

## APPLICATIONS OF STOCHASTIC METHODS IN EUTROPHICATION

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### ABSTRACT

Recognition of man's increasing power to affect his environment has resulted in formulation of mathematical models to describe physico-chemical-biological interactions. Stochastic theory can be applied to deterministic models of eutrophication to include consideration of the inherent variability of biological responses. A conceptual model format for this stochastic simulation is presented.

### Introduction

Within the domain of the scientific method are three theories of practice which are concerned with the search for truth [1]. Bounded by the extremes of the pure and the applied scientist are the intermediate or *modus operandi* investigator who bridges theory and practice. The environmentalist performing at the level of *modus operandi* recognizes man's increasing power to affect his environment and his destruction potential. It thus becomes increasingly more important for man to be able to evaluate the probable results of a given set of actions. This paper is designed to show how stochastic theory can be applied to quantify the accelerated rates of eutrophication which are spoiling our waterways.

Eutrophication refers to a natural or artificial addition of nutrients to a body of water as well as the effects of increased nutrients [2]. Although inherently a natural process relating directly to the aging of a lake, it can be greatly accelerated by man. Limnologists are uncertain as to whether consequences of natural eutrophication parallel those of eutrophication accelerated by man, or whether eutrophication is reversible within a reasonable time span. This latter uncertainty underscores the urgent need to understand eutrophication and to be able to predict the effects of artificially adding nutrients to lakes, streams and rivers.

### Simplified Aquatic System

The impact of water resources development projects on aquatic ecosystems, measured in terms of accelerated eutrophication and resulting economic and social losses, has become a matter of rising concern both in the United States and abroad. If we consider the potential combined effects of increased domestic sewage, salinity increases, and agricultural drainage effects we are led to conclude that the environment would experience greatly accelerated eutrophication. There is little doubt that a serious need exists for methods and tools which will permit assessment of the shifts in rates of eutrophication and in the merits or demerits of alternatives for control of eutrophication. Realizing the need for such a capability in dealing with eutrophication, we find it necessary to understand biotic and abiotic relationships in the aquatic system. A simplified aquatic model (Figure 1) deals with a nutrient source, primary producers (phytoplankton), and primary consumers (zooplankton). Usually very general parameters such as temperature and levels of a few nutrients are the variables of interest. Most of the inputs are lumped, e.g., fish grazing is represented by one factor. Models of fish population dynamics have been expanded by Patten [3].

A more complete model of an aquatic ecosystem is given in Everett [4]. The higher plants have been omitted. Although we conceptually *understand* the paths in Figure 1, postulating functional relationships is difficult because of the lack of complete simultaneous data acquisition and other sampling problems.

### Stochastic Model

Although the modeling of biological phenomena must be considered an infant science, numerous mathematical constructs have

