Chapter 18

Improving Computational Models and Practices:
Scenario Testing and Forecasting the Spread of Infectious Disease

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ABSTRACT

Since infectious diseases pose a significant risk to human health many countries aim to control their spread. Public health bodies faced with a disease threat must understand the disease's progression and its transmission process. From this understanding it is possible to evaluate public health interventions intended to decrease impacts on the population. Commonly, contingency planning has been achieved through epidemiological studies and the use of relatively simple models. However, computational methods increasingly allow more complex, and potentially more realistic, simulations of various scenarios of the control of the spread of disease. However, understanding computational results from more sophisticated models can pose considerable challenges. A case study of a system combining a complex infectious disease model with interactive visualization and computational steering tools shows some of the opportunities this approach offers to infectious disease control.

INTRODUCTION

Planning for epidemics of human disease is a highly complex task. In the case of an emerging disease little is known about the epidemiology ahead of an outbreak. For ongoing or re-emerging disease much can be learnt about the disease's natural history from epidemiological analysis of the outbreak or from the study of historical records of previous outbreaks. Planning may be undertaken for many reasons, such as determining the logistics for healthcare provision or surveillance. Perhaps more importantly, modelling can be applied to assess the likely impact of a disease outbreak

and the effect of any mitigation strategies. This *contingency planning* can inform the purchase or production of vaccine stockpiles or evaluate proposed public health policies. These analyses could consider the impact of the contingency on morbidity or mortality or its full economic impact.

Surveillance is a vital tool of the epidemiologist. From case records information on the course of the disease, its impact on various demographic groups and any geographic clustering can be determined. However in the case of rapidly spreading diseases which have the potential to affect large numbers of people, such as pandemic influenza, the time scales are so short that real-time surveillance, which underpins the necessary short- and mid-term contingency planning, is too highly resource intensive.

For longer term contingency planning, undertaken well ahead of an outbreak, historical records give some idea of the course of an entire outbreak although many uncertainties surrounding transmission still remain. For example, since the certification in 1980 of the eradication of smallpox (Fenner, 1988) social structures and population movement have changed markedly and, with no further widespread vaccination campaigns, the immunity of the population has waned. This means that there would be difficulties in predicting the spread of a virus should it reappear in a human population. Additionally, research in public health science has increased the range of available treatment and prophylactic agents such as vaccines and antibiotics, introducing further uncertainties. Insight into these uncertainties, and those from changing behavioural patterns, can come from developing computational models allowing different scenarios to be run and estimates to be made of the effects of any interventions that may be adopted in an attempt to control the spread of an epidemic or mitigate its impact.

Mathematical and computational models are abstractions and their results are explored through various types of human-computer interactions (many of which can be made interactive through the use of visualization systems and, where appropriate, computational steering). The developmental path for computational science applications follows a typical route:

[Note: the conditions are numbered numerically and the developmental steps under each condition alphabetically (the steps under condition 2 may iterate and change order)]

1. Traditional observational/experimental methods are too costly, do not produce useful results in a timely fashion or are not accessible to experimentation (for example, it would be unethical to produce an experiment on the spread of a lethal disease in a human population).

    a. A computationally simple model is developed that allows the observations/experiments to be simulated, typically on a desktop machine; results are produced that the developer can understand and report (these may be visual or numeric and may be analysed in real-time as the simulation runs).

2. The model and the analysis of the model results lack details that limit its usefulness so steps a. b. below occur iteratively while the model is improved.

    a. Improving the complexity of the model requires it to be re-engineered to run on a specialist machine, typically a high performance computing (HPC) system rather than a desktop. Such machines and systems often have a batch queue system and are remote from the developer's desktop so real-time analysis is no longer practical. This step occurs each time the simulation is ported to run on a more powerful platform.

    b. Analysis of the simulation results is now more complex—the datasets are larger, containing more detail, and possibly with more parameters and there are more individual datasets—so

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