

Shape of Ecological Networks

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We study the statistics of ecosystems with a variable number of coevolving species. The species interact in two ways: by prey-predator relationships and by direct competition with similar kinds. The interaction coefficients change slowly through successful adaptations and speciations. They are treated as quenched random variables. These interactions determine long-term topological features of the species network, which are found to agree with those of biological systems.

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Population dynamics is a classical subject of evolutionary biology. The mutually dependent dynamics of two or more populations or species is often described by coupled differential equations governing the relative change of the population sizes $N_i(t)$,

$$\frac{1}{N_i} \frac{dN_i}{dt} = \sum_{j=1}^s g_{ij} N_j + h_i \quad (i = 1, \dots, s). \quad (1)$$

The interaction coefficients g_{ij} can represent a prey-predator relationship ($g_{ij} < 0$, $g_{ji} > 0$), direct competition ($g_{ij} < 0$, $g_{ji} < 0$), or mutualism ($g_{ij} > 0$, $g_{ji} > 0$) between species i and j , and the terms h_i denote intrinsic production or decay rates. These so-called *Lotka-Volterra* equations, as well as many generalizations thereof, have been used to model coexistence, invasions, and adaptive change of populations. Of great importance is their conceptual connection to mathematical *game theory* [1]. A set of populations N_1, \dots, N_s represents a mixed strategy. For given interactions g_{ij} , an optimal strategy—called Nash equilibrium—can often be realized as a stable fixed point N_1^*, \dots, N_s^* of an associated Lotka-Volterra dynamics. This explains how strategic optimization is reached in biological systems through reproductive success, with no need for rational thinking.

These equilibria determine the species' fate. For a given set of equations (1), a species is viable if $N_i^* > 0$ and becomes extinct if $N_i^* = 0$. Even the viable species is not perennial, however. Successful adaptations, migrations, and speciations (the splittings of a single species into a pair) eventually change the number of players as well as the rules of the game, i.e., the couplings g_{ij} . On large time scales, the observed dynamical patterns can be quite intermittent. Correlated extinctions and speciations alternate with periods of relative stasis, leading to large fluctuations in the number of species [2]. Little is known on how this long-term behavior is connected to the underlying interactions between species in (1).

The best studied natural ecosystems are *food webs*, i.e., communities of animal species in a closed environment where food chains can be observed. Figure 1(a) shows the graph of such a network, each arrow representing

a prey-predator relationship. Despite large variations in size and environmental conditions, large ecosystems share a few important topological characteristics: (i) Every species lives at a certain *trophic level*. The level number can be defined as the minimum, the maximum, or a suitable average length of its relevant “downward” food chains; the differences between these definitions turn out not to be significant. Species at level one feed from external resources. (ii) The number of trophic levels is small, typically between three and seven. (iii) Most species have a small number of relevant prey species (typically around three), mainly from the next lower level. (iv) The number of species at level l increases with l for lower values of l and decreases again sharply for higher l [3,5]; see Fig. 1(b). Networks of coevolving species thus have a characteristic *shape*.

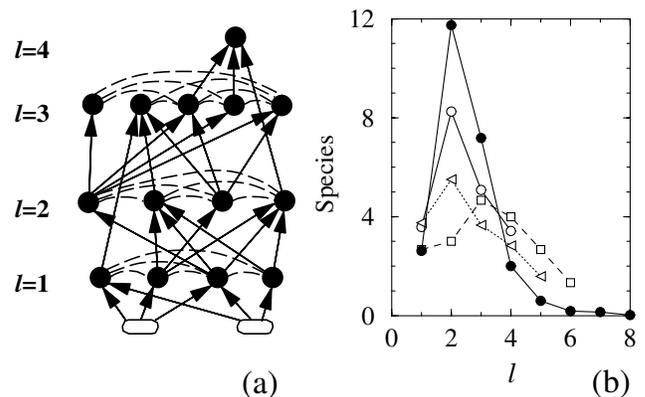


FIG. 1. (a) The Pamlico estuary food web in North Carolina, consisting of 14 species (filled circles) at four trophic levels. *Detritus*, *dinoflagellates*, and *diatoms* are at the bottom level ($l = 1$) and feed from external resources (empty symbols). There is a single trophic group at the highest level ($l = 4$), formed by the predatory fishes *Roccus* and *Cynoscion*. Arrows point from prey to predator; dashed lines connect species pairs with a nonzero link overlap (see text). Data from [3]; the level is defined here by the longest relevant food chain. (b) Average species numbers per level for a set of natural ecosystems, taken from Ref. [3] (empty symbols) and [4] (filled circles). This last case corresponds to an average over 61 food webs, most of which are empty at high levels.

