A NOTE ON ABSTRACT RELATIONAL BIOLOGIES*

ROBERT ROSEN COMMITTEE ON MATHEMATICAL BIOLOGY THE UNIVERSITY OF CHICAGO

It is shown that the class of abstract block diagrams of $(\mathfrak{N},\mathfrak{R})$ -systems which can be constructed out of the objects and mappings of a particular subcategory \mathfrak{S}_0 of the category \mathfrak{S} of all sets depends heavily on the structure of \mathfrak{S}_0 , and in particular on the number of sets of mappings H(A,B) which are empty in \mathfrak{S}_0 . In the context of $(\mathfrak{N},\mathfrak{R})$ -systems, therefore, each particular category \mathfrak{S}_0 gives rise to a different "abstract biology" in the sense of Rashevsky. A number of theorems illustrating the relation between the structure of a category \mathfrak{S}_0 and the embeddability of an arbitrary mapping $\mathfrak{AE}\mathfrak{S}_0$ into an $(\mathfrak{R},\mathfrak{R})$ -system are proved, and their biological implication is discussed.

In previous work (Rosen, 1958a; 1958b; 1959) we have shown how to construct a class of metabolic models which we have called $(\mathfrak{N},\mathfrak{R})$ -systems, and with which we suppose the reader to be familiar. The definition of the abstract block diagram of a system of this type, as presented in Rosen 1958b, 1959, makes sense over an arbitrary subcategory \mathfrak{S}_0 of the category \mathfrak{S} of all sets. In our previous studies, we have always supposed a category \mathfrak{S}_0 to be given initially and held fixed throughout the discussion, and we then proceeded to investigate the properties of individual $(\mathfrak{N},\mathfrak{R})$ -systems formed from the objects and mappings in \mathfrak{S}_0 .

There are, however, problems of considerable biological interest which cannot be approached by means of "local" studies of this type. In the present note, we shall consider in detail one such question, which may roughly be stated as follows: under what conditions can an arbitrary component be embedded in an $(\mathfrak{A}, \mathfrak{R})$ -system?

This research was supported by the United States Air Force through the Air Force Office of Scientific Research of the Air Research and Development Command, under Contract No. AF 49(638)-917.

We shall see that problems of this nature depend very sensitively on the structure of the category in which we are working. In fact, we shall see that each subcategory \mathfrak{S}_0 of \mathfrak{S} gives rise to a different class of $(\mathfrak{M},\mathfrak{R})$ -systems, and thus to a different "abstract biology," in the sense of Rashevsky (1956, 1961). In the present context, it thus becomes clear that the relation between the structure of a category \mathfrak{S}_0 and the class of $(\mathfrak{M},\mathfrak{R})$ -systems which can be formed from the objects and maps of \mathfrak{S}_0 is one of the central problems in relational biology.

Let us now return to the question enunciated above, and let us proceed informally for a moment. Given a mapping $\alpha:A\longrightarrow B$ in an arbitrary but fixed subcategory \mathfrak{S}_0 of the category of all sets, what does it mean to say that α is embedded in an $(\mathfrak{M}, \mathfrak{R})$ -system? By definition, α must be a map in the abstract block diagram of an $(\mathfrak{M}, \mathfrak{R})$ -system, satisfying the axioms set down in Rosen 1959, p. 115. However, there remain two possibilities for the role played by α in an $(\mathfrak{M}, \mathfrak{R})$ -system: if the range B of α is of the form H(X, Y), where X and Y are objects in \mathfrak{S}_0 , then α may play the role of a "genetic" component; in our previous terminology, we may write $\alpha = \Phi_f$ for some "metabolic" mapping f of the system. If this is not the case, then α itself plays the role of a "metabolic" mapping f.

Let us first suppose that α is to play the role of a "metabolic" mapping f, and let us see under what circumstances we can find an $(\mathfrak{M},\mathfrak{R})$ -system (always constructed out of objects and maps in \mathfrak{S}_0) which contains f. By definition, we know that there must be a map Φ_f the range of which contains f. However, it may well be the case that in \mathfrak{S}_0 , every set of maps of the form H(X,H(A,B)) is empty. If this situation obtains, then it is clear that the mapping f can never be a "metabolic" mapping of an $(\mathfrak{M},\mathfrak{R})$ -system in the category \mathfrak{S}_0 .

