

The Global Dynamics of Cellular Automata

by Andrew Wuensche and Mike Lesser, Addison-Wesley, 1992. £39.69 hbk (xvii + 250 pages) ISBN 0 201 55740 1

Since the pioneering work by J. Neumann¹ on the theory of self-reproducing machines, and especially after the appearance of Conway's 'Game of Life'², the prototype of cellular automaton (CA) games, many dif-

ferent types of CA models have been developed for scientific purposes in quite a few disciplines, as tools for the study of spatiotemporal dynamical processes. The penetration of CAs into theoretical ecology is mostly due to the fact that they offer a relatively simple conceptual and technical framework for animating spatial-pattern-dependent population and community dynamical processes that would be very difficult to approach otherwise.

Despite the structural simplicity of most CA models, they produce complex dynamics not tractable by closed mathematical formalism. Therefore, the study of CA dynamics is a typical problem of experimental mathematics that, one might think, has hardly anything to do with biology whatsoever. Wuensche and Lesser show it does, although they do it in an 'implicit' manner. Their results are of metaphorical value from the point of view of possible

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applications, for two separate reasons. One is that the range of the types of CA studied is very limited – in fact, it is limited to a single type of the simplest imaginable models: one-dimensional, deterministic, binary CA only. Most objects of biological research deviate all these postulates, as they are normally two- or three-dimensional, stochastic and not binary. This means that no predictive model of this kind can be developed for actual situations. The other reason is that the authors themselves stick to their subject rigorously (which they are not to be blamed for at all), and do not explicate any possible applications of the models they study. Therefore, those who expect something more directly applicable should look for a practical treatment of the subject.

The book consists of three main components. The first contains the 'essence': it is a general description of the dynamics of three- and five-neighbour CA, as represented by the topology of the set of basins of attraction. The models are discussed in full depth, and the authors make their arguments very easy to understand. The reader is not supposed to possess a knowledge of mathematics beyond the secondary school level – each concept, and most relations, are explicated verbally or illustrated by diagrams. This makes the comprehension of seemingly complicated concepts, like the 'basin of attraction field', painless.

This part includes the description of the so-called reverse algorithm, which is a new, efficient, tool for the exploration of the topology of the basins of attraction related to a given rule. The second component is a computer diskette with two programs. One of these generates spatiotemporal patterns for a given rule and initial pattern, the other is the software implementation of the reverse algorithm, designed to visualize the topology of the basins of attraction for any given rule. The programs are spectacular and very easy to use. The manual of the programs is included in the Appendix. The third component is an atlas containing the complete topology of the basin of attraction fields for all one-dimensional, deterministic, binary CA with three-neighbour rules, and a subset of those for five-neighbour rules. The atlas is produced with the programs.

Although there are no direct references to any possible biological applications of CA, it is demonstrated well that even very simple sets of local rules may generate astonishingly complicated global dynamics with a large number of possible pattern realizations. It is just this type of locally generated global complexity that the biologist has to face when trying to explain processes such as the morphogenesis of an embryo or that of a forest. Those who devote time and effort to read the book through will gain an inspiring insight into an abstract structure

representing an analogue of some natural mechanisms that lead to complex patterns. The analogy of CA with biological systems becomes apparent in the chapter dealing with the relation of rule spaces and basin of attraction fields. Following the idea of Kauffmann and others^{3,4}, who regard the set of transformation rules of a given CA as 'genotype', and the resulting spatiotemporal pattern as 'phenotype', the authors propose an analogy between the topological form of the basin of attraction fields and the morphology of an organism. This analogy is again not to be taken very seriously, only as a loose metaphore, since the mechanisms underlying the morphogenesis of an organism and that of a CA are in many respects different. Still, the melody is the same.

Tamás Czárán

Ecological Modelling Research Group,
Hungarian Academy of Sciences and ELTE,
H-1083 Budapest, Ludovika tér 2, Hungary

References

- 1 von Neumann, J. (1966) *Theory of Self-reproducing Automata* (edited and completed by A. W. Burks), University of Illinois Press
- 2 Conway, J.H. (1970) in *Mathematical Games* (Gardner, M., ed.), pp. 120–123, Scientific American
- 3 Kauffmann, S.A. (1984) *Physica D* 10, 52–58
- 4 Li, W. and Packard, N.H. (1990) *Complex Syst.* 4, 281–297