



Quantitative analysis of the local structure of food webs

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Abstract

We analyze the local structure of model and empirical food webs through the statistics of these webs' subgraphs. We study analytically and numerically the number of appearances of each subgraph for a simple model of food web topology, the so-called generalized cascade model, and compare them with 17 empirical community food webs from a variety of environments, including aquatic, terrestrial, and microbial ecosystems. We obtain analytical expressions for the probability of appearances of each subgraph in the model, and also the randomizations of the model that preserve species numbers of prey and number of predators; these distributions allow us to quantify which subgraphs are over- or under-represented in both the model and the empirical food webs. We find agreement between the model predictions and the empirical results. These results indicate that simple models such as the generalized cascade can provide a good description not only of the global topology of food webs, as recently shown, but also of its local structure.

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1. Introduction

Food web theory seeks to understand the functioning of ecosystems by studying the trophic relations among its species (Cohen et al., 1990). To this end, in the last years great effort has been devoted to the compilation of comprehensive empirical food webs just for instance (Dunne et al., 2002). The statistical treatment of these data has revealed several regularities among food webs belonging to quite diverse habitats, such as deserts, lakes and islands, suggesting that some robust mechanism common to most ecosystems is at work (Williams and Martinez, 2000; Camacho et al., 2002b; Swaffler et al., 2005).

Several models have been proposed to describe the structure of food webs and clarify the origin of these patterns. They differ in the mechanisms underlying them and in the level of description. Some of them describe the dynamics of the network according to evolutionary rules

(Amaral and May, 1999; Rensborg et al., 2005; Rensborg et al., 2006a,b), population biology (Yodanis, 1981), or mixtures of both (Caldwell et al., 1998; Lässig et al., 2001). Other so-called static models do not contain the explicit dynamics of the ecosystem, but provide some mechanistic rules aiming to generate food webs with a statistically similar structure to the empirical ones (Cohen and Newton, 1985; Williams and Martinez, 2000; Carré et al., 2004; Swaffler et al., 2005).

Two of these static models, the niche model (Williams and Martinez, 2000) and the neutral-hierarchy model (Carré et al., 2004), yield good predictions for a wide number of statistical measures of empirical food webs. Indeed, it has been demonstrated analytically that the two models yield the same distributions for the number of prey and number of predators (Swaffler et al., 2005), which imply, for example, the same fractions of top and basal species or the standard deviations of generality and vulnerability, just as observed numerically (Carré et al., 2004). Remarkably, these distributions are in good agreement with most of the highest quality empirical food webs in the literature, providing a general picture of food web topology (Camacho et al., 2002a,b; Swaffler et al., 2005).

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