This remarkable structure calls for a theoretical explanation. The classical work on Lotka-Volterra equations has established stability criteria for networks with random interactions g_{ij} [6]. In a real ecosystem, however, the interactions are not random, but are themselves subject to selection. Recently, Lotka-Volterra systems coupled to speciation [7] and immigration [8] dynamics have been studied by numerical simulations, and food web structures have indeed been found. Another class of models focuses directly on the dynamics of extinctions and speciations. These models have no explicit population dynamics and mostly random topology, with the important exception of Ref. [9].

In this Letter, we present elements of a statistical theory for large ecosystems, using concepts and methods of theoretical physics. We discuss the population dynamics with the *minimal* species interactions consistent with the observed complexity of ecosystems. These interactions are *prey-predator relationships*, which establish a flux of biomass between species, and *direct competition* between similar species, which leads to their mutual exclusion from ecological niches. The interaction coefficients g_{ij} in (1) are modeled as random variables that change through successful mutations. We focus on the (often realistic) case that these mutations are sufficiently rare so that the populations can reach stable equilibria in between. In the language of statistical physics, the species interactions are *quenched* random variables on the time scales of population dynamics. The statistics of such ecosystems is thus governed by a quenched distribution of Nash equilibria. This distribution in turn emerges from a long-term balance between adaptations, speciations, and extinctions. The topology of the resulting networks is found to be closely related to the underlying dynamics of coevolution. In the following, we concentrate on generic topological features amenable to an approximate analytical treatment; in particular, we derive the shape of ecosystems. A detailed analysis of structure and dynamics of these networks will be published elsewhere [10].

To describe generic features of ecological networks, we choose the simplest population dynamics containing predation and direct competition. The interaction matrix in (1) is decomposed accordingly, $g_{ij} = \gamma_{ij} - \beta_{ij}$. Predation is parametrized by the constants $\gamma_{ij} = \gamma_+$ if j is prey of i and $\gamma_{ij} = -\gamma_-$ if i is prey of j , with $0 < \gamma_+ < \gamma_-$. Competition takes place for nesting places, mating opportunities, and other resources not explicitly represented in the model. It is strongest between individuals of the same species, but also occurs between different species that interfere in each other's livelihood [11]. This interaction turns out to be a limiting factor for the coexistence of species in a common network [12]. We set $\beta_{ii} = 1$ [this normalization amounts to an appropriate choice of the time scale in (1)] and $\beta_{ij} = \beta \rho_{ij}$ for $i \neq j$, with $0 < \beta < 1$. The *link overlap* ρ_{ij} measures the degree of competition between the species. It can be defined as $\rho_{ij} \equiv c_{ij} / \sqrt{c_i c_j}$,

where c_i, c_j are the numbers of links with i, j as predator, and c_{ij} is the number of common links. (Species pairs with a nonzero link overlap are connected by dashed lines in Fig. 1.) Furthermore, all species are assigned a uniform decay rate $h_i = -\alpha$. The external resources are represented as a small number of extra "populations" N_i with $h_i = \gamma_+ R$ and predators only (i.e., $\gamma_{ij} \leq 0$ and $\beta_{ij} = 0$ for all j).

With these interactions, the fixed point populations given by (1) can be written in the form

$$N_i^* = P_i - Q_i + h_i, \quad (2)$$

where $P_i = \gamma_+ \sum_{j \in \pi(i)} N_j^* - \gamma_- \sum_{j \in \Pi(i)} N_j^*$ is the *productivity* of species i from predation [with $\pi(i)$ the set of its prey and $\Pi(i)$ the set of its predators] and $Q_i = \beta \sum_{j \neq i} \rho_{ij} N_j^*$ is its competition load. Furthermore, we require a minimum population size $N_c \ll R$ for viable species, and count all species with $N_i^* < N_c$ as extinct. Indeed, natural populations are known to be unstable under short-term environmental fluctuations or adverse mutations if they are too small or too dilute [13].

Of course, an ecosystem is not determined by its population dynamics alone but also by the long-term processes of successful mutations, in particular, speciations [7,14]. In this model, a mutation is represented as a stochastic change of predation links that is consistent with existing food chains. It turns out that details of this process are not relevant for our present purpose of deriving global network characteristics. It is sufficient to assume that speciations and adaptations maintain a broad distribution of productivities P_i , and hence, of population sizes N_i^* (in a sense made precise below). This is well supported by field observations and by our numerics [10,15]. An increase in the number of species reduces the average productivity and increases the average competition load. Hence, such an ecosystem admits only a certain number of viable species, whose productivities satisfy $P_i > Q_i + \alpha + N_c$. The number of these *ecological niches* depends on the interaction parameters $\beta, \gamma_+, \gamma_-$, and on the dimensionless ratios $R/N_c, \alpha/N_c$. Once the niches are filled, ongoing speciations and the subsequent adaptations reshuffle the productivities and the population numbers N_i^* of all the species, forcing the least viable ones into extinction. On large time scales, this is a stationary stochastic process. The relative success of an individual species keeps changing as a result of its own adaptations and those of the other species, resulting in a continuous threat of extinction called the *red queen* effect [16]. The shape of these mature networks is determined essentially by the distribution of ecological niches. To see this, consider the first two cases of simple networks with fixed topology.

