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Modelling on Human Disease Control

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Abstract: Treatment of diseases pertaining to all has moved from each and individualistic. Like this the mathematical modeling should also move from deterministic to stochastic to suit each and ever individual.

Key words: Pertaining, inddividualistic, deterministic, disease

INTRODUCTION

Last few years computer modelling has gone from being an esoteric interest of a few people (with little understanding by others of its value and application) to being a recognized tool both for research and policy formulation in human disease and its control. As with most innovations in research method, acceptance and application of the technique has been patchy and slower than might have been hoped, but both the number of people using the technique and the range of practical application has grown rapidly over the last ten years. This study reviews the techniques which have been used in computer modelling and the degree to which the method has received practical application. Examples will be provided of different types of models and their application.

The simplest models incorporating disease information have been at the level of individual They have also been used quite extensively as teaching tools in order to allow students to gain experience of making complex decisions without influencing the real-life outcome.

Regional and national models have received far greater practical use. A wide range of these 'policy models' have been developed to answer questions about individual diseases and countries, or to investigate other situations where modelling has specific application. The range of diseases and situations covered has been quite wide. Current developments include the integration of models with other precisely targeted software to form a complete decision-support system which can assist in the management of national disease control program.

Models: The objective of modelling is to build a simplified representation of a complex system within the real world, in order to test procedures which would be too costly or impractical for various reasons to test on the real world system. Such models can include physical replicas, mental or conceptual models, mathematical representations which are solved by analytical methods and representations within a computer which can be investigated by mathematical or purely computational methods.

A variety of modelling methods were used with varying degrees of success. As computing has moved to minicomputers and then to personal computers, models have followed. They have become far more comprehensive and realistic and in most cases far more accessible to non-modellers through the design of easily used interfaces for setting parameters and the development of more visual methods of presenting results. These now include spatial as well as temporal trends in disease occurrence, plus other relevant items such as economic consequences. There are two fundamentally different ways of representing disease processes in computer models. The first is deterministic, in which the processes built into the model are fixed by the coefficients set for each variable and no biological variability is allowed for. Such models will always produce the same outcome for any given set of parameters and initial conditions. The second is stochastic or probabilistic, in which outcomes of at least some of the processes are obtained by drawing samples randomly from standard statistical distributions (binomial, normal, etc.), or empirical distributions based on field data. Such models produce different outcomes for each run and it is necessary to run the model a number of times (commonly five and in some cases as many as ten) in order to represent the range of likely outcomes and provide a reasonable estimate of the mean outcome. Deterministic models are faster to run, but it is more difficult to make them realistically represent the disease control issues of interest at a practical rather than a theoretical level. In some cases they are incapable of realism-for example in estimating the proportion of cases in which a disease

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would be successfully eradicated by a particular control strategy. They will always predict either success or failure under such circumstances-not a probability of success.

Both of the approaches have their uses and the one chosen should depend on the nature of the problem and the kinds of answers required; deterministic models are valuable for deriving general principles, while stochastic models are applicable to analyzing specific practical problems.

Differential and difference equation models: The classical deterministic mathematical approach to analyzing time-varying processes such as disease occurrence is through the formulation of differential equations (for continuous processes) or difference equations (for step processes) and using integration to predict the future values of the variable of interest. Over the years this has been a very fruitful approach for systems with relatively few important variables, provided that the equations describing the system were mathematically tractable (Anderson, 1982; Anderson and May,1981). The approach is very valuable for deriving general principles about the behaviour of simplified 'representative' systems. As the model system being described is allowed to approach reality and hence increases in complexity, at some point for any system the set of differential equations becomes insoluble by standard mathematical methods.

Computer simulation is then normally used to solve the equations, in which case the approach becomes closer to other forms of simulation modelling, although the solutions derived are still deterministic. In some differential equation models certain of the coefficients have biological interpretations which are helpful in understanding fundamental systems dynamics. However again the insights offered through such coefficients tend to lose their clarity as model systems become more complex and approach closer to field reality. Some have argued (Onstad, 1988) that this general approach is inadequate to handle ecological systems modelling, because the coefficients are highly aggregated and not representative of true relationships and because the equilibrium solutions sought may be largely imaginary as far as real world systems are concerned.

Markov chain models: These are well suited to the deterministic description of disease transmission processes and can be formulated in terms that are mathematically manageable and realistically handle infectious disease epidemiology. They are not as well suited to other types of disease, such as cholera diseases, where the issue of interest is the severity of disease rather than its presence or absence (Kristensen,1987).

Other mathematical approaches: A wide variety of other specific mathematical techniques have found application in various specific instances for investigating disease, but in general they have been used because they fitted a particular special case and they have not found wide applicability.

Models electronic spreadsheet: Although electronic spreadsheets were originally designed as accounting tools, they have evolved into very powerful methods for representing many different types of quantitative problems, using the capacity to embed mathematical equations within individual cells of the spreadsheet. It is not difficult to build various forms of simulations within spreadsheet software and this can be a good structure within which to formulate a disease model. If appropriate it can subsequently be converted to a standard computer program, but the development process will always benefit from the design work done within the spreadsheet format.

