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Growth Rate Dependencies for Computerized Identification of Ecological Associations

HENRY BUNGAY,*
PETER GOSTOMSKI, AND STEVEN FRALEIGH

*Department of Chemical Engineering,
Rensselaer Polytechnic Institute, Troy, NY 12180-3590*

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ABSTRACT

When all possible permutations of specific growth rates vs concentrations are graphed, roles of members of an ecosystem become evident. A scatter plot indicates that the organism is not consuming the other constituent, whereas points that fall in line define the relationship of specific growth rate to the food for that organism.

Index Entries: Predation; models; spreadsheets; expert systems; ecosystems.

INTRODUCTION

Identifying and enumerating in a real ecosystem is difficult, controversial, time-consuming, and expensive. Continuous observation of even a few members of the ecosystem is essentially impossible. If data were available, there would be sequences of samples at, perhaps, daily or weekly intervals with much effort expended for resolution and counting. These data would reflect diurnal changes and variations owing to climate, season, and events, such as pollution or rain. When analytical errors are included, noisy population data may need to be filtered or smoothed somehow. When population graphs become available, there will still be a major problem in interpretation. Nutritional interdependencies are studied

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*Author to whom all correspondence and reprint requests should be addressed.

in many ecosystems by examining feces or the contents of the digestive system, but this is impractical for most microorganisms. They are too numerous and too tiny. Sectioning and examination are tedious, and identification of dead and partially digested materials would be tenuous, even with relatively large microorganisms. It is difficult to decide which organisms are prey, predators, or play other roles. Some lever is needed to pry into ecological associations. Relating apparent specific growth rate to concentrations of other constituents of the system throughout an experiment tells how organisms interact in food chains. Although this would be computationally frightening for manual analysis, it is trivial for computers.

The definition of specific growth rate coefficient, μ, in batch culture is

$$\mu = \frac{dX/dt}{X} \tag{1}$$

where X is cell mass concentration and t is time. In well-mixed continuous culture, there is a correction for dilution rate D, the flow rate divided by the volume of culture fluid

$$\mu = \frac{dX/dt}{X} + D \tag{2}$$

Mass balance equations for cell mass may have terms for natural death and for losses to predation. Our proposed analysis based on apparent specific growth rate may fail when other effects are overlooked. Usually, natural death is important only late in batch culture, and organisms may be eaten so rapidly that natural death is small by comparison. Natural death is assumed negligible in continuous cultures for which organisms tend to be washed out before reaching old age. Input of organisms is assumed zero as for systems with sterile feed.

Specific growth rate relates to concentration of limiting substrate, and the Monod equation or other expression may fit the data well. For the purpose of this discussion, the equation does not matter as long as there is a unique value of μ for each concentration of nutrient. The Lotka-Volterra analysis of predation considers predator increase to be a function of the product of prey concentration times predator concentration. Dividing through by predator concentration to get specific growth rate shows that it is directly proportional to prey concentration. We have worked with simulated ecosystems, calculated specific growth rates, and plotted vs all concentrations of possible foods in the system. The graphs are meaningless scatter plots except for the true limiting nutrient or prey where a relationship is obvious.

Computer Programs

Continuously cultured microbial ecosystems with up to eight constituents have been modeled using equations for predation and competition, but five organisms plus one limiting organic nutrient develops graphs