Let us suppose, however, that at least one set of the form H(X, H(A, B)) is not empty in \mathfrak{S}_0 . If in particular we let X = B, and find that $H(B, H(A, B)) \neq \emptyset$ in \mathfrak{S}_0 , then f can be embedded into the $(\mathfrak{M}, \mathfrak{R})$ -system consisting of the pair of mappings $\{f, \Phi_f\}$, where $\Phi_f \in H(B, H(A, B))$. Thus, we see trivially that, if the set of maps of the form H(B, H(A, B)) is not empty, then any map $f: A \longrightarrow B$ can be embedded into an $(\mathfrak{M}, \mathfrak{R})$ -system.

On the other hand, if H(B, H(A, B)) is empty, but H(X, H(A, B)) is not empty for some object $X \in \mathcal{G}_0$, we can proceed by adjoining to f any mapping Φ_f in H(X, H(A, B)). The pair $\{f, \Phi_f\}$ is not now an $(\mathfrak{M}, \mathbb{R})$ -system, since the set of outputs of f does not provide inputs

to Φ_f . However, we may attempt to adjoin to the pair $\{f,\Phi_f\}$ some further mappings g, whose ranges provide appropriate inputs to Φ_f . In order to accomplish this, we must once again require that not all sets of the form H(Z,X) be empty in \mathfrak{S}_0 . If this condition is fulfilled, so that the appropriate mappings g can be found, we shall have to adjoin appropriate mappings Φ_g . Once again it may be the case that not all the Φ_g receive an input from the "metabolic" mappings f, g, so that we may have to adjoin further "metabolic" mappings h (if this is possible in \mathfrak{S}_0), further "genetic" mappings Φ_h , and so on. Under what conditions can we be sure that this process always terminates to give us an $(\mathfrak{M}, \mathfrak{R})$ -system after a finite number of such adjunctions?

Next, let us turn to the case in which the initially given mapping $\alpha: A \longrightarrow B$ is to play the role of a "genetic" mapping. This means that B is of the form H(X,Y), where X, Y are objects in \mathfrak{S}_0 , as we noted earlier. If $Y \ne A$, however, we find ourselves back in precisely the same situation as has just been discussed; the details of this situation may therefore be left to the reader.

The heuristic discussion presented above leads us to expect that it is, in some sense, the relative abundance of empty sets of mappings in a category \mathfrak{S}_0 which limits the class of $(\mathfrak{M}, \mathfrak{R})$ -systems that can be formed from the objects and mappings in \mathfrak{S}_0 . Let us now attempt to see whether this expectation can be made precise.

Definition: A sequence A_1 , A_2 , A_3 , ... of objects in a category \mathfrak{S}_0 will be called *normal* if no pair A_i , A_{i+1} recurs infinitely often in the sequence. The category \mathfrak{S}_0 will be called *normal* if every normal sequence of objects in \mathfrak{S}_0 has the property that the associated sequence $H(A_1, A_2)$, $H(A_2, A_3)$, ... contains only a finite number of empty sets.

Theorem 1: If \mathfrak{S}_0 is a normal category, then every mapping $\alpha \in \mathfrak{S}_0$ can be embedded in an $(\mathfrak{M}, \mathfrak{R})$ -system in \mathfrak{S}_0 .

Proof: We begin by proving an auxiliary Lemma.

Lemma: If \mathfrak{S}_0 is normal, then to each object $X \in \mathfrak{S}_0$ there corresponds at least one object $Z \in \mathfrak{S}_0$ such that H(Z,X) is not empty.

Proof: Let Z_1 , Z_2 , Z_3 , ..., be a sequence of pairwise distinct objects in \mathfrak{S}_0 . Consider the sequence Z_1 , X, Z_2 , X, Z_3 , X, It follows immediately that not all the sets $H(Z_i, X)$ can be empty, and thus the Lemma follows. We note in passing that we have actually proved much more than is asserted in the Lemma, but since we shall not require the full generality which is obtainable, we shall not pursue the matter further here.

Let us now return to the proof of the main theorem. We suppose that the hypotheses enunciated above are satisfied, and that there exists a mapping $f: X_0 \longrightarrow Y_0$ in \mathfrak{S}_0 which cannot be embedded into an $(\mathfrak{M}, \mathfrak{R})$ -system in \mathfrak{S}_0 . (We shall consider here only the case in which f is a "metabolic" map; the case in which the given mapping is a "genetic" map differs from the "metabolic" situation only in minor details, and is left to the reader.) Since by hypothesis f is not embeddable into an $(\mathfrak{M}, \mathfrak{R})$ -system, we must have in particular

$$H(Y_0, H(X_0, Y_0)) = \emptyset.$$
 (1)

However, we know from our Lemma that there exists an object Y_1 in \mathfrak{S}_0 such that $H(Y_1, H(X_0, Y_0)) \neq \emptyset$. Hence to the given f, we can correspond a mapping $\Phi_f \in H(Y_1, H(X_0, Y_0))$. Our Lemma now tells us that there exists an object $X_1 \in \mathfrak{S}_0$ such that $H(X_1, Y_1) \neq \emptyset$. Let $g_1 \in H(X_1, Y_1)$.

