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A MARKOV CONTINGENCY-TABLE MODEL FOR REPLICATED LOTKA-VOLTERRA SYSTEMS NEAR EQUILIBRIUM*

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1. INTRODUCTION

This paper proposes a translation of the deterministic Lotka-Volterra equations for the interaction of populations of two species in a single environment into a formally equivalent Markovian model for the interaction of populations of two species in an ensemble of similar environments. Unlike several discussions of the Lotka-Volterra equations, this paper explores the evolution of such an ensemble of interacting populations when some of the parameters of interaction are considered as subject to natural selection. The purpose of this theoretical development is eventually to illuminate interactions of infections in parasitized, particularly human, hosts, and the following exposition will speak of individuals (hosts) with various kinds of infections. But interactions of any species distributed in discrete, or patchy, and approximately similar environments could also be studied in the same way (Section 6).

The general motivation for this undertaking is in part empirical, in part theoretical. The empirical motivation is that studying even moderately complex associations of species, when it is possible, is difficult and costly. Evaluating experimental interventions in ecology requires knowledge of how a system would have behaved in the absence of intervention and hence, for want of adequate theory, requires replication of the original system. Small laboratory systems, though replicable with effort, may not always illuminate situations outside laboratories adequately (Smith 1952).

Moulder (1969) has ingeniously combined the advantages of a natural system with small size and replicability by studying intracellular parasitism, using uniform populations of single susceptible cells as hosts. The problem of generalizing to the impact of a parasitemia on the whole organism remains, however, as Moulder points out.

Ecological investigations of the interspecific interactions within ensembles of human beings exposed to infection by a variety of species offer one convenient and important solution to the problems of size, naturalness, and replication, because many such systems have been extensively studied.

A theoretical motivation for the following approach is that, when it has

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been difficult to understand the behavior of unique systems, it has sometimes been easier to understand ensembles of such systems. Kerner (1961) and Leigh (1965) have attempted to extend the machinery of statistical mechanics to ecological theory. The following, though using analytical tools more tailored to the systems at hand, is another attempt in the same spirit.

The absence of interaction between the presence of one species of occupant or parasite and the presence of a second in a population of replicated quadrats, or units of habitat, or parasitized individuals is defined here by saying that, if α_1 and α_2 are the respective probabilities of finding species 1 and 2 present in an individual host, then the probabilities P_0 of an individual having no species present, P_1 of an individual having only species 1 present, P_2 of an individual having only species 2 present, and P_3 of an individual having both species present are given by

$$\begin{aligned} P_0 &= (1-\alpha_1)(1-\alpha_2), \\ P_1 &= \alpha_1(1-\alpha_2), \\ P_2 &= (1-\alpha_1)\alpha_2, \\ P_3 &= \alpha_1\alpha_2. \end{aligned} \tag{1}$$

Estimates of the probabilities P_i are obtained by recording observations in the form of a 2×2 contingency table (fig. 1). Pielou (1969, p. 159–168) has reviewed the usual statistical tools for deciding whether the sample estimates of P_i are consistent with the model (1) of no interaction within the population of individuals, or with a model of no interaction within just the sample of individuals.

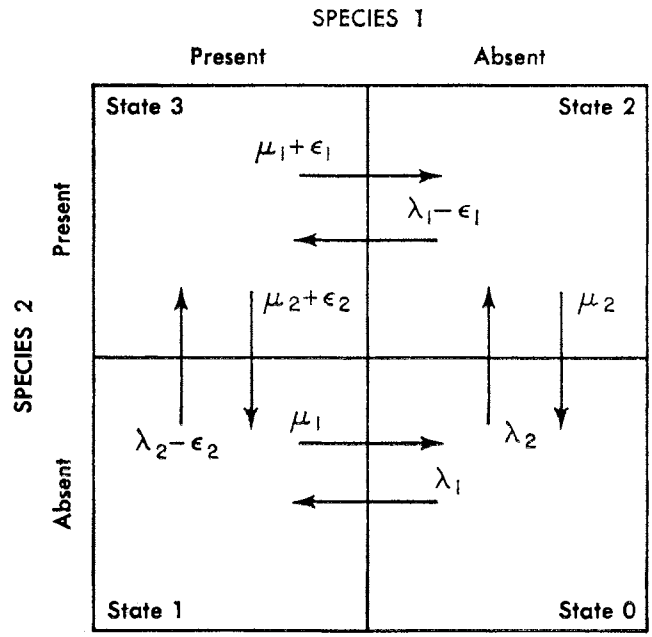

FIG. 1.—Schema of the Markov-chain model for interaction between two species.

