**Towards a general interest high level publication on our research**

John McCaskill and Norman Packard

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**Nature:**

“Articles have a summary, separate from the main text, of up to 150 words, which does not have references, and does not contain numbers, abbreviations, acronyms or measurements unless essential. It is aimed at readers outside the discipline. This summary contains a paragraph (2-3 sentences) of basic-level introduction to the field; a brief account of the background and rationale of the work; a statement of the main conclusions (introduced by the phrase 'Here we show' or its equivalent); and finally, 2-3 sentences putting the main findings into general context so it is clear how the results described in the paper have moved the field forwards.”

Assuming we can show all these things:

1. 342 word version
2. 258 word version
3. 151 word version

**How robust ecosystems maintaining diversity emerge in spatial evolutionary dynamics.**

(342 words)

Simple models of the maintenance and diversification of information processing in spatial evolution allow an improved analytical understanding of the long-term implications of changes to the environment induced by population density and their impact on species interactions and diversity. Simple models that are strong in the analysis of potentially universal information processing, like the discrete cellular automata family that includes Conway’s Game of Life, are weak in evolutionary robustness and genetic realism, and more biological models do not yet possess a coherent framework for analysing the interplay of genetic and spatial information. Questions of the origin and robustness of biological complexity involving interactions between species necessarily involves spatial ecological in addition to genetic information. While there is an accepted hierarchy of increasingly complex models for the genetic component of biological information, the interplay of genetic information with spatial information, which is vital for understanding the evolution of species diversity and complexity, is not so seamlessly resolved. Whereas separately tools like coalescence theory have been used successfully to understand genealogies and extrapolate from current genetic information backwards in time, and stochastic spatial information analysis tools like epsilon machines have been employed to capture the information processing in complex spatial systems, there is currently not yet a unified framework for studying the interplay of spatial and genetic information effects. Here we show that such a unified framework is possible and useful in understanding complex spatial evolutionary phenomena including the maintenance of diversity. To exemplify this development we introduce a new family of simple models open to computational analysis, which include the Game of Life and various well studied evolutionary and ecological models as special cases. We show that the analysis of the genealogies of spatial patterns represents an achievable and vital complement to genetic sequence genealogies in understanding the evolution of such systems. It is expected that this new approach to modelling will pay dividends in the analysis of big data in both local and global populations and be applicable to a broad range of increasingly critical societal problems involving sustainability and species diversity.

**How robust ecosystems maintaining diversity emerge in spatial evolutionary dynamics.**

(258 words)

Simple models of the diversification of information in spatial evolution can improve our understanding of environmental impact on species interactions and diversity. Simple models that are strong in the analysis of information processing, like Conway’s Game of Life, are weak in evolutionary robustness and genetic realism, and models in evolutionary ecology miss the computational interplay of genetic and spatial information. The hierarchy of increasingly complex models and tools for the genetic component of biological information is not matched for spatial information, which is vital for understanding the evolution of species diversity and complexity. Whereas separately tools like coalescence theory have been used successfully to understand genealogies and extrapolate from current genetic information backwards in time, there is currently not yet a unified framework for studying the interplay of spatial and genetic information evolution. Here we show that such a unified framework is possible and useful in understanding complex spatial evolutionary phenomena including the maintenance of diversity. To exemplify this development, we introduce a new family of simple models open to computational analysis, which include the Game of Life and various well studied evolutionary and ecological models as special cases. We show that the analysis of the genealogies of spatial patterns represents an achievable and vital complement to genetic sequence genealogies in understanding the evolution of such systems. It is expected that this new approach to modelling will pay dividends in the analysis of big data in both local and global populations and be applicable to a broad range of increasingly critical societal problems involving sustainability and species diversity.

**How robust ecosystems maintaining diversity emerge in spatial evolutionary dynamics.**

(151 words)

Simple models of the diversification of information in spatial evolution can improve our understanding of environmental impact on species interactions and diversity. Simple models that are strong in the analysis of information processing, like Conway’s Game of Life, are weak in evolutionary robustness and genetic realism. The hierarchy of increasingly complex models and tools for genetic information is not matched for spatial information. Whereas tools like coalescence theory enlighten our understanding of genealogies, there is currently not yet a unified framework for studying the interplay of spatial and genetic information evolution. Here we show that such a framework is useful in understanding complex evolution, introducing a new family of simple computational models, which include the Game of Life and known evolutionary and ecological models as special cases. We show that the analysis of the genealogies of spatial patterns represents an achievable and vital complement to genetic sequence genealogies in understanding evolution.