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GUEST EDITORIAL: GRAEME WAKE

Graeme Wake is a New Zealander by birth and completed his Ph.D. in applied mathematics at Victoria University of Wellington in 1967. After a postdoctoral year at the University of Oxford, Professor Wake was successively a Lecturer, Senior Lecturer and then Reader in Mathematics at Victoria University. In 1986 he moved to Massey University in Palmerston North to take up a new chair of mathematics. Currently he is Head of the Mathematics Department which is one of four Departments in Massey's School of Mathematical and Information Sciences. Professor Wake's early work was in the field of mathematical chemistry, especially the study of the reaction-diffusion equations which describe heat and mass transfer in physical, chemical and biological systems. He has, since coming to Massey University, developed intensive interests in biological systems as well as chemical processes. His publications number over eighty refereed publications in these areas and he has spent extensive periods in England. Also he is Director of an Industrial Mathematics Group at Massey University which acts as a focal point for academic-industry links for problem-solving partnerships.

THE SYMBIOSIS OF MATHEMATICS AND BIOLOGY

Setting the Scene

When I was at college, biology was set as an alternative to mathematics. Was this Hobson's choice? Not really: it was a reflection that biology, or at least elementary biology education, was largely non-quantitative. Have things changed? Well yes, but it will take a generation to have an effect. This will be hindered further by the lack of progress that mathematics has made in being accepted as the vehicle for mechanistic modelling, simulation and prediction in non-mathematical situations in biology and elsewhere. My schoolboy experience of biology was that of an eighteenth century taxonomist, and no one told me otherwise.

I do know better now. Mathematics can be a great asset in modelling biological phenomena. The whole area of dynamical systems (differential-difference equations - tools from core curriculae in algebra and calculus, see later) provides a really good mind-set for biologists of all kinds - ecologists, plant physiologists, agronomists etc. My own time at Massey University has provided a wealth of challenges in areas like:

Determination of food-chain dynamics in seawater.

Explanation of distributions of cells in plant roots and bacteria cohorts,

Determination of optimal grazing strategies for farming,

Maximising wool growth,

Explanation of spatial patterns ("patchiness") in the occurrence of animal diseases like tuberculosis in possums.

The success of mathematics in these areas and others like genetics. plant development and so on needs to be recognised generally, and especially in the curriculum in secondary schools.

It is one thing to describe biological phenomena but it is really much better to operate at a deeper level and be able to predict and explain as one might, given a real understanding of the mechanism involved. Data gathering without a theory and interpretation is really a very small step.

The three main steps involved in the process of mathematical modelling are:

FORMULATION SOLUTION INTERPRETATION.

Of course a poor or even incorrect formulation will lead to a bad explanation - "garbage-in, garbage-out" as they say. But the iterative process of going through these steps with better and better approximations to the mechanisms involved can and does lead to better understanding. The process of mathematical modelling is one which has much to offer biology as it now stands. Thus mathematicians need to get more into the biological action.

We need to encourage the exchange of knowledge across this discipline barrier. This is especially so at University level. Many groups have made a tentative start in this area. An example of this has just occurred here at Massey University. We have designed a course on Biological Modelling for 1993, and thereafter, principally for majors in Biology. The course will include sections on key areas like:

Fitting data to models,

Systems approach - population theory and harvesting.

Evolutionary trees - a combinatorial approach, Theoretical biology - optimisation problems and sequence analysis.

The difficulty is the diversity of these areas, but this is the sort of methodology needed in biological problems.

The disciplines meet in an example

Recent developments in the analysis of continuous and discrete dynamical system models has shown that the complex phenomena shown by various biological systems can be explained by surprisingly simple models. Given the phenomena of catastrophe theory (with the concept of the "onset of gross parametric sensitivity") and chaos shown by quite simple dynamical systems, the mind set which came from physics:

complex situations \leftrightarrow complex mathematics

is open to re-examination. The application of these ideas to biological problems has stimulated mathematicians to rethink our approach to these methodologies with really positive results.

An example of this is the recent discovery of strange behaviour in the discrete (c.f. continuous)

$$dN$$
 — = N(a-bN), with initial value when we start dt the clock N(O) = N₀

with a, b constant, depending on the population, species or environment. Here a is the growth rate per capita, and b is an over-crowding parameter. Now dN/dt is just the rate of change of N with t (like speed is the rate of change of distance). This equation can be s hown to have the solution

$$N(t) = \frac{aNo}{bNo + (a-No)e^{-at}}$$

after some involved mathematics (at last we're useful!) and which has $N(\infty) = a/b$ as the preferred long-term value for all No > O. This is demonstrated in Fig. 1. When this equation is written in discrete form with t = 1,2,3,4,..., that is, we look at the population by generations, Nt satisfies the difference equation

$$N_{t+1} = N_t(a+1 - bN_t)$$
, again with initial condition $N_{t=0} = No$

Here N_t represents the population at time t (compare N(t) above) and N_{t+1} is the population at one time interval later, say a year for humans or a day for insects. This is the discrete analogue of our logistic equation above. Now here we have to admit defeat! No one has succeeded in solving for a simple formula for N_t , like that above. There is scope for a Nobel prize here!!

