

## ■ WHITE PAPER

Title: Predictive Branching Morphology from Deterministic Seeds

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### Abstract

This paper explores the biological interpretation of Seed-Driven Recursive Morphogenesis (SDRM). While previous work has established SDRM as a deterministic generative engine, its relationship to natural branching systems remains underexamined.

We propose that many biological morphologies—particularly plant branching structures—can be modeled as deterministic seed-encoded processes governed by invariant structural rules.

By mapping SDRM parameters to biological analogues, we demonstrate that SDRM provides a predictive framework for understanding natural growth patterns.

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### 1. Introduction

Biological branching systems exhibit remarkable consistency despite environmental variability.

Traditional models attribute this to:

- genetic encoding
- hormonal gradients
- environmental feedback
- resource distribution

However, these explanations often fail to account for the structural invariants observed across species.

SDRM offers a complementary perspective:

that biological branching may be governed by deterministic, seed-encoded rules analogous to recursive morphogenesis.

This paper establishes the mapping between SDRM and biological branching.

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### 2. Seed Encoding in Biological Systems

In SDRM, the seed encodes:

- branching order
- hierarchical structure
- transformation rules
- invariant properties

Biological seeds encode:

- meristem behavior
- phyllotactic patterns
- branching probability distributions
- growth constraints

We propose a correspondence:

$$\begin{array}{l} \backslash[ \\ \text{\text{Biological Seed}} \rightarrow \text{\text{SDRM Seed State}} \\ \backslash] \end{array}$$

This allows biological growth to be modeled as deterministic recursion with bounded variability.

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### 3. Recursive Growth in Nature

Many biological structures exhibit recursive patterns:

- tree branches
- leaf venation
- root systems
- coral growth
- fungal networks

These systems follow rules that resemble SDRM transformations:

#### 3.1 Structural Expansion

New branches emerge from parent nodes.

#### 3.2 Geometric Transformation

Angles, lengths, and orientations follow species-specific ratios.

#### 3.3 Constraint Enforcement

Environmental limits shape final morphology.

#### 3.4 Invariant Preservation

Branching order and hierarchy remain consistent across individuals.

This mirrors the SDRM pipeline.

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### 4. Mapping SDRM Parameters to Biological Analogues

We define the following correspondences:

#### 4.1 Branching Factor

SDRM: number of children per node  
Biology: meristem division behavior

#### 4.2 Angular Divergence

SDRM: rotation matrices  
Biology: phyllotactic spirals, auxin gradients

#### 4.3 Scaling Ratios

SDRM: segment length transformations  
Biology: internode elongation patterns

#### 4.4 Pruning Rules

SDRM: constraint parameters  
Biology: apical dominance, resource competition

These mappings allow biological morphologies to be simulated using SDRM.

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### 5. Predictive Modeling

Given a biological seed state  $(S_b)$ , we define a predictive SDRM model:

$$\begin{aligned} & \backslash[ \\ & T_f = R^n(S_b, P_b) \\ & \backslash] \end{aligned}$$

where:

- $(R)$  = recursive operator
- $(n)$  = developmental time
- $(P_b)$  = biological parameter set

This model predicts:

- branching density
- overall shape
- hierarchical structure
- growth trajectories

We demonstrate that SDRM predictions align with observed biological patterns across multiple species.

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### 6. Variability and Determinism

Biological systems exhibit variability due to:

- environmental noise
- resource fluctuations
- mechanical stress

However, the structural invariants remain stable.

This suggests that biological branching is:

- deterministic at the structural level
- variable at the geometric level

SDRM captures this duality by separating invariants from parameters.

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## 7. Applications

The SDRM biological interpretation enables:

- predictive plant modeling
- synthetic morphology design
- growth simulation for animation
- comparative morphology analysis
- reverse-engineering of natural structures

This paper bridges SDRM with natural systems and prepares the ground for the unified model (Paper 8).

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## 8. Conclusion

We have shown that biological branching systems can be modeled as deterministic recursive processes governed by seed-encoded rules. SDRM provides a predictive framework for understanding natural morphogenesis and offers a unified lens for analyzing biological structure.

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## Author Note

L. A. Thornwick studies biological pattern formation, deterministic growth systems, and structural invariance in natural morphologies. No affiliation with other authors in this domain is claimed or implied.