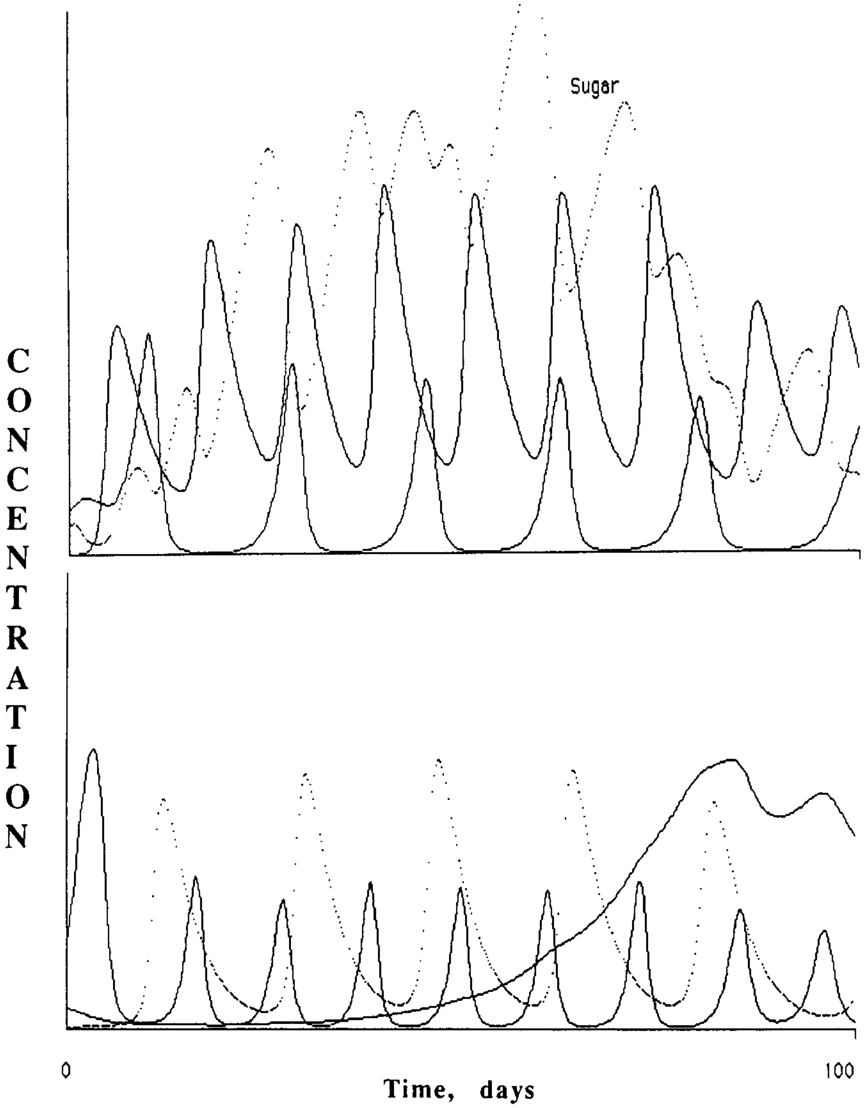

Fig. 1. Simulation of population behavior in continuous culture (5 organisms and one limiting nutrient).

that illustrate well the complicated population behavior of even such simple ecosystems. Figure 1 is typical of our simulations. Actual data would not be continuous. In a previous paper, we set the differential equations to zero and analyzed the curves at peaks and valleys where the slope was zero (*1*). This approach made use only of data for the peaks and valleys.

Figure 2 shows the apparent specific growth rate of each of the organisms plotted against the concentrations of each other component. Amidst the scatter, a few lines are defined. These are strong proof of a relationship between the specific growth rate of one component and the concentration of the other component. Furthermore, scatter to minus