(1) A *single food chain* is a community of L species on L trophic levels. The species at level one feeds from an external resource, the species at level l from that at level $l-1$ ($l = 2, 3, \dots, L$). The productivities of this chain are given by the equations

$$P_l = \gamma_+ N_{l-1}^* - \gamma_- N_{l+1}^* \quad (l = 1, \dots, L), \quad (3)$$

and $P_0 = -\gamma_1 N_1^*$, with the boundary condition $N_{L+1}^* = 0$. They determine directly the population numbers $N_l^* = P_l - \alpha$ since all competition loads vanish. The entire chain is viable if $P_l > P_c$ for all species l , with the minimum productivity

$$P_c = \alpha + N_c. \quad (4)$$

Equation (3) can be solved exactly by recursion starting from the top level $l = L$. For the biologically important case of small γ_+ , we find that the maximum value of L compatible with (3) is

$$L = \frac{-1}{\log \gamma_+} \log \left(\frac{R}{\text{const} \times \alpha + N_c} \right) - 1 + O(\gamma_+) \quad (5)$$

by applying the condition (4) at the top level.

The parameters α and N_c are seen to be equivalent viability cutoffs for the chain since they reduce primarily the top population N_L^* . More generally, the population numbers N_l^* are found to be rapidly decreasing with increasing l for all relevant parameter values. Hence, as observed in nature, viable chains are always short [17].

(2) A *single trophic level* is a group of S species that may have a significant overlap in their predation links and a resulting competition load. First we consider the productivities P_i as fixed by the interactions with other trophic levels and concentrate on the effects of the direct competition terms Q_i . In a “mean field” approximation, we replace the individual link overlaps by an expectation value \bar{p} depending on the predation clusters. In the simplest case of random predation, Eq. (2) then determines the fixed point populations

$$N_i^* = \frac{P_i - \beta \bar{p} S \bar{N} - \alpha}{1 - \beta \bar{p}}, \quad (6)$$

with the average $\bar{N} \equiv S^{-1} \sum_{i=1}^S N_i^*$ given by

$$\bar{N} = \frac{\bar{P} - \alpha}{1 + \beta \bar{p} (S - 1)}. \quad (7)$$

The viability of all species ($N_i^* > N_c$) again sets a minimum productivity

$$P_c = \alpha + (1 - \beta \bar{p}) N_c + \beta \bar{p} S \bar{N}. \quad (8)$$

We now use the assumption that the productivities P_i are drawn from a broad probability distribution given by $\Phi(q) \equiv \text{Prob}(P_i/\bar{P} < q)$. [The qualitative results do not depend strongly on the form of $\Phi(q)$; here we use a simple approximation [18].] The species community becomes unstable if the least viable species has a productivity below P_c . The number of species in a mature trophic level can therefore be estimated from the relation $S\Phi(P_c/\bar{P}) = O(1)$. Equation (8) then becomes an implicit relation for S as a function of \bar{P}/N_c , α/N_c , and the average pairwise competition load $\beta \bar{p}$. Consider, for example, a trophic level with random predation from a set of S' prey species from the levels below. Using a simple approximation for the average link overlap $\bar{p}(S, S')$ [19], it

can be shown that the solution of Eq. (8) always satisfies $S \leq \max[a(\beta)S'/\bar{c}, 1]$, where $a(\beta) \geq 1$ is a monotonically decreasing function of α and \bar{c} is the average number of prey species per predator species. That is, competition determines the number of ecological niches in a trophic level as a function of the prey diversity and the competition strength β . For sufficiently large β , only nonoverlapping species can coexist, i.e., $S = \max(S'/\bar{c}, 1)$. This result generalizes the well-known theorem of competitive exclusion [20], which states the condition for coexistence of two competing species. Note that this limiting effect on the number of species exists independently of the population numbers. It is indeed crucial for the buildup of high population numbers at the lower trophic levels. For example, a trophic level feeding from resources of size $R \gg \alpha, N_c$ acquires an extensive population number per species, $\bar{N} \sim R/S$ with S asymptotically independent of R . Without competitive exclusion ($\beta = 0$), speciations would further increase S and eventually lead to an extensive number of marginally viable species, $S \sim R/\bar{N}$ with \bar{N} of order N_c . Such a level could not support sizable predation from above.