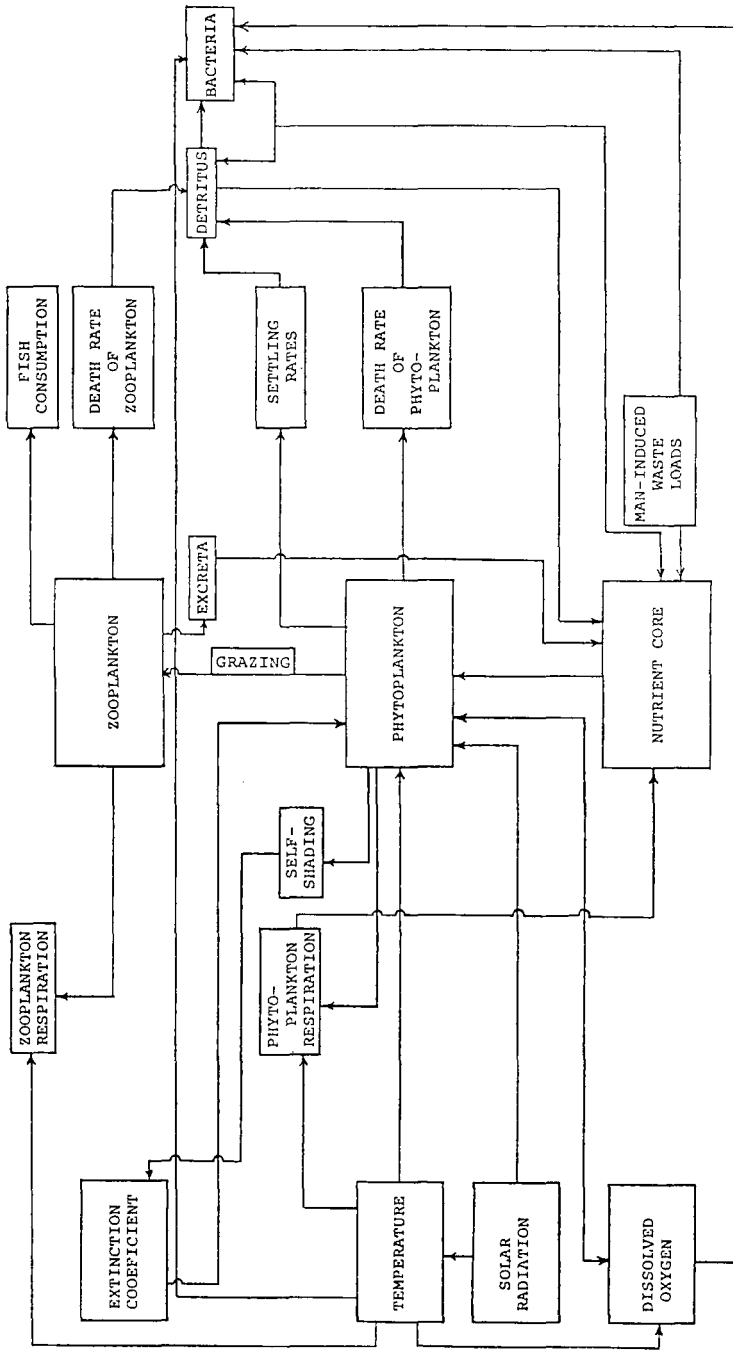


Figure 1. Simplified diagram of an aquatic ecosystem (after Everett 1972).

been formulated and have proven useful for describing (within fairly reasonable error limits) the dynamics of aquatic systems [5-7]. Like any mathematical description of ecological processes, these formulations have necessarily included numerous simplifications which have varying effects on the realism and utility of the models. One common characteristic is the treatment of large organism groups (at various trophic levels for example) as homogeneous populations with identical patterns of response to variations in such environmental characteristics as temperature, nutrients, availability of food materials and predation pressure. This is clearly an oversimplification as the response of an organism is dependent upon genetic make-up and its environmental history (disease, nutrition, exposure to various environmental stresses, etc.). As these factors are variables within each individual of even a mono-specific population, the response of even this mono-specific group may thus be viewed as a stochastic process.

Lewontin stressed that the understanding of ecological and evolutionary influences is not possible if populations are regarded as homogeneous collections of individuals [8]. In fact, shifts in biotic populations occur via selection processes which act upon phenotypic variation. This paper describes a methodology for dealing with this stochastic character of biotic populations response.

We will consider a stochastic model of a phytoplankton-zooplankton population where  $x$  and  $y$  represent the respective sizes of the two populations. The state of the system at any time can be represented by the ordered pair  $(x, y)$ . The system can change state as a result of either births or deaths of either species. Migrations will not be considered, although they do not pose serious additional difficulties. We will assume that these births and deaths are independent events that individually satisfy the following four assumptions of the Poisson process:

1. The probability of exactly one event occurring in the time interval  $(t, t+\delta t)$  is  $r\delta t - O(\delta t)$ ;
2. The probability of more than one event occurring in the time interval  $(t, t+\delta t)$  is  $O(\delta t)$ ;
3. The probability of zero events occurring in the time interval is  $1 - r\delta t + O(\delta t)$ ; and
4. The above probabilities are independent of the state changes of the system during an interval of time  $(T, T+\Delta T)$  where  $\Delta T \gg \delta t$ .

The usual form for the last assumption is that the probabilities in the first three assumptions are totally independent of the state

of the system [9]. Since our birth and death rates are somewhat state dependent, we need the modified form given above where  $\Delta T$  is chosen such that the probability that there is a significant percentage change in a state within the time interval is arbitrarily close to zero. In practice, it is convenient to attempt a simulation with a prescribed value of  $\Delta T$  and examine the results to check the validity of the fourth assumption rather than trying to derive an analytical expression for  $\Delta T$ . With a proper choice of  $\Delta T$ , if the state changes within the time interval do not appreciably change the birth and death rates, then we can treat these rates as constants that depend only upon the state at the beginning of the time interval.

