Chapter 11
A Genetic Approach to the Study of Self-Replication

INTRODUCTION

The basic mechanisms underlying development have long been a focus of attention for biological research. Development - or morphogenesis - involves a special sequence of transformations determined by a wide range of elementary processes. It is these processes - genetic regulation, changes in cell morphology, self-replication and proliferation of cells, cooperation among cells (Gierer and Meinhardt, 1972) - that allow organisms to adapt to their environment and to survive.

One of the processes most commonly studied is cellular replication. The results of these studies pose interesting questions. Is it possible to identify the basic mechanisms of biological self-replication, and apply them to artificial organisms? If so, is it possible to use such organisms as experimental models? Can models of their behavior provide new insights into biological processes?

The first authors to investigate this interplay between biological behavior and mathematical models of mechanism were d’Arcy Thompson (1917) and Alan Turing (1952). D’Arcy Thompson hypothesized that the creation of new structures is determined by the mathematical and physical properties of living matter, in this way laying the foundations for theoretical analyses of morphogenesis. Alain Turing, for his part, proposed a reaction-diffusion model of molecular dynamics, showing...
how patterns could develop from an initial homogeneous state. The model makes no explicit mention of growth. Rather it describes chemical reactions between substances that diffuse through an organism. According to Turing’s main hypothesis, pattern formation is determined by reaction-diffusion reactions that take place when certain specific chemicals (morphogens) are present at specific densities. Turing’s model provides a paradigm for the study of morphogenesis. Examples of Turing’s reaction-diffusion reactions have been found both in biological organisms (Kondo and Asay, 1995; Meinhardt, 1982; Meinhardt et al. 2003; Murray, 1989; 2003) and in artificial systems systems (Kauffmann, 1993; 1995; Adamatzky & Komosinski, 2005; Miyashita & Murata, 2005; Goras et al., 1995a; 1995b; Goras & Chua, 1995; Arena et al. ; 1999; Bedau et al., 2000).

The study of biological behavior using artificial systems, (inspired by classical work in cybernetics, systems theory and dynamic systems by authors such as Ashby (1952), Rosen (1991), Hacken (1977), Kelso (1995) involves a wide range of disciplines including mathematics, biology, psychology and philosophy. The majority of research is based on a conceptual framework, involving the steps listed below

a. Collection of evidence (from observation and experiment), providing a (partial and incomplete) picture of the behavior of biological systems.

b. Construction and validation of simplified models of biological behavior, based either on observational and experimental evidence or on engineering approaches with no direct link to experimental data.

c. Construction and validation of artificial laboratories, dedicated to the development of algorithms, simulations or embodied artificial agents that can be validated using mathematical analysis and benchmark problems. The construction of these laboratories requires new computational metaphors, providing appropriate representations for system components, effective methods for evaluating interactions among components and processes to control and modify components. The laboratory should also supply descriptions of the characteristics of biological systems it seeks to represent and interfaces allowing the visualization, manipulation or physical implementation of these characteristics. Artificial laboratories may also define principles for the design and analysis of bio-inspired algorithms. Some of these algorithms may be suitable for application to non-biological problems; others are specifically designed to address issues in a specific domain of knowledge (Bonabeau et al., 1999; Dorigo & Stützle, 2004). But even in these cases, the end-results is new data that can be fed back into biological research. At this point, the cycle repeats, starting from step 1.
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