Section 2 of this paper will present a discrete-time, finite-state Markov-chain model (in the manner of Coleman 1964) to aid the measurement and interpretation of the interactions such contingency tables may reveal, and will derive a continuous-time, finite-state Markov-chain equivalent to it. Section 3 will show that under a certain interpretation (in the manner of White 1970) of the variables in the Lotka-Volterra model, this continuous-time Markov chain is formally identical to the Lotka-Volterra model near its equilibrium point in which both species are present. The parameters of the Lotka-Volterra model will be calculated from those of the Markov chain. Section 4 will review the statistical procedures for estimating the parameters in the discrete-time Markov model and will present tests required to reject some of the assumptions of the Markov model. Section 5 will explore the evolution of the equilibrium of the Markov chain when the parameters measuring interspecific interaction are allowed to change in response to a representation of natural selection. Finally, Section 6 will evaluate this new Markov-chain interpretation of the Lotka-Volterra model and the techniques used to make the interpretation.

2. A MARKOV-CHAIN MODEL FOR INTERSPECIFIC INTERACTION

The model to be presented, a Markov chain in discrete time and a derived Markov chain in continuous time, is a special case of the class of models discussed and applied in a different context by Coleman (1964, p. 103–188).

For convenience, I will speak of individuals getting infected with a species or losing that infection and as having single or mixed infections. Readers interested in islands are requested to translate into islands getting colonized by or suffering the extinction of a species and as having single- or mixed-species faunas or floras.

Suppose two species are available to infect individuals. Consistent with the notation in (1), an individual is said to be in state 0 if he is infected with neither, in state 1 if he is infected with species 1 but not species 2, in state 2 if he is infected with species 2 but not species 1, and in state 3 if he is infected with both species. Suppose that transitions among these states occur as diagramed in figure 1. The labels attached to the arrows may be interpreted either as transition probabilities, when the changes of state occur in discrete time, or in the limit as transition rates when the changes occur in continuous time.

In discrete time, figure 1 means that between time t and some later time $t + \tau$, where τ is the unit of time, the row vector $\boldsymbol{P}(t) = [P_0(t), P_1(t), P_2(t), P_3(t)]$, which gives the probability distribution of individuals over states, will change by $\boldsymbol{P}(t + \tau) = \boldsymbol{P}(t) \cdot \boldsymbol{T}$, where the transition matrix $\boldsymbol{T}$ is

$$\boldsymbol{T} = \begin{pmatrix} 1 - \lambda_1 - \lambda_2 & \lambda_1 & \lambda_2 & 0 \\ \mu_1 & 1 - \mu_1 - \lambda_2 + \varepsilon_2 & 0 & \lambda_2 - \varepsilon_2 \\ \mu_2 & 0 & 1 - \mu_2 - \lambda_1 + \varepsilon_1 & \lambda_1 - \varepsilon_1 \\ 0 & \mu_2 + \varepsilon_2 & \mu_1 + \varepsilon_1 & 1 - \mu_1 - \varepsilon_1 - \mu_2 - \varepsilon_2 \end{pmatrix} \tag{2}$$

and the parameter values are restricted by the requirement that all elements T_{ij} in the matrix fall in [0, 1].

As a model, such a Markov chain assumes that there is no interaction among individuals making transitions among these states, so that one may speak indifferently of an individual's probability of being in a state or of the probability distribution of individuals among states. Hence, the model approximates the role that the density of other infected individuals may play in the incidence of infection by a constant. The model also assumes that an individual's probabilities of transition from a given state are independent of what states he occupied previously. Such a model neglects immunity acquired from previous infection. Hence, in order for it to be relevant to actual immunogenic parasitic diseases, it may be necessary to define the states of the contingency table (fig. 1) in terms of the presence or absence of species-specific antibodies in sera rather than in terms of the presence or absence of the parasites themselves. The two assumptions just described may not be so bad when, for example, the individuals are not human beings but separate lakes and the inhabitants are Ectoprocta (Bushnell 1966).

