ANALYSIS OF THE BEHAVIOUR OF KAUFFMAN BINARY NETWORKS—I. STATE SPACE DESCRIPTION AND THE DISTRIBUTION OF LIMIT CYCLE LENGTHS

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The basis of an analytical description of the behaviour of large random nets of binary elements of the type first investigated in detail by S. A. Kauffman is presented. It is shown that information about the network dynamics can be deduced from quite general considerations of the properties of the state transition graph and matrix. An expression for the matrix elements of the state transition matrix in terms of the Boolean function specification of the net is derived. Using these ideas the distribution of limit cycle lengths $l$ for a completely random net is calculated and shown to be $\propto 1/l$, a result which agrees well with experimental data.

1. Introduction. Numerous attempts have been made to apply concepts and properties of 'random networks' of various kinds to the understanding and simulation of aspects of the behaviour of biological systems. Of these attempts the work of Kauffman (1969a, b; and 1970a, b; 1971) stands out for the ingenuity and novelty of its approach, and most of all for the unexpected and surprising nature of its results. The central feature of this work, which is outlined in some detail in the next section of this paper, is the finding that large networks of binary elements, having literally astronomical numbers of possible states, exhibit remarkably restricted, ordered and stable behaviour without requiring any special organisation in their structure. They very rapidly enter stable limit cycles in their state space, the length of the limit cycles and the number of different limit cycles both being extremely small numbers when expressed as fractions of the total number of possible states.

Kauffman (1969a, b; 1970a) presented his original work in this area in terms of metabolic stability and epigenesis in genetic nets, making the plausible analogy between the known features of (at least bacterial) genetic
control systems (Jacob and Monod, 1961) and the formal ‘binary genes’ of his network. Quite impressive agreement between the behaviour of the model in this context and that of a very wide range of biological organisms was demonstrated by Kauffman (1969a) and further evidence of the generality of ‘Kauffman’s law’ (as it seems to have become!) has been given recently by Cavender (1977). However, it has also been clearly recognised by Kauffman and others that the underlying mathematical structure and properties of the Kauffman nets may well be relevant and useful in the development of theories of other aspects of biological systems, e.g. the ‘evolution’ of biological macromolecules from their precursors (Pattee, 1969), neural networks (Aleksander and Atlas, 1973), developmental biology (Kauffman, 1973) and biochemical control networks (Glass and Kauffman, 1973).

Unfortunately, despite the considerable initial interest, Kauffman’s work does not seem to have had as much impact on the development of theoretical biology as, in the present author’s opinion at least, it should have. Almost certainly this undesirable situation is not due to any lack of biological relevance of the basic model, but rather to what Goodwin (1976) describes as its ‘weakness in relation to the possibilities of mathematical analysis’. The two published attempts (Kauffman, 1971; Aleksander, 1973) to understand the origins and develop predictive models of Kauffman net behaviour have not been particularly successful in elucidating the general properties, although they have produced some useful concepts and insights.

In this and the following paper a formal analysis is presented which appears to provide a basis for a more detailed understanding of the Kauffman results than has hitherto been available. It differs fundamentally from the analyses presented so far in that it concentrates on understanding the system behaviour in terms of constraints imposed by topological features of the systems’ state space trajectories rather than in terms of actual structures in the network topology—the ‘forcing structures’ of Kauffman (1971) or the ‘live rings’ of Aleksander (1973). Although the present approach is initially more abstract it seems to provide a more useful conceptual framework in which to formulate the statistical and probabilistic descriptions which are unavoidable in analysing such large systems. Ultimately of course the two approaches should lead to the same goal.

2. Kauffman Nets—Definitions and Properties. A Kauffman net (see Figure 1) of size \( \mu \) and connectivity \( \kappa \) consists of \( \mu \) interconnected elements, each having \( \kappa \) inputs and one output. (The elements are described as ‘formal genes’ by Kauffman (1969a) but in view of the relevance of the model to systems other than genetic systems this restrictive nomenclature will be