Although simple spreadsheet models are deterministic in nature, it is also possible to build stochastic models within a spreadsheet, using the random number generator built into current spreadsheets. This can be done from scratch, but it is now possible to use add-on modules which integrates with selected spreadsheets and adds to them the capacity to run full stochastic simulations involving sampling on any one of about 20 statistical distributions, with automated processing of sequences of runs using both standard Monte Carlo procedures and the faster variant termed Latin hypercube simulation. Although such models are slower to run than those which are written in a programming language, the flexibility and speed of development and adjustment make them an attractive option for some modelling activities.

Monte carlo models: These use random number generators to sample from statistical distributions and hence create the sequence of events and results which form the model outcome. Each single outcome is a chance event (hence the gambling association which produced the name of the technique), but in current Monte Carlo systems where millions of such random number selections take place in a single run, the behaviour of the system is stable yet reflects the variability seen in real-world systems. By repeating runs five or more times with different random number seeds to start the process, estimates of natural variability can be made. The technique has advantages over analytical approaches in that it is far easier for non-mathematicians to understand and use, it can approximate much more closely to the real nature of events and processes using a mix of analytical

and empirical representations and it can far better represent sequences over time and conditional probabilities. It does not however have the mathematical purity and same potential for providing conceptual insights which mathematical analyses can in some cases offer, nor does it automatically identify optimal parameter settings for disease control. However the optima it identifies through structured sensitivity analysis are usually more realistic for practical applications than analytical solutions, so this is not a major disadvantage.

A Monte Carlo model is structured by defining the biological processes believed to be involved in the system of interest and then creating a computer program which carries out a simulation of all the relevant processes in the time sequence believed to occur in reality. The structure of the model is based on the nature of the data resources which can be used to construct it and hence it is normally possible to get data for most aspects of the model from published research. Where an essential item is unavailable, a guesstimate is used and a decision made in the light of initial model runs whether field data collection will be necessary to refine the estimate.

Optimizing models: For some disease control purposes, it may be useful to have a true optimizing procedure which mathematically finds the best combination of resource inputs to achieve the desired goal. Linear programming, parametric programming and dynamic programming have all been used in such applications. Dynamic programming is the most powerful of the techniques, but requires considerable mathematical understanding to apply and is not yet readily available as a package procedure on microcomputers. It is likely to find increasing use in the future as a goal-seeking tool in the definition of control policies in combination with more traditional simulation methods (Huirne *et al*., 1992).

CONCLUSION

Each of the modelling approaches is gradually finding its niche in the spectrum of techniques, as modelling matures as a research tool. Analytical mathematical models are best suited to identifying central issues in relation to a particular disease and establishing broad principles concerning constraints to the effectiveness of alternative approaches to control. As the focus moves from principle to specific guidance on the detailed merits and risks of specific control measures, the mathematical methods reach a point where they cannot approach realism much closer than they have already done because the issues which determine differences between strategies are not capable of adequate representation within a tractable mathematical function.

Another factor is that the people who must make use of the information at the practical level must be able to understand and believe what has been done and in most cases they have difficulty with mathematical approaches in which typically some of the variables and many of the coefficients do not translate into measurable items in the field situation.

Decision-makers are also very interested in the probability of failure, as well as the expected outcome, since a control policy which succeeds 'on average' may fail a substantial proportion of the time. A model which fails to make estimates of variability around expected outcomes is not very helpful in practice.

Thus as the investigation of a major disease problem moves from establishment of principles to field implementation of control policies, modelling support needs to move from deterministic to stochastic and from a mathematically solved solution to a solution by repeated simulation with sensitivity analysis. The extent to which model parameters match items which are measurable in the field also becomes increasingly important. In selected cases optimizing rather than evaluative models can offer useful insights.

The point along this continuum where modelling stops is usually determined by money, as far as investment in research and evaluation models is concerned. If the problem is an easy one or not of great importance then a simple mathematical or spreadsheet approach may be adequate. If the problem is a biologically difficult one or is seen to be very important, then a larger investment in more detailed modelling may be justified, as a continuing aid to decision-making and to justification for the chosen research and control strategy. The selection of approach is always a compromise between ease and speed of development on one hand, versus realism and power to investigate approaches in detail on the other hand. The background of the modeller will also be very influential, with those from a mathematical background espousing the mathematical approach and those with a biological training seeking closer approximation to the reality they see in the field. Unfortunately there have been very few examples where the two approaches have been compared effectively in dealing with the same problem, so intuition rather than evidence largely determines the approach adopted.

With Current Computing Techniques, it is possible to achieve high speed of model operation and prompt output

of results, without sacrificing biological validity. Interactions between factors in complex biological systems are usually crucial in determining actual system behaviour and Monte Carlo models can represent such interactions in a much more biologically realistic manner than alternative approaches. Because the model is formulated around current understanding of the particular problem, it is relatively easy to incorporate new knowledge as it becomes available. It is also much easier to represent biological heterogeneity, including spatial variability, through various procedures such as the use of multiple sub-models and linking models to geographical information systems. It is far easier to provide a model interface which is easy to use and requests information in a familiar form and to explain to potential users what the variables are and how the model operates. As modellers at the applied end of the spectrum, we find that these advantages justify the additional development effort and allow the models to be useful over a longer time period and a wider geographical area.

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