The particular model (2) embodies two additional strong assumptions. First, because of the zero minor diagonal, it assumes that in the period of time τ, there can be no direct diagonal transitions (between states 0 and 3 or 1 and 2) in figure 1; that is, only one infection at a time can be lost or gained. Second, it assumes that the decrease in the probability of infection with species 1 when species 2 is present compared with when species 2 is absent is equal to the increase in the probability of loss of infection with species 1 when species 2 is present compared with when species 2 is absent, and similarly when 1 and 2 are reversed. (A less confusing mathematical statement of this assumption appears as [15] below.)

That the model (2) is a strong model embodying a very restrictive set of assumptions may be seen by comparing the small number, six, of arbitrary parameters it contains relative to the possible number, 12, of different parameters such a four-state Markov chain could assume.

If $P(t)$ is subtracted from both sides of the identity $P(t + \tau) = P(t) \cdot T$ which precedes (2) and if the unit of time τ is allowed to approach zero, the continuous rates of change P_i' in the state probabilities are obtained as a function of the infinitesimal matrix of transition rates of the process (Karlin 1968, p. 218–225). The resulting set of equations for P_i' shares two important properties with the epidemic models, which are also first-order differential equations whose variables are fractions of a population, proposed by Muench (1959): the equations are linear in the state probabilities (or in the categories of the population); and the models are "conservative" (Karlin 1968, p. 223) in that, roughly speaking, the probability gains (or losses) of each state are always exactly balanced by the probability losses (or gains) of the remaining states. When P_0 has been eliminated by noticing that $P_0 = 1 - P_1 - P_2 - P_3$, the continuous-time Markov chain becomes

$$P_1' = \lambda_1 - P_1(\mu_1 + \lambda_1 + \lambda_2 - \varepsilon_2) - P_2\lambda_1 + P_3(\mu_2 + \varepsilon_2 - \lambda_1),$$

$$P_2' = \lambda_2 - P_1\lambda_2 - P_2(\mu_2 + \lambda_2 + \lambda_1 - \varepsilon_1) + P_3(\mu_1 + \varepsilon_1 - \lambda_2), \quad (3)$$
$$P_3' = P_1(\lambda_2 - \varepsilon_2) + P_2(\lambda_1 - \varepsilon_1) - P_3(\mu_1 + \varepsilon_1 + \mu_2 + \varepsilon_2).$$

The proportion of individuals who are infected with species i, whether or not the other species is present, is $Y_i = P_i + P_3$, $i = 1, 2$. From (3), the rates of change Y_i' in the proportions Y_i infected with each species are

$$Y_1' = \lambda_1\left[1 - \left(1 + \frac{\mu_1}{\lambda_1}\right) Y_1 - \left(\frac{\varepsilon_1}{\lambda_1}\right) Y_2\right],$$
$$Y_2' = \lambda_2\left[1 - \left(\frac{\varepsilon_2}{\lambda_2}\right) Y_1 - \left(1 + \frac{\mu_2}{\lambda_2}\right) Y_2\right]. \quad (4)$$

At equilibrium, the rates of change on the left sides of (3) and (4) are zero, and the equilibrial values of the P_i and Y_i may be found by Cramer's rule. In particular,

$$P_3^* = \frac{\lambda_1\mu_2(\lambda_2 - \varepsilon_2) + \lambda_2\mu_1(\lambda_1 - \varepsilon_1) + (\lambda_1 + \lambda_2)(\lambda_1 - \varepsilon_1)(\lambda_2 - \varepsilon_2)}{(\mu_1 + \mu_2 + \lambda_1 + \lambda_2)[(\mu_1 + \lambda_1)(\mu_2 + \lambda_2) - \varepsilon_1\varepsilon_2]} \quad (5)$$

and

$$Y_1^* = \frac{\lambda_1(\lambda_2 + \mu_2) - \varepsilon_1\lambda_2}{(\lambda_1 + \mu_1)(\lambda_2 + \mu_2) - \varepsilon_1\varepsilon_2},$$
$$Y_2^* = \frac{\lambda_2(\lambda_1 + \mu_1) - \varepsilon_2\lambda_1}{(\lambda_1 + \mu_1)(\lambda_2 + \mu_2) - \varepsilon_1\varepsilon_2}. \quad (6)$$

The equilibrial values P_0^*, P_1^*, and P_2^* may be found from (5) and (6).