Invoking our Lemma once again, we can find an object Y_2 in \mathfrak{S}_0 such that the set $H(Y_2, H(X_1, Y_1)) \neq \emptyset$. Let us observe, however, that we cannot have $Y_2 = Y_1$, for otherwise it is readily verified that the system of mappings

$$\{f, g_1, \Phi_f, \Phi_{g_1}\},\$$

where $\Phi_{g_1} \in H(Y_1, H(X_1, Y_1))$, would be an $(\mathfrak{M}, \mathfrak{R})$ -system containing f, contrary to our hypothesis. Hence we must have

$$H(Y_1, H(X_1, Y_1)) = \emptyset.$$
 (2)

Knowing that Y_2 is distinct from Y_1 , our Lemma assures us that there exists an object X_2 in \mathfrak{S}_0 such that $H(X_2, Y_2)$ is not empty. Let $g_2 \in H(X_2, Y_2)$. Once again, we notice that if the set $H(Y_2, H(X_2, Y_2))$ were not empty, we could find an element Φ_{g_2} in that set such that the system

$$\{f, g_1, g_2, \Phi_f, \Phi_{g_1}, \Phi_{g_2}\}$$

is an (M,R)-system containing f. Therefore we must have

$$H(Y_2, H(X_2, Y_2)) = \emptyset.$$
 (3)

Invoking our Lemma again, we can find an object $Y_3 \neq Y_2$ such that $H(Y_3, H(X_2, Y_2)) \neq \emptyset$, and an object X_3 such that $H(X_3, Y_3) \neq \emptyset$, and proceed exactly as before. We continue this process ad infinitum, constructing the objects X_n , Y_n in the obvious manner.

Consider now the sequence of objects

$$Y_0, H(X_0, Y_0), Y_1, H(X_1, Y_1), Y_2, H(X_2, Y_2), \dots$$
 (4)

which is a sequence of pairwise disjoint objects in \mathfrak{S}_0 . Comparing the relations (1), (2), (3), ... with the initial hypothesis on \mathfrak{S}_0 leads to an immediate contradiction, from which our theorem follows.

Theorem 1 may be regarded as an answer to the question, "when can an arbitrary mapping of a category \mathfrak{S}_0 be embedded into an $(\mathfrak{R},\mathfrak{R})$ -system over the category?" We might, however, have asked ourselves the more general question: given any arbitrary finite family of mappings of a category \mathfrak{S}_0 , under what conditions can this family be embedded into a (connected) $(\mathfrak{R},\mathfrak{R})$ -system over the category? It is by no means evident a priori that the embeddability of arbitrary single mappings implies the embeddability of finite families of mappings. However, in the present situation, we can readily verify that the technique employed in the proof of Theorem 1 can be modified to yield a proof of the more general

Theorem 2: Under the hypothesis of Theorem 1, if $\mathfrak{F} = \{\alpha_1, \alpha_2, \ldots, \alpha_n\}$ is a finite family of mappings in \mathfrak{S}_0 , there exists a connected $(\mathfrak{M}, \mathfrak{R})$ -system in which \mathfrak{F} can be embedded.

Proof: Suppose that no such $(\mathfrak{M}, \mathfrak{R})$ -system exists. Just as in the proof of Theorem 1 above, we begin by adjoining mappings to \mathfrak{F} in an attempt to make the augmented system \mathfrak{F}' take on the structure of an $(\mathfrak{M}, \mathfrak{R})$ -system. By hypothesis we know that \mathfrak{F}' is not an $(\mathfrak{M}, \mathfrak{R})$ -system, from which it follows as before that certain sets of mappings must be empty in \mathfrak{S}_0 . We then adjoin further mappings to \mathfrak{F}' to obtain a new augmented system \mathfrak{F}'' , which again cannot be an $(\mathfrak{M}, \mathfrak{R})$ -system, and from which we find a further collection of empty sets of mappings in \mathfrak{S}_0 . Proceeding in this manner, we shall ultimately be able to construct a sequence of objects in the category \mathfrak{S}_0 which violates our initial hypothesis on \mathfrak{S}_0 . The details of the argument are somewhat complex but involve no new principles, and are therefore left to the reader.

