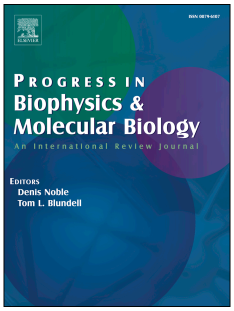

Modeling the peak of emergence in systems: Design and katachi

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Modeling the Peak of Emergence in Systems: Design and Katachi.

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Abstract

It is difficult to model emergence in biological systems using reductionist paradigms. A requirement for computational modeling is that individual entities can be recorded parametrically and related logically, but their *transformation* into systems cannot be captured this way. The problem stems from an inability to formally represent system-level interactions and implicit influences, such as context, shifts in causal agency or scale, and self-reference. This hampers biological systems modeling and its computational counterpart, indicating a need for new fundamental abstraction frameworks that include system-level characteristics.

We develop an approach that formally captures these characteristics, focusing on the way they come together to enable transformation at the ‘peak’ of an emergent process. An example from virology is presented, in which two seemingly antagonistic systems – the herpes cold sore virus and its host – are capable of altering their basic biological objectives to work together. The usual barriers to modeling this interaction are overcome through the addition of mechanisms from practices centered on emergent organization: design and *katachi*.

In the Japanese science of form, *katachi* refers to the emergence of structure from real situations, where an optimal balance between implicit influences is achieved. Design indicates how such optimization is guided by principles of flow. These practices leverage qualities of situated abstraction, and are complemented by an example from the sciences, in the intuitive method of physicist Kôdi Husimi.

Early results indicate that this approach can capture functional transformations during biological emergence, whilst being reasonably computable. Due to its geometric foundations, reliance on formal principles of flow and realization as narrative-based mechanisms, the method can also generate speculative predictions. This research forms the foundations of a new biomedical modeling platform, which is discussed.

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