One might have expected that the differences in these two models would be only cosmetic. To some extent this is right -

$$N\infty = \frac{a}{b}$$
 is still the preferred long-term solution for small a.

But if a is large enough, strange things happen.

Firstly let's change things a bit with a couple of simple transformations. We change the basic growth rate a and write A = a + 1. Then we scale N_t to be a related value, X_t , say

$$X_t \alpha N_t \text{ or } X_t = \frac{b}{a}$$
 N_t .

Then the difference equation for N_t becomes (multiplying the difference equation by b/(a+1) and substituting X_t for N_t as above, and A for a+1)

$$\begin{split} X_{t+1} &= AX_t(1-X_t), & X_{t=0} &= X_o = \frac{b}{A} N_o \ (*) \\ &= F(X_t) & (\text{that is, a function of } X_t). \end{split}$$

So this is the rule that gives the population a time interval later, say 1993 from that in, say, 1992.

Now we note that X must remain on the interval 0 < X < I, otherwise the population will become extinct. Since y = F(X) obtains a maximum of A/4 at

Fig. 1: Graph of N(t) versus t for various N_0

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Table 1: Period 2 solution for A = a+1 = 3.2

t	0	1	2	3	4	5	10	X_{2n}	X_{2n+1}	X_{2n+2}	X_{2n+3}
\mathbf{X}_{t}	0.5	0.8	0.512	0.800	0.513	0.799	0.513	0.513	0.799	0.513	0.799

X = 1/2 (it is an upside-down parabola) we need

for practical biological situations; otherwise we do get $X_t < 0$ after a few generations. (Try it and see.) The equilibrium value of (*) is still, as in the continuous case (see Fig. 1),

$$X = \frac{A-1}{B} = \frac{a}{a+1}$$
 which is, of course, $N = \frac{a}{b}$

Also $F'(X\infty) = 2-A$, so we have stability of $X\infty$ (given by $-1 < F'(X\infty) < 1$) for

$$1 < A < 3 (0 < a < 2)$$
.

What happens for 3 < A < 4? By looking at the relation of X_{t+2} to X_t from (*) we find after some not too difficult **algebra** using (*) at t **and** t + 1 that the population two intervals later is

$$X_{t+2} = A^2 X_t (1-X_t)(1-AX_t(1-X_t))$$

This has "fixed points" (a period 2 solution where the population number repeats itself every two intervals — see below) which is a stable dynamic "equilibrium" when A is slightly greater than 3. The same things happen again and again as, for larger A (but still less than 4), period 4 solutions appear and are stable for some values of A etc., etc. Thus we have the period-doubling phenomenon and the onset of chaos at the point of accumulation of period 2ⁿ cycles. This happens when A=3.5700.

Beyond this point (for 3.57 < A < 4) there are an infinite number of fixed points with different periods,

and an infinite number of different periodic cycles. This is then the onset of chaos.

The term "chaos" evokes an image of dynamical trajectories which are indistinguishable from some stochastic process. Simulations tend to confirm this. But the underlying fact is that for all values of A there is one unique cycle that is stable and that attracts essentially all initial points.

The fact that such rich behaviour comes from a simple (discrete) dynamical system underlines one of my points:

"Simple models can describe complex behaviour". A simple iteration (of hand calculator variety) for A=a+1=3.2 gives the solution in Table 1. This has a period 2 cycle which is attracting, that is, the population prefers to settle down to the pattern on the right of the table, which shows a period 2 solution. This means the steady state X = a/(a+1) = 2.2/3.2 = 0.69 is still there but never attainable as the system never prefers this state.

What lesson do we learn from this? We have used two different methodologies to describe the "same" situation. It could be disturbing to have different outcomes for the same situation. But periodic situations occur all over the biological landscape.

If a population shows periodic behaviour the lesson learnt is that this could be modelled by a simple (discretised - the N_t one) equation. This was startling to mathematicians when this was first revealed. But the long term situation is good. Biologists and mathematicians do not need complicated dynamics to describe complicated outcomes like periodic solutions.

By this kind of partnership development; matching reality with simple models, understanding will follow. This is the way ahead.