In the language of this model, the hypothesis of no interaction between species 1 and 2 means that the rates of infection or loss of infection with one species are not affected by the presence or absence of the other and hence that $\varepsilon_1 = \varepsilon_2 = 0$. When $\varepsilon_1 = \varepsilon_2 = 0$,

$$P_3^* = \frac{\lambda_1\lambda_2}{(\mu_1 + \lambda_1)(\mu_2 + \lambda_2)} = Y_1^*Y_2^*. \quad (7)$$

If Y_i^*, the equilibrial proportion infected with species i, is identified with α_i, an individual's probability of infection with species i, then the model of no interaction (1) is reproduced exactly. The deviation between (5) and (7) is one measure of the strength of the interaction.

3. LOTKA-VOLTERRA SYSTEMS NEAR EQUILIBRIUM

The classical Lotka-Volterra equations for the competition of two species in a limited environment (Keyfitz 1968, p. 288–291) are

$$X_1' = r_1X_1(1 - aX_1 - \alpha X_2),$$
$$X_2' = r_2X_2(1 - \beta X_1 - bX_2), \quad (8)$$

where X_i (assumed nonnegative) is a measure of the abundance, and X_i' is a measure of the rate of change in abundance, of species i, $i = 1, 2$, and all parameters are assumed positive.

The system (8) has four stationary points where $X_i' = 0$: when $X_1 = X_2 = 0$; when $X_1 = 0$, $X_2 = 1/b$; when $X_1 = 1/a$, $X_2 = 0$; and when

$$X_1^* = \frac{b - \alpha}{ab - \alpha\beta},$$
$$X_2^* = \frac{a - \beta}{ab - \alpha\beta}. \tag{9}$$

This last stationary point, the only one of interest henceforth, is a stable equilibrium if

$$ab > \alpha\beta. \tag{10}$$

The stability of the system (8) at this stationary point (9) is completely determined by the stability of the linear approximation obtained from expanding the right side of (8) in a Taylor series about (9) and truncating all nonlinear terms.

The linearized approximation to (8) at the point (9) is

$$X_1' = (X_1 - X_1^*)(-ar_1X_1^*) + (X_2 - X_2^*)(-\alpha r_1X_1^*),$$
$$X_2' = (X_1 - X_1^*)(-\beta r_2X_2^*) + (X_2 - X_2^*)(-br_2X_2^*), \tag{11}$$

or

$$X_1' = \frac{r_1(b - \alpha)}{ab - \alpha\beta}(1 - aX_1 - \alpha X_2),$$
$$X_2' = \frac{r_2(a - \beta)}{ab - \alpha\beta}(1 - \beta X_1 - bX_2). \tag{12}$$

These equations (12) are formally identical to the equations (4) for the Markov chain under the identification:

$$\begin{aligned} X_i &= Y_i, i = 1, 2, \\ a &= 1 + \mu_1/\lambda_1, \\ b &= 1 + \mu_2/\lambda_2, \\ \alpha &= \varepsilon_1/\lambda_1, \\ \beta &= \varepsilon_2/\lambda_2, \\ r_i &= \lambda_i/X_i^*, i = 1, 2, \end{aligned} \tag{13}$$

where X_i^* are given by (9). Thus, if the abundance X_i of species i is taken as the proportion Y_i of all individuals who are infected with species i, then the behavior of a Lotka-Volterra competitive system in the vicinity of its stable point (9) is given exactly by the Markov-chain model of Section 2. The six parameters of the Lotka-Volterra system are uniquely specified by, and uniquely specify, those of the Markov model as in (13). If the param-

eters a, b, α, β, r_1, and r_2 are assumed positive when (8) describes competition, then ε_i, λ_i, and μ_i, $i = 1, 2$, must also be positive.

Under this identification of X_i with Y_i, the usual measure of abundance as the density of malarial parasites in the blood of an infected child or the number of birds of a species on an island is replaced with the number of individuals (children or islands) in which the species is present. The idea of replacing a continuously varying property of a single system with the proportion of replicated systems having an all-or-none attribute is due to White (1970), who proposes and carries out the technique in a different context.

The condition for stability (10) becomes, in the parameters of the Markov model,

$$(\lambda_1 + \mu_1)(\lambda_2 + \mu_2) > \varepsilon_1\varepsilon_2, \tag{14}$$

which is always satisfied because $\lambda_i \geqslant \varepsilon_i$ and $\mu_i > 0$ under (13). This is hardly surprising, since the Markov-chain model to which the linearized Lotka-Volterra system is equivalent has a single stationary point which is stable.