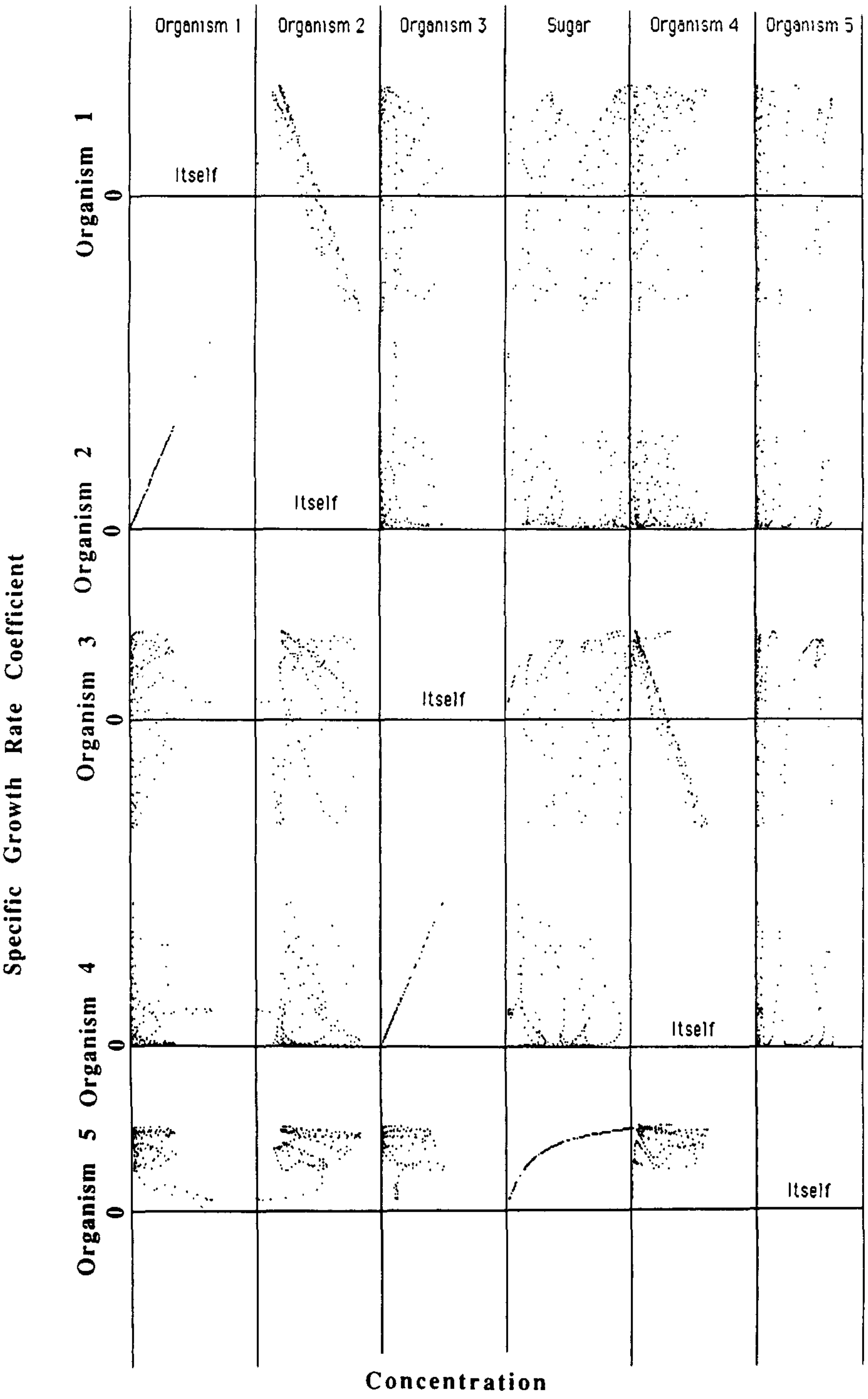

Fig. 2. Plots of apparent specific growth rates.

Table 1
Specific Growth Rate Correlation
for Organism 2 on Organism 1

Interval between data	Correlation coefficient
0.5 days	1.00
2	0.994
7	−.305

values is strong proof of consumption, and prey are thus identified. In other words, there must be death when the specific growth rate is negative. The conclusions are: Organism 2 eats Organism 1, 4 eats 3, and 5 eats sugar while being involved in no predations. Organisms 1 and 3 compete with 5 for sugar.

Spreadsheet Approach

Although many highly-sophisticated expert systems are written in a powerful language, such as LISP, the analysis of large amounts of tabular data usually works well with a spreadsheet program. In fact, reasonably advanced expert systems have been written with Lotus 1-2-3 (2). We use a simple program for modeling simultaneous, ordinary different equations (3), and send data of concentrations of constituents of the ecosystem to a computer file at regular intervals. Such data files are easily accepted by a spreadsheet in much the same manner as collecting and entering real data. Calculations of slopes at various times and correcting for the dilution rate for use as dX/dt in Eq. 2, and correlations with concentrations of other constituents of the ecosystem, are carried out automatically within the spreadsheet. The equations we selected for the correlations are a straight line (Lotka-Volterra Model), the Monod Equation, and a transformation of the Monod Equation in the manner of Lineweaver and Burke. Our expert system displays correlation coefficients, and the user decides which relationships merit further attention.

When a consumer has been identified, the graphing features of the spreadsheet come into play. This could be automated, but human decisions about what to analyze in detail seem more appropriate. We have been surprised to find that simulated data at two-day intervals are nearly as useful as data taken twice per day. When the interval is 7 d, we get a negative correlation coefficient (no correlation). Typical results are in Table 1.

DISCUSSION

An ecological expert system using rules based on specific growth rate needs population data over a period of time. It would seem that the longer the time, the better the analysis. This may not be true if the organisms mutate or adapt so that the equations do not hold or the coefficients change.

In a sense, it is unremarkable that a contrived ecosystem can be analyzed and picked apart. Nevertheless, our simulations employ the sorts of equations being used by modelers and ecologists, and the equations should apply sometimes well and sometimes poorly for real ecosystems. This approach provides a method to evaluate equations and some powerful rules for expert systems.

Obviously, computer models that add more interactions and strive for more realistic terms (perhaps with structure) can generate population graphs that are overwhelming. Unfortunately, real ecosystems are even more complicated. Only with computerized analysis can we hope to unravel the interactions. Neither perfect mixing or ideal plug flow is encountered in real ecosystems, but this approach can be valid whenever there are enough data for calculating specific growth rates corrected for flow, and for relating them to concentrations. With smooth data generated by the computer, the maximum interval between samples is roughly 2 d. It would be interesting to investigate the effects of noisy data, interaction other than predation, density-dependency of specific growth rates, and the like. Unfortunately, only a small amount of relevant information has been published.

In real ecosystems, organisms can play several roles, such as preying on some organisms while being victims of others. Our approach can still succeed because of the relative abundance in real ecosystems, where a few types of organisms can constitute a very high percentage of the total. We are finding with simulations of more complicated ecosystems in which a predator eats two different organisms that there are times when some concentrations are low, so that terms drop out of the population equations and analysis based on specific growth rate becomes useful. Furthermore, when the contribution to specific growth rate of one organism is recognized, it can be subtracted so that the contribution of the other organism becomes more obvious. In summary, brute force in relating specific growth rate to concentrations or permutations of concentrations of other members of an ecosystem is easily carried out with computers, and can be a powerful tool for analysis, especially in combination with other ecological tools.

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