A consequence of these four assumptions is that the probability of exactly  $k$  events of a given type occurring within the interval  $(T, T+\Delta T)$  follows a Poisson distribution:

$$p(k,r) = \frac{(r\Delta T)^k}{k!} \exp(-r\Delta T).$$

Let  $r_{x+}$  and  $r_{y+}$  be the respective birth rates of the phytoplankton and zooplankton populations, and  $r_{x-}$  and  $r_{y-}$  the respective death rates. If the system is in the state  $(x,y)$  at the  $T$ , the probability  $\Pr((x,y), (x+a,y+b), \Delta T)$  of a transition to a state  $(x+a,y+b)$  at time  $T+\Delta T$  can be evaluated as follows:

$$\Pr((x,y), (x+a,y+b), \Delta T) = \left[ \sum_{i=a}^x p(i,r_{x+}) p(i-a,r_{x-}) \right] \left[ \sum_{j=b}^y p(j,r_{y+}) p(j-b,r_{y-}) \right]$$

It is not, however, practical to evaluate these probabilities in order to obtain a transition matrix, since the transition probabilities are not stationary in time, and the transition matrix is infinite dimensional. Instead, we will develop a Monte Carlo simulation of the system. Since we know the distributions of the number of births and deaths of each species within a time interval  $(T, T+\Delta T)$  as a function of the state at time  $T$ , we can generate values from these distributions to simulate the number of births and deaths occurring in the time interval, and then very simply calculate the state at time  $T+\Delta T$ . We can then recalculate the birth and death rates for the next time interval in terms of the state at time  $T+\Delta T$ , and proceed with our simulation. The accuracy of the simulation relative to assumption number four can be improved by reducing the size of  $\Delta T$ . The limit of reducing the size of  $\Delta T$  would involve recalculation of the birth and death rates after each birth or death,

which is the standard Monte Carlo simulation procedure. Since we will be dealing with phytoplankton and zooplankton populations whose sizes will normally be extremely large, this standard procedure is infeasible for a practical simulation.

We will modify the above stochastic population model by introducing the limiting nutrient supply into the state vector. This is necessary because the phytoplankton birth rate depends strongly upon the limiting nutrient supply. Since changes in limiting nutrient supply depend to a large extent upon births and deaths of phytoplankton, we cannot treat the nutrient "births" and "deaths" as events independent of phytoplankton births and deaths. We will, therefore, treat the limiting nutrient supply in a deterministic fashion as described below.

After our simulation generates the number of births and deaths of each population in a given time interval  $(T, T+\Delta T)$ , we will calculate the changes in nutrient supply based upon these events as well as other contributing factors such as external nutrient inputs. This enables us to calculate the limiting nutrient supply at time  $T+\Delta T$  in terms of the state and input at time  $T$ .

We are now prepared to describe our model in rigorous system theoretic terms. The terminology used in the model is from Wymore [10, 11].

### System Theoretic Model

From phytoplankton-zooplankton-nutrient interactions, it becomes apparent that any model we develop lacks analytical tractability primarily because of the nonstationary character of the transition rates. We, therefore, must develop a model which lends itself readily to computer simulation in order to have a useful model. The following system theoretic form of the model was chosen because it illustrates both the biological interactions and the logic of the Monte Carlo simulation in a reasonably concise, clear, and rigorous fashion. A finite state machine model is insufficient because there are an infinite number of possible states of the system. References will be made to some constants and functions which are explained below.

The function POISSON( $x$ ) is defined uniquely by the following relationships:

1. POISSON( $x$ )  $\in$  FUNCTIONS  $([0,1], \text{NONNEGATIVE-INTEGERS})$ ;
2. For every  $r \in \text{REALS } [0,1]$ ,

$$\sum_{k=0}^{(\text{POISSON}(x)) - 1} \exp(-x) \frac{x^k}{k!} \leq r \leq \sum_{k=0}^{(\text{POISSON}(x))} \exp(-x) \frac{x^k}{k!}.$$

If  $r$  is a random observation from a uniform distribution on  $(0,1)$ , then  $\text{POISSON}(x)$  is a random observation from a Poisson distribution with parameter  $x$  by the inverse transformation method of generating values from a probability distribution [12]. An alternative scheme is available for generating observations from a Poisson distribution when the mean is large, based on the normal approximation to the Poisson.

The following constants and functions are also used:

zbirthrate = growth rate function for zooplankton

(organisms/hr.-organism-°C)

zdeathrate = assumed constant value of the fraction of zooplankton lost to predation by higher species, poisoning, etc.