Let T_{ij} be the elements of the transition matrix T in (2), where rows and columns are indexed starting from zero. Under the assumption that the minor diagonal is zero (barring two changes in the state of infection at once, a reasonable assumption for the continuous-time Markov chain), it may be shown that the necessary conditions for (4) to be formally identical to (12) are

$$\begin{aligned} T_{01} - T_{23} &= T_{32} - T_{10} \quad (=\varepsilon_1), \\ T_{02} - T_{13} &= T_{31} - T_{20} \quad (=\varepsilon_2). \end{aligned} \tag{15}$$

4. ESTIMATION AND TESTING

The data in the four cells of figure 1 make possible the estimation of three independent proportions, such as P_0, P_1, and P_2, or Y_1, Y_2, and P_3. The data are obviously insufficient to estimate separately the six parameters of the Markov model, let alone to test the assumptions underlying it.

The necessary theory and techniques for estimating and testing the discrete-time and continuous-time Markov chains presented here appear compendiously in Billingsley (1961, p. 23–32, 45–51). The analysis of independence in a discrete-time Markov chain on a contingency table is even carried out explicitly (Billingsley 1961, p. 29–30). Coleman (1964, p. 177–188) also discusses the estimation of transition rates apparently unaware of Billingsley's work.

For the discrete-time model, the essential idea is to observe a sample of transitions among states from one time to the next. If N_{ij} is the number of transitions which begin in state i and go to state j (i and j are not necessarily distinct) and $N_{i.}$ is the number of transitions which begin in state i,

then the maximum-likelihood estimate t_{ij} of the transition probability T_{ij} from state i to state j is $N_{ij}/N_{i.}$. The conditions and tests related to this estimation procedure need not be repeated here from Billingsley (1961).

To test whether the observed transitions are consistent with the conditions (15), we note that given $N_{i.}$, the N_{ij} are multinomially distributed with the probabilities T_{ij} given by the ith row of the transition matrix T in (2). Hence, $E(t_{ij}) = T_{ij}$, $\text{var}(t_{ij}) = T_{ij}(1 - T_{ij})/N_{i.}$, and $\text{cov}(t_{ij}, t_{kl}) = (-T_{ij} T_{kl}/N_{i.})\delta_{ik}$.[1] On the null hypothesis that the observations come from a Markov chain with transition matrix T as in (2), the expectation of the random variables

$$\begin{aligned} \theta_1 &= t_{01} + t_{10} - t_{23} - t_{32}, \\ \theta_2 &= t_{02} - t_{13} + t_{20} - t_{31}, \end{aligned} \tag{16}$$

is $E(\theta_1) = E(\theta_2) = 0$ and the variances may be estimated by

$$\text{var}(\theta_1) \approx \frac{t_{01}(1 - t_{01})}{N_{0.}} + \frac{t_{10}(1 - t_{10})}{N_{1.}} + \frac{t_{23}(1 - t_{23})}{N_{2.}} + \frac{t_{32}(1 - t_{32})}{N_{3.}},$$

$$\text{var}(\theta_2) \approx \frac{t_{02}(1 - t_{02})}{N_{0.}} + \frac{t_{13}(1 - t_{13})}{N_{1.}} + \frac{t_{20}(1 - t_{20})}{N_{2.}} + \frac{t_{31}(1 - t_{31})}{N_{3.}}. \tag{17}$$

An observed value of θ_i, divided by its estimated variance (17), may then be assigned the distribution function of a standardized normal variate to see whether the observations are consistent with conditions (15). The two tests, one for θ_1 and the other for θ_2, are not independent, because

$$\text{cov}(\theta_1, \theta_2) = -\frac{\lambda_1\lambda_2}{N_{0.}} + \frac{\mu_1(\lambda_2 - \varepsilon_2)}{N_{1.}} + \frac{\mu_2(\lambda_1 - \varepsilon_1)}{N_{2.}} - \frac{(\mu_1 + \varepsilon_1)(\mu_2 + \varepsilon_2)}{N_{3.}}. \tag{18}$$

Hence, the power of the test of the compound hypothesis (15) against the alternative that equality does not hold in either or both relations cannot be found simply by multiplication of the powers of the two separate tests of the hypotheses that each equation holds against the separate alternate hypotheses of inequality.

5. EVOLUTIONARY DYNAMICS

So far in this paper, the parameters μ_i, λ_i, and ε_i, $i = 1, 2$, have been treated as given and fixed and the units of time have been interpreted as shorter than those in which the parameters change measurably. In order to study the effects of selection on the parameters, we now assume that the system of two parasite species and their host species is locked on to its equilibrium (5) and (6). We consider how the parameters evolve, in time units on the evolutionary scale, to affect that equilibrium.

