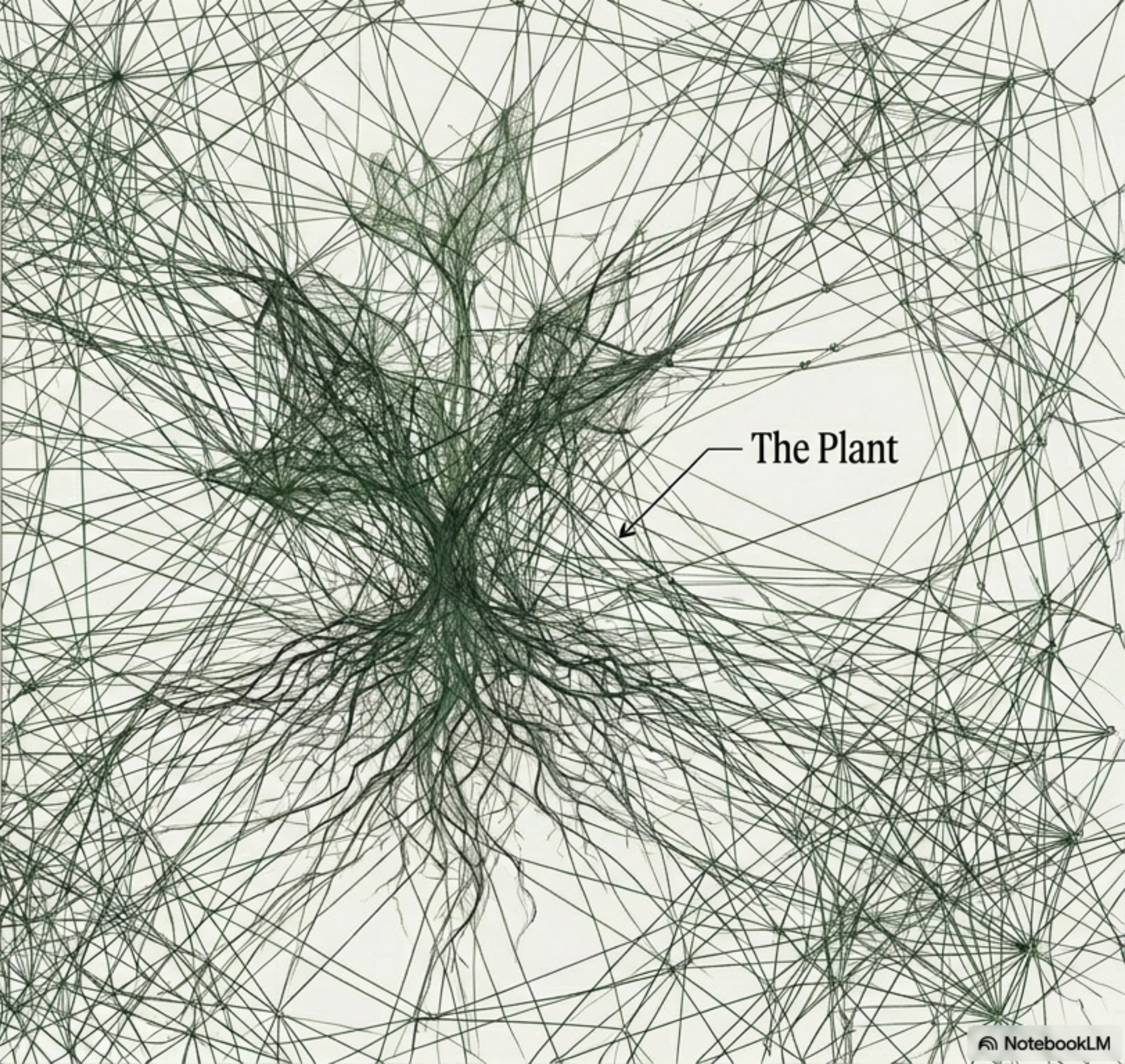
The plant is merely a partially stabilized sub-network within an infinite ecological web

The Assemblage: $P \approx C(S_1, S_2, \dots, S_n)$

Coherence over Boundaries: The plant is not an agent that recruits a microbiome. It is a temporary stabilization of processual dynamics.

The Event: What appears to be a stable object is actually a highly coordinated ecological event maintained by continuous exchange relations.

The Plant



The evolution of biological paradigms demands new ontological commitments

	Classical ($G \times E$)	Extended (GEM)	Ecological Assemblage
Unit of Analysis	The Bounded Organism	The Holobiont	The Sub-Network Assemblage
Treatment of Microbiome	Unstructured Noise (ϵ)	Additive Variable (M)	Co-constitutive Constraint Field
Selection Target	Instantaneous Yield Point	Yield + Recruitment Capacity	Trajectory Robustness Basin
Underlying Math	Lossy Projection ($P = G+E$)	Expanded Projection ($P = GEM$)	RSVP Coupled Fields

We are recovering lost ecological structure, not discovering new facts

The Integration Deficit:

The microbiome did not hide from plant breeding. The biological knowledge always existed.

The Blindness of the Bounded Form:

The breeding framework hid the microbiome from itself by insisting that the bounded organism was the only thing to see.

“Advances arise not from more sophisticated statistics – but from revising the ontological commitments that determined what counted as signal and what counted as background in the first place.”