We now turn to a full ecological network with L trophic levels. In the mean field approximation, we treat all species at the same level on an equal footing and derive self-consistent equations for the level averages of population and species number, \bar{N}_l and S_l ($l = 1, \dots, L$). The average productivities \bar{P}_l satisfy the recursion relations

$$\bar{P}_l = \gamma_+ \bar{c} \bar{N}_{l-1} - \gamma_- \bar{c} (S_{l+1}/S_l) \bar{N}_{l+1}, \quad (9)$$

where we assume that the species at every level predate randomly on the species at the next lower level. The average number \bar{c} of predation links per predator is taken to be independent of l ; this is indeed suggested by field data. The average number of predators per prey is then simply $\bar{c} S_{l+1}/S_l$. The productivity \bar{P}_l is linked to \bar{N}_l and S_l as in (7), using for $\bar{p}(S_l, S_{l-1})$ the same approximation as above [19]. Hence, the relations (9) determine the population numbers given the species numbers. The latter are again limited by the stability criteria $S_l \Phi(P_{c,l}/\bar{P}_l) = O(1)$ with the minimum productivities $P_{c,l}$ given as in (8); these relations determine the S_l given the \bar{N}_l . The coupled set of equations can be solved iteratively. Finally, the number of levels L follows from the condition $\bar{N}_L \approx N_c$, which is equivalent to $S_L \approx 1$.

Over a wide range of relevant parameters, these networks have the characteristic shape shown in the example of Fig. 2: The species numbers S_l increase with l at low levels due to the increasing prey diversity, which opens up more and more niches. They reach a maximum at an intermediate level and decrease again at higher levels, because more and more species have population numbers too low to support further predation. Hence, these two regimes reflect the two kinds of species interactions. The population numbers show an approximately exponential decrease in both regimes, just as for a single vertical

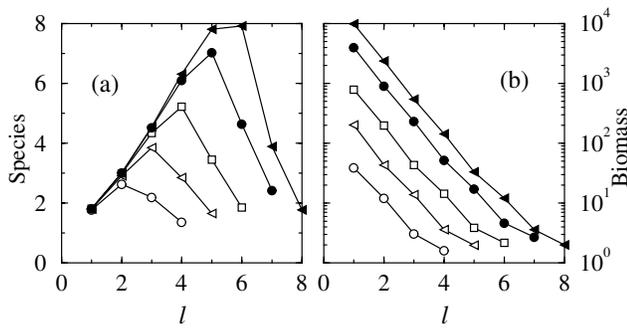


FIG. 2. The shape of ecosystems. (a) The species numbers S_l ($1 \leq l \leq L$) for networks with L trophic levels. Parameters are $\bar{c} = 3$, $\gamma_+ = 0.3$, $\gamma_- = 2.0$, $\beta = 0.2$, $q_0 = 0.35$ (see [18]), $\alpha/N_c = 1$, and $R/N_c = 2 \times 10^3, 10^4, 4 \times 10^4, 2 \times 10^5$, and 5×10^5 for the cases $L = 4, 5, 6, 7$, and 8 , respectively. (b) The average population numbers \bar{N}_l for the same cases.

chain. Hence, L is always small, in agreement with observations and with the results of [7,8]. The functional form of the patterns S_l, \bar{N}_l can be described by various analytical approximations.

Species networks are thus quite far from randomly connected. Their topological shape is dynamically generated by the coupled evolution of populations and the slower adaptative changes. The ubiquity of this shape suggests that predation and competition of similar species are the fundamental interactions governing the long-term coevolution of large ecosystems. They are remarkably simple. Predation is the basic transport of energy in the system; competition forces the species into states with little overlap. In physics, mutual avoidance is a well-known property of fermions. Competitive exclusion may thus be regarded as the Pauli principle of coevolution: It generates the complexity of species networks just as its quantum-mechanical counterpart does for atoms and molecules.

We have discussed here the *global* shape of these networks. It remains a challenging task to explore the connection between dynamics and topology *locally*, that is, at the level of individual species and their genealogies.

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 [19] For $S \leq \max(S'/\bar{c}, 1)$, a configuration with zero overlap exists. For larger values of S , we assume random predation. This gives $\bar{\rho}(S, S') = 0$ if $S \leq \max(S'/\bar{c}, 1)$ and $\bar{\rho}(S, S') = \min(\bar{c}/S', 1)$ if $S > \max(S'/\bar{c}, 1)$. Other approximations of the predation clusters are possible.
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