[1] The Kronecker delta δ_{ik} satisfies $\delta_{ik} = 1$ if $i = k$ and $\delta_{ik} = 0$ if $i \neq k$.

A full analysis would model the evolution of all six parameters. As a first step, we will model the evolution of ε_i, assuming fixed, positive λ_i, μ_i, $i = 1, 2$. Whereas the identification (13) of the Markov-chain proportions (4) with the competitive Lotka-Volterra equations (8) required ε_i to be positive, the Markov-chain model (2) of interspecific interaction imposed no restriction on the sign of ε_i, and hence neither will the following. The index j will refer below to one of the two parasite species, and the index k will refer to the other, while i will refer to both species, $i = 1, 2$. The decision to model only the evolution of the ε_i means that the parameters λ_j, μ_j are assumed to have been determined in the absence of species k by the joint evolution of species j and its environment, where the environment consists of the host and all parasites other than species 1 and 2.

If the presence of species k changes species j's infection rate from λ_j to $\lambda_j - \varepsilon_j$ and the defection rate from μ_j to $\mu_j + \varepsilon_j$, we assume that the change ε_j is under the control of species k in the sense that species k will evolve to bring about a value of ε_j most favorable to species k. As a crude approximation, we assume that species k measures how good a value of ε_j is by the equilibrium abundance Y_k^* determined by (6) from ε_j. Because the elements of T in (2) are not allowed to be negative, the values of ε_i must lie in a closed box B in the $(\varepsilon_1, \varepsilon_2)$-plane,

$$B = \{(\varepsilon_1(t), \varepsilon_2(t)) \mid -\mu_i \leqslant \varepsilon_i(t) \leqslant \lambda_i, i = 1, 2\}. \tag{19}$$

Thus, species k is assumed to face the following simplification of natural selection:

$$\begin{gathered}\text{find } \varepsilon_j \text{ in } B \text{ that maximizes } Y_k^*, \\ \text{given } \varepsilon_k \text{ in } B \text{ and positive } \lambda_1, \lambda_2, \mu_1, \mu_2.\end{gathered} \tag{20}$$

Though the global optimal ε_j in B will be rewarded with the largest abundance Y_k^*, we assume that selection can act only through gradients in Y_k^* associated with local neighborhoods of ε_j. Hence, the effective procedure by which evolution seeks to carry out the maximization (20) could be represented by equations of the form

$$\frac{d\varepsilon_j}{dt} = C_k \frac{\partial Y_k}{\partial \varepsilon_j}, \quad C_k > 0, \tag{21}$$

or some similar form in which $d\varepsilon_j/dt$ has the sign of $\partial Y_k^*/\partial \varepsilon_j$. The solution to (21) or a similar form is a trajectory in the $(\varepsilon_1, \varepsilon_2)$-plane traced out in time by the current value of $(\varepsilon_1(t), \varepsilon_2(t))$. The qualitative features of any such solution may be readily sketched by noting from (6) that

$$\frac{\partial Y_k^*}{\partial \varepsilon_j} = \frac{\varepsilon_k Y_k^*}{(\lambda_1 + \mu_1)(\lambda_2 + \mu_2) - \varepsilon_1 \varepsilon_2} \tag{22}$$

Hence, within the box B, where Y_k^* and the denominator in (22) are always positive, the sign of $\partial Y_k^*/\partial \varepsilon_j$ equals to sign of ε_k. Four cases may be considered.

First, if $\varepsilon_k < 0$, then species k increases Y_k^* by decreasing ε_j, in the limit to $-\mu_j$. Since species j then faces a negative ε_j, it increases Y_j^* by lowering ε_k to $-\mu_k$. Thus, species k maximizes its abundance by ensuring that no individuals infected with species k and with species j lose their infection with species j. At equilibrium in evolutionary time, $\varepsilon_i = -\mu_i$; the system moves to the lower left corner of B, and all individuals have double infections ($P_3 = 1$). This equilibrium is locally stable since small perturbations of these negative values of ε_i will still leave ε_i negative; hence, the equilibrium will be reestablished.

