Developing the Use of Process Algebra in the Derivation and Analysis of Mathematical Models of Infectious Disease
Extended Abstract

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1 Summary

Mathematical models of infectious disease systems are used to address specific and important problems in the dynamics, persistence and control of those systems. Here we bring together two contrasting modelling approaches: a population based approach from mathematics and an individual based approach from computing science, and apply these to epidemiological problems.

Systems of non-linear coupled differential equations are often used to describe the spread of infectious diseases from a population level. Mathematical techniques are available to analyse algebraically the long-term behaviour of these models. However, once the level of realism in these models increases the mathematical techniques currently in use often cannot give a full picture of the system dynamics. Computing science techniques (based on process algebras) allow us to rigorously describe the same systems from the level of individuals but the question of how those models relate to the population level models has not yet been fully explored.

Our long-term research programme addresses three open questions: Can we improve the mathematical models which describe infectious diseases by comparing and combining the individual and population approaches? Can process algebras yield more tractable analyses than the differential equation based models for realistic models of disease spread? How does the ability to model explicit rules of behaviour and interaction of individuals, permitted by the process algebra, affect model results? This paper describes our initial investigations into these questions.

2 Mathematical Modelling

Mathematical models have been used extensively for more than 20 years to describe dynamical infectious disease systems. Many of the models of directly transmitted diseases are based on the simple susceptible-infectious-recovered (SIR) model [1]. The population is divided up into those who are susceptible to the disease, those who are infectious, and those who have recovered and are immune.

This system can be described by three coupled non-linear differential equations. These equations cannot be solved directly: the standard method of analysis is to look at their long-term behaviour. For the simple SIR model we have a full understanding of the possible long-term behaviours of the system for all combinations of parameter values [1]. However, once we start to add more realism to the model analysis may become algebraically intractable and we have to resort to simulation [2]. Simulation can easily miss interesting dynamical behaviour since it is difficult to explore the whole parameter space.

Implicit and explicit modelling assumptions affect the validity of the model. Common assumptions include: all individuals in the population are loosely coupled, and individuals behave in an average way. More crucially, this is an a priori approach in which we assume that we understand the behaviour of the system at the population level, whereas realistically we may have more experimental information about the behaviour of individuals.

3 Process Algebra

Process algebra allows description of the rules of behaviour and interaction for an individual. Individuals are loosely coupled together to describe a system. Typically, process algebras are used to describe concurrent distributed computer systems, such as communications protocols, but some have already been applied to biological systems. The discrete time process algebra Weighted Synchronous Calculus of Communicating Systems (WSCCS) [3] has been useful in describing dynamics of social insect populations [4, 5], supported by use of the tool Probability Workbench. Process algebra allows creation of an individual-based model, but with the advantage of a formal mathematical semantics, thereby allowing formal analysis. Both long and short term behaviours of the population as a whole may be rigorously explored by examining the Markov chain resulting from the description, or by derivation of a mean field model (MFE) [5].

4 The Combined Approach

Our approach is illustrated in Figure 1. The focus of our work is developing methods of deriving accurate MFEs from the process algebra (the dotted arrow), the comparison of the two sets of MFEs obtained (the thick double headed arrow), and the comparison of the results with real world data.

Sumpter [5] describes a heuristic for deriving MFEs from the process algebra specification. We take some simple disease systems previously been described using differential equation models and describe rules of individual behaviour in WSCCS. We carry out analyses of these systems using the Probability Workbench, manual probabilistic analysis, and Sumpter's technique for deriving MFEs, comparing these with the population level MFEs in the literature. This allows us to better understand the correlation between individual and population level behaviour. By beginning with such simple, well-understood systems we also gain a better understanding of the relationship between the rules of individual

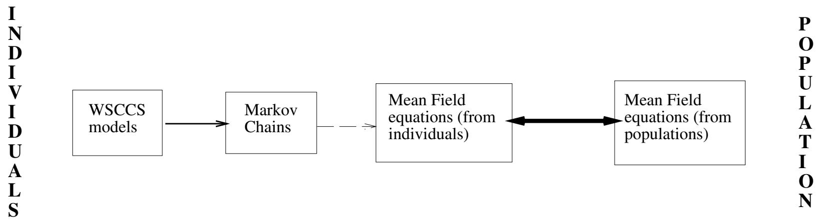

Fig. 1. The Relationship between the Process Algebra and PDE Approach

behaviour as expressed in process algebra, and the derived MFEs. We expect that different modelling assumptions, especially the population view versus the individual view, will result in different models. This may additionally enhance our understanding of disease systems.

5 Conclusions and Future Work

We have examined a simple SIR system with births and deaths, comparing the use of process algebra (WSCCS) with the use of differential equations. Our main aim was to test the use of process algebras in describing infectious disease systems since they may provide an accessible method of deriving individual based models that may be analysed algebraically to yield population level results. Initial studies have shown process algebra to be an intuitive and useful way to describe disease systems. To fully investigate the questions posed above, we need to consider more complex models with decreasing levels of algebraic tractability (from the viewpoint of traditional analyses).

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