(organisms/hr.-organism-°C)

pbirthrate = growth rate function for phytoplankton population

(organisms/hr.-organism-°C)

knut = Michaelis-Menton constant for limiting nutrient

psink = phytoplankton sinking rate [/hr.-°C]

pmass = average mass of phytoplankton organism (grams)

npratio = nutrient to biomass ratio of phytoplankton

volume = volume of water in section to be modeled (liters)

kphytoresp = phytoplankton respiration coefficient (/hr.-°C)

nutlossrate = fraction of total nutrients lost to sediment per hour

kgraz = zooplankton grazing rate (liters/organism-hr.-°C)

nother = nutrient release rate per hour by death and excretion of higher food chain elements

depth = distance below surface of section to be modeled (meters)

klight = coefficient expressing light intensity for maximum phytoplankton growth (langleys per hour)

kext = light extinction coefficient (/meter)

zooconveff = conversion efficiency of zooplankton at low phytoplankton concentrations

kmp = Michaelis-Menton constant for phytoplankton

We will define a system LAKE = (S,P,F,M,T, $\sigma$ ) as a discrete system as follows:

1. S=ZOOPLANKTON X PHYTOPLANKTON X NUTRIENTS

where

ZOOPLANKTON=PHYTOPLANKTON=NONNEGATIVE-INTEGERS, and NUTRIENTS=NONNEGATIVEREALS.

The units of the plankton components of the state are number of organisms, whereas the nutrient component is specified by weight.

$$2. P = \text{TEMPERATURE} \times \text{LIGHT INTENSITY} \times \text{NUTRIENT} \\ \text{IN} \times \text{DEPTH} \times \text{RANDOM}_1 \times \text{RANDOM}_2 \times \text{RANDOM}_3$$

where

$$\text{TEMPERATURE} = \text{REALS}, \text{LIGHT INTENSITY} = \text{NUTRIENT} \\ \text{IN} = \text{DEPTH} = \text{NONNEGATIVEREALS}, \text{ and} \\ \text{RANDOM}_i = \text{REALS}[0,1] \text{ for } i \in \text{INTEGERS}[1,3].$$

The units of temperature  $t$  and light intensity at the surface ( $Li$ ) are respectively degrees Centigrade and langleys per hour, while the nutrient input is measured in grams, and the  $\text{RANDOM}_i$  are random numbers generated from a uniform  $[0,1]$  distribution and for  $(zoo, phy, nut) \in S$ ,

$$p = (t, Li, n, depth, r_1, r_2, r_3) \in P,$$

$$3. (\sigma(c_p, l)) (zoo, phy, nut) = (zoo + \text{deltazoo}, phy + \text{deltaphy}, \\ nut + \text{deltanut})$$

where

$$\text{deltazoo} = (\text{POISSON}(z_{\text{birth}} - z_{\text{death}})) (r_1)$$

$$\text{deltaphy} = (\text{POISSON}(p_{\text{birth}} - p_{\text{sink}} - p_{\text{grazed}} - p_{\text{resp}})) (r_2)$$

$$\text{deltanut} = (\text{POISSON}(n + n_{\text{zooexcr}} + n_{\text{other}} - n_{\text{phyassim}} - n_{\text{sedloss}})) (r_3)$$

$$z_{\text{birth}} = z_{\text{birthrate}} \cdot zoo \cdot t$$

$$z_{\text{death}} = \text{Min}(z_{\text{death}} \cdot zoo \cdot t, zoo)$$

$$p_{\text{birth}} = p_{\text{birthrate}} \cdot phy \cdot t \cdot \left[ \frac{\text{nut}}{k_{\text{nut}} + \text{nut}} \right] \cdot \frac{\text{light}}{k_{\text{light}}} \cdot \exp \left[ 1 - \frac{\text{light}}{k_{\text{light}}} \right]$$

$$\text{light} = Li \cdot \exp(-k_{\text{ext}} \cdot \text{depth})$$

$$p_{\text{sink}} = \text{Min}(t \cdot k_{\text{sink}} \cdot phy, phy)$$

$$p_{\text{grazed}} = \text{Min}(t \cdot k_{\text{graze}} \cdot zoo \cdot phy / \text{volume}, phy)$$

$$n_{\text{zooexcr}} = \left[ \frac{p_{\text{grazed}}}{n_{\text{pratio}}} \right] \left[ 1 - \left[ \frac{zoo_{\text{conveff}} \cdot k_{\text{mp}}}{k_{\text{mp}} + (phy / \text{volume})} \right] \right]$$