The equilibrium associated with this first case might be identified as a symbiosis between two parasites which is obligatory for the host. Such a situation might obtain, for example, with a pair of rumen ciliates which digest cellulose for a ruminant (Croll 1966, p. 4–5). In the course of evolution toward this equilibrium, a 2×2 contingency table of observations of the state of infection of the hosts would reveal a positive association between the infecting parasites. At equilibrium, there would be no observations to enter in states 0, 1, and 2 and hence no use for a contingency table.

In the second case, if $\varepsilon_k > 0$, then species k increases Y_k^* by increasing ε_j to the limit of λ_j. Since species j then faces a positive ε_j, it increases Y_j^* by similarly increasing ε_k. Thus, species k maximizes its abundance by ensuring that no individuals infected with species k become infected with species j. At equilibrium in evolutionary time, $\varepsilon_i = \lambda_i$ (the upper right corner of B), and no individuals have double infections ($P_3 = 0$). Then

$$Y_k^* = \frac{\lambda_k \mu_j}{\lambda_1\mu_2 + \lambda_2\mu_1 + \mu_1\mu_2} \tag{23}$$

This case, in which species k faces a positive ε_j, was identified as the case of competition in Section 3. Though the complete exclusion in evolutionary time of double infections follows mathematically from the schema of evolution assumed, the rationale underlying this outcome is easily grasped intuitively. Suppose I, species 2, seek to maximize my abundance and you, species 1, impose a positive ε_2. Then I have worse luck infecting hosts who are already infected with you (lower infection rate, higher defection rate) than I have infecting hosts who are free of you. Hence, I want to make sure that as many hosts as possible are free of you. So I will try to make things hard for you by imposing a positive ε_2 in those hosts which I can manage to infect.

The pursuit of this logic leads to an equilibrium ($P_3 = 0$) which may be partially identified with MacArthur's broken-stick or ordered-random-intervals model (1957). The competing parasites here may be identified with MacArthur's competing species, and the complete mutual exclusion of parasites here may be identified with MacArthur's assumption of no overlap in the use of resources. However, whereas MacArthur assumed that none of the resource (here the hosts) went unused, here an equilibrium fraction $P_0 = \mu_1\mu_2/(\mu_1\lambda_2 + \mu_2\lambda_1 + \mu_1\mu_2)$ of hosts remains uninfected.

The equilibrium of this second case is locally stable since small perturbations of positive values of ε_i still leave ε_i positive; hence, the equilibrium will be reestablished. While a system evolves toward this evolutionary equilibrium, a 2×2 contingency table of observations of the state of infection of hosts reveals a negative association between the infecting parasites.

In the third case, if $\varepsilon_k = 0$, then $\partial Y_k^*/\partial\varepsilon_j = 0$ regardless of ε_j. If ε_j is negative, then species j will decrease ε_k and case 1 takes over. If ε_j is positive, then species j will increase ε_k and case 2 takes over. If $\varepsilon_k = 0$, the system is at equilibrium and there is no interaction whatsoever between species 1 and 2; $P_3 = Y_1^* Y_2^*$. This lack of interaction corresponds to the interspecific relations assumed in an "exponential" model (Cohen 1968) which predicts the same relative abundances as MacArthur's. But the exponential model assumes identical underlying abundance distribution functions for all species, while here $Y_i^* = \lambda_i/(\lambda_i + \mu_i)$, so the exponential model differs from this equilibrium of the Markov-chain model. This third equilibrium is unstable since, if small perturbations drive the ε_i both positive or both negative, a different equilibrium will become established.

In the fourth and final case, if $\varepsilon_1\varepsilon_2 < 0$, the parasites will evolve so that $\varepsilon_1\varepsilon_2 = 0$, that is, to the axes within B. Unless the trajectory of the system passes through the origin (case 3), the values of ε_i will cross the axes so that $\varepsilon_1\varepsilon_2 > 0$ and the system will go to the equilibria of cases 1 or 2.

The equilibria of cases 1, 2, and 3 should not be confused with the equilibria of the usual Lotka-Volterra equations with fixed parameters mentioned before (9). Because $\lambda_i > 0$, at no equilibrium of (3) is a parasite extinct from the ensemble of hosts, though either parasite may be absent from a particular host.

