Chapter VII

Computing Bacterial Evolvability Using Individual-Based Models

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ABSTRACT

This chapter describes two approaches to individual-based modelling that are based on bacterial evolution and bacterial ecologies. Some history of the individual-based modelling approach is presented and contrasted to traditional methods. Two related models of bacterial evolution are then discussed in some detail. The first model consists of populations of bacterial cells, each bacterial cell containing a genome and many gene products derived from the genome. The genomes themselves are slowly mutated over
time. As a result, this model contains multiple time scales and is very fine-grained. The second model employs a coarser-grained, agent-based architecture designed to explore the evolvability of adaptive behavioural strategies in artificial bacterial ecologies. The organisms in this approach are represented by mutating learning classifier systems. Finally, the subject of computability on parallel machines and clusters is applied to these models, with the aim of making them efficiently scalable to the point of being biologically realistic by containing sufficient numbers of complex individuals.

INTRODUCTION

A systemic approach to the study of biological systems has been pursued for many decades, with its modern roots in a number of developing areas of nineteenth century science such as physiology (homeostasis, histology), tissues and systems, and ecology (lake as a microcosm). In the twentieth century we see major integrative developments, especially with the rise of General Systems Theory and cybernetics. More recently, with the increase in data available from molecular biological experiments, it has become important to describe an emerging field of systems biology. We wish to place our work within this long tradition of interdisciplinary science.

The approach to modelling biological systems that is presented here includes evolutionary and ecological perspectives. Coupled with this is an approach from the “bottom up” that seeks to model individual entities and processes as individuals rather than averaged aggregates. We shall explore some ways in which an individual-based approach that seeks to include ecological and evolutionary dimensions can be implemented by describing two systems we have developed that model (at different levels of biological granularity) bacterial systems in simple environments. Some of the many computational challenges to these approaches are described, as well as the biological realism we wish to incorporate in the models. A further challenge, and opportunity, is the increasing access to very large computational power. We discuss a number of aspects for using grid-enabled systems.

Individual-based modelling (IbM) provides an important complementary approach to biosystems modelling that relies on population-based (averaging) techniques (DeAngelis & Gross, 1992). Levins (1984) made the very important comment that no model can simultaneously optimise for generality, realism, and precision. There is always a trade-off between at least two of these modelling dimensions. Whereas some model developers may wish to provide
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