$$n_{\text{phyassim}} = p_{\text{birth}} \cdot p_{\text{mass}} \cdot n_{\text{pratio}}$$

$$n_{\text{sedloss}} = \text{nutlossrate} \cdot \text{nut}$$

$$p_{\text{resp}} = k_{\text{phytoresp}} \cdot phy \cdot t$$

The above model is, of course, only a point model. For practical use, a number of point models should be used and linked together appropriately. In order to accomplish the linkage, movement of phytoplankton, zooplankton, and nutrients from the vicinity of one point to another must be considered. These transport terms



must then be encompassed into the state transition function  $\sigma$  either in a deterministic or stochastic fashion. Chen and Orlob consider vertical migration in their differential equations [7], and Ditoro et al. consider horizontal migration in their model [5], both using a deterministic approach. Either of these approaches can be formulated in the system theoretic framework by defining systems for each point and coupling them.

### Conclusions

Model evaluation is an extremely important and extremely difficult part of the modeling process. The previously discussed model has not yet been applied to a real world situation, so our model evaluation will be restricted to comparisons between our model and other models that have been evaluated.

Basically, our model is a stochastic version of the differential equation model developed by DiToro et al. [5]. Differences occur because DiToro et al. concern themselves with biomass [5], whereas we keep track of number of organisms. Therefore, changes in state in our model occur as a result of births and deaths, while growth causes changes in state in the DiToro model. Since neither model distinguishes between growth and reproduction, this difference is not very significant.

Our approach to determining changes in nutrient level is also slightly different. We treat these changes as being a function of the changes in phytoplankton and zooplankton population levels rather than the population levels themselves. This difference is necessary for maintaining the mass balance viewpoint adopted by DiToro et al. [5]. In the deterministic case, there is a one-to-one correspondence between changes in population levels and the actual levels, whereas in the stochastic case the one-to-one correspondence is between the mean rate of change of population and the actual population size.

The birth-death approach used in our stochastic model has never previously been used to describe phytoplankton-zooplankton interactions, but it has successfully been used in biological modeling. The same is true concerning Monte Carlo simulation. Beyer et al. set up a birth-death model describing wolf-moose-plant interactions and ran a Monte Carlo simulation [13], and Bartlett used a birth-death approach combined with Monte Carlo simulation to describe the competition between two species of flour beetles [14].

Several problems occur in attempting to apply such a model. Several of the constants such as  $k_{mp}$  and  $k_{nut}$  have no physical basis and must be estimated empirically. Other constants such as

zooplankton grazing rates are species dependent, and we are forced to use some sort of average grazing rate. The model also requires as input the water temperature, incident light intensity, and external nutrient supply at all times. These data are frequently unavailable.

Since these problems are shared with the standard differential equation approach used by DiToro et al., Chen and Orlob, and many others, they do not represent a severe limitation upon our modeling approach [5-7]. Several conclusions can be drawn from our literature search and model development. We have found that system theory provides a clear and precise language for describing a complicated model. In addition, a computer simulation can easily be constructed from this form of the model.

We have formulated a stochastic model of phytoplankton-zooplankton interactions that seems to be an alternative approach. A final comparison of the two approaches must await a real world application.

As indicated earlier, the simplest way of controlling excess algal growths seems to be limiting the external nutrient input. Monte Carlo simulation can be used to evaluate the effects of different amounts of nutrient inputs.

Finally, our model has indicated a deficiency in the type of data generally available. In order to calibrate our model or a differential equation model, it is necessary to have data taken much more frequently than every two or three weeks.

Water temperature, solar radiation, and nutrients from external sources are inputs to the model. These should be measured as frequently as deemed necessary to obtain an acceptable approximation to the actual input stream. The constants— $p_{mass}$ ,  $k_{ext}$ ,  $k_{light}$ ,  $n_{other}$ ,  $zooconveff$ ,  $k_{mp}$ ,  $n_{pratio}$ ,  $n_{sedlossrate}$ , and  $k_{sink}$ —should either be estimated from the available literature or estimated empirically. Frequent measurements of the state are necessary in order to preform the empirical estimation and laboratory data might provide a satisfactory basis for this estimation in many cases.

Further work is, of course, necessary. As interactions between different species of phytoplankton and zooplankton as well as phytoplankton affinities for specific nutrients are understood, the state description can be modified to include each species separately. More work is also needed in the area of model calibration. Finally, a careful comparison should be made between the differential equation approach and the use of Monte Carlo simulation as a tool for studying the complicated problem of eutrophication.

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