Comparison of the equilibria attained in evolutionary time shows that the abundances of the parasites are largest in the first case of universal double infection where $Y_i^* = 1$, are less in the third case of no interaction where $Y_i = \lambda_i/(\lambda_i + \mu_i)$, and are least in the second case of complete competitive exclusion where Y_i^* are as in (23). Therefore, if simple abundance is the criterion of adaptive advantage, the parasite species should favor ensembles of hosts which permit negative values of ε_i—hosts in which the presence of one parasite paves the way for the other. At the same time, if parasitic infection injures the host, the host should seek to effect the largest possible threshold (T_1, T_2) which restricts the region within B which the parasites can reach to that satisfying $\mu_i < T_i \leqslant \varepsilon_i \leqslant \lambda_i$. If the host can evolve so that neither parasite confers any advantage on the other, that is, so that $T_i = 0$, then it is to the parasites' advantage to maintain the unstable equilibrium $\varepsilon_i = 0$ by diverging so far that the host cannot use its means of limiting λ_j to produce a positive ε_k.

In summary, pairs of parasites being selected for abundance should seek to prevent their hosts from exploiting one as a defense against the other. If the host's defenses depend on characters of the parasite which are partly or wholly specific to the species of parasite (as is widely the case with specific immunity), then it is to the advantage of each parasite to diverge

from the other. In turn, it is to the advantage of the host to develop defenses (such as those labeled "cross-specific immunity" or "heterologous immunity") which, when aroused by infection with one parasite, have some effect against the other and hence create the formal equivalent of competition ($\varepsilon_i > 0$) between the two.

Experimental studies of malaria (Cox and Voller 1966), schistosomiasis (Nelson et al. 1968; Amin, Nelson, and Saoud 1968; Amin and Nelson 1969; Amin, Saoud, and Nelson 1969), and trypanosomiasis (Ford 1970, p. 95) and epidemiological studies under way (Cohen, in press) and in preparation may demonstrate that, though the Lotka-Volterra equations are inadequate as an epidemic model of such diseases, these general conclusions are useful in understanding the interspecific interactions in some widespread genera of parasites of men.

6. CONCLUSION AND SUMMARY

Information about the presence or absence of each of a number of species in ecological systems or patches of environment can be represented in a contingency table with as many dimensions as there are species, and available statistical methods can reveal interactions among the species (Goodman 1964). The analysis through contingency tables of interspecific interactions in replicated systems has long been practiced in general ecology (Edmondson 1944; Bushnell 1966 [I thank Thomas W. Schoener for these references]). Parasitologists have used the distribution of different parasites in an ensemble of hosts to reveal interactions of the parasites since not later than 1916 (Croll 1966, p. 110–113). This paper offers a description of what may be implicit in this common analysis of interaction and explores some evolutionary consequences of that description.

A standard model (1) for the analysis of interaction in 2×2 contingency tables has been related to a discrete-time (2) or continuous-time (3) Markov chain, which in turn has been related to a linearized equilibrial approximation (12) to the classical Lotka-Volterra model (8) for the competition of species. Identification of the variables representing abundance in the Lotka-Volterra equations with the proportions in the Markov chains of ecological systems in which species were present, makes it possible to estimate, via the parameters of the Markov chain, all the parameters of the linearized Lotka-Volterra equations.

Whether the parameters obtained in this way would also predict the course of interaction in a single system when a species' abundance was measured by its numbers or biomass remains an open empirical question.

When the parameters in the Markov chain that measure interaction between species are made subject to changes by which each parasite seeks to maximize its own abundance, the system of hosts and parasites is found to move to one of three equilibrial states. In order of descending abundance for the parasites, the equilibria are: universal double infection of hosts (stable equilibrium), no interaction between parasites (unstable equilib-

rium), and complete competitive exclusion between parasites (stable equilibrium). If the parasites are injurious to the host, it is thus to the host's advantage to bring about competitive (or cross-immune) interactions between its parasites.

One advantage of the identification between the Markov chain and the Lotka-Volterra equations is that it makes clear that dynamic information about rates of infection (immigration) and defection (emigration) is required to estimate the Lotka-Volterra parameters. An advantage of the Markov chain over the Lotka-Volterra equations is that, for the same number of parameters, the Markov chain gives information about the proportions of systems with each kind (mixed, single, or null) of infection, whereas the Lotka-Volterra equations give only information about the margins of the contingency table, which describe each species regardless of the other.

In addition to providing a means of putting one interpretation of the Lotka-Volterra equations to empirical test, the methods used here illustrate more general techniques for the analysis of systems of dynamic equations in which the variables are difficult to measure with precision in a single case but can reliably be measured as all-or-none attributes of numerous ecological systems.

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