Chapter 7

Structural and Dynamical Heterogeneity in Ecological Networks

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ABSTRACT

Diversity is a key feature of biological systems. In complex ecological systems, which are composed of several components and multiple parallel interactions among them, it is increasingly needed to precisely understand structural and dynamical variability among components. This variability is the basis of adaptability and evolvability in nature, as well as adaptive management-based applications. The authors discuss how to quantify and characterize the structural and dynamical variability in ecological networks. They perform network analysis in order to quantify structure and we provide a process algebra-based stochastic simulation model and sensitivity analysis for better understanding the dynamics of the studied ecological system. They use a large, data-rich, real ecological network for illustration.

INTRODUCTION

Diversity is one of the few concepts of biology that are familiar also to politicians and laymen. There is a common belief that diversity is "good" and should be maintained at several levels of biological organization, from genes to ecosystems. In order to decide whether it is true, we need to understand diversity much better, and not only at a descriptive (mostly structural) level but also, and much more, from a functional and more dynamical point of view.

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Since the diversity of biological objects is valuable primarily in the context of their populations, it may be useful to ask these questions in a systems biology context. The hierarchical organization of life means that most biological systems are composed of subsystems and compose supersystems, for example populations are composed of individuals and compose an ecological community. Interactions are of key importance in connecting lower-level systems and, thus, interactions themselves determine the subsystem-system or system-supersystem relationships (Allen & Starr, 1982). Without relevant interactions, lower-level components remain only a set of components, instead of being subsystems forming a system. The explicit study of hierarchy is a key issue but frequently missed in modern systems biology, that normally focuses on the huge amount of components without considering the relationship with the lower and higher levels. On the contrary, classical systems biology was unable to analyze huge amounts of components but was more sensitive to hierarchy.

If we aim to understand the diversity of some biological components from this systems view, we cannot neglect the composition and topology of the system they build up. Heterogeneity of positions in anisotropic networks is a key to understand diverse roles of components. If we aim to understand a human social group, we need some information on the number of individuals, on their sex ratio and age distribution, but the key information is whether they form a social system (e.g. a classroom) or they are only a set of people (e.g. travelling on the same bus). The same applies for social animals, where the paradigm of group size is recently being exchanged with the paradigm of the social network. As we know more about the global topology of animal social networks as well as we identify their key players based on local network indices, we begin to understand the relevance and limits of group size and network-independent attributes of individuals. The same question here is not only how many species we have and what are their abundance distributions, but also how are they connected to each other and how does their network position determine what roles they play in the ecological community. Here, the big challenge is to translate taxonomical knowledge (identities) to ecological language (roles).

In this chapter, we present a real network to illustrate how structural and dynamical heterogeneity can be studied. We discuss some novel approaches to systems ecology and systems-based conservation, based on stochastic dynamical modeling of ecosystems.

A SYSTEMS VIEW ON VARIABILITY: COMPUTATIONAL CHALLENGES

Systems Biology and Systems Ecology

Both real databases and computational power are growing continuously in biological research. Still, what we call systems biology today is mostly based on collecting huge amounts of information without a hierarchical perspective and coherent integration. However, real integration needs also qualitative, not only quantitative changes in dynamical systems models. A major qualitative change could be the parallel analysis of multiple hierarchical organizational levels (e.g. genes in individuals, individuals in ecosystems). In order to improve the predictive power of biological models, novel computational tools would be important. Apart from managing huge databases and visualising complex systems, new types of algorithms could link community and systems ecology by providing tools for process-based approaches. The solution to these problems will become computable by increasing computer power and introducing novel conceptual and computational tools (Levin et al., 1997; Pascual, 2005; Green et al., 2005; Seth, 2007).

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