Let us note that the converse of Theorems 1 and 2 is false; that is, the embeddability of every mapping (or finite family of mappings) in a category \mathfrak{S}_0 into an $(\mathfrak{M},\mathfrak{R})$ -system over \mathfrak{S}_0 does not imply that \mathfrak{S}_0 satisfies the conditions of Theorem 1, nor even the weaker condition appearing as the conclusion of our Lemma above. However, certain instructive partial results in this direction may be stated. The following two results are typical; as they follow immediately from the definitions, the proofs are omitted:

Theorem 3: If every mapping $\alpha \in \mathfrak{S}_0$ is embeddable in an $(\mathfrak{M}, \mathfrak{R})$ system, and if A, B are objects in \mathfrak{S}_0 such that $H(X, H(A, B)) = \emptyset$ for each object $X \in \mathfrak{S}_0$, then $H(A, B) = \emptyset$.

Theorem 4: If every mapping $\alpha \in \mathfrak{S}_0$ is embeddable in an $(\mathfrak{M}, \mathfrak{R})$ -system, and if there exists an object $X \in \mathfrak{S}_0$ such that for every obobject Z we have $H(Z, X) = \emptyset$, then $H(X, H(A, B)) = \emptyset$ for every pair of objects A, B in \mathfrak{S}_0 .

In physical terms, these theorems assert that no "Garden of Eden" objects or mappings, which cannot be fabricated by the effective procedures available in the base category \mathfrak{S}_0 , can play a role in a theory of $(\mathfrak{M}, \mathfrak{R})$ -systems.

There is one further aspect of the influence of the structure of the base category on the embeddability of mappings of the category into (M.R)-systems which must be considered. Namely, given an arbitrary mapping a in the category, what can be said about how many mappings occur in the smallest (M, R)-system in which α can be embedded? It is readily seen that if \mathfrak{S}_0 is a category in which H(B, H(A, B)) is not empty for any pair of objects A, B in \mathfrak{S}_0 , then every mapping $f: A \longrightarrow B$ in the category can be embedded into an $(\mathfrak{M},\mathfrak{R})$ -system of the form $\{f,\Phi_f\}$, where we have $\Phi_f \in H(B,H(A,B))$. Conversely, if \mathfrak{S}_0 is such that for every pair A, B we have H(B, $H(A,B) = \emptyset$, then there can exist no $(\mathfrak{M},\mathfrak{R})$ -systems of the form $\{f, \Phi_f\}$, and the question as to the minimal size of an $(\mathfrak{A}, \mathfrak{R})$ -system containing a given mapping in \mathfrak{S}_0 is a highly non-trivial one. We can see roughly that the more empty sets of mappings there are in \mathfrak{S}_0 , the greater will be the size of the minimal $(\mathfrak{R},\mathfrak{R})$ -systems which can be formed over \mathfrak{S}_0 . Moreover, there will, in general, be a kind of "quantization" in the size of these (M,R)-systems, in the following sense: we know that, if \mathfrak{S}_0 satisfies the hypothesis of Theorem 1, then, given an arbitrary $(\mathfrak{R},\mathfrak{R})$ -system Λ and an arbitrary mapping $\alpha \notin \Lambda$ in \mathfrak{S}_0 , there exists (by Theorem 2) an $(\mathfrak{M}, \mathfrak{R})$ system Λ' such that the set of mappings $\{\alpha, \Lambda\}$ can be embedded into Λ' . If N, N' are the number of mappings in Λ , Λ' respectively, it may be possible to preassign an integer k such that we always have (N'-N) > k; moreover, k may be taken arbitrarily large by suitably choosing the category \mathfrak{S}_0 . It is clear, therefore, that the relation between the structure of a category \mathfrak{S}_0 and a number k of the type just described furnishes important information about the set of $(\mathfrak{M}, \mathfrak{R})$ -systems constructible in \mathfrak{S}_0 . It would be most instructive to be able to derive a relation between the number of empty sets in the category \mathfrak{S}_0 (for example by imposing a condition such as the hypothesis of Theorems 1 and 2 above) and the magnitude of k. No such results are presently available, although studies in this direction are currently in progress. It seems to be

crucial in such studies to take account not only of the number but also the *distribution* of the empty sets in \mathfrak{S}_0 , which is tantamount to putting a topology on \mathfrak{S}_0 .

We must now briefly discuss the biological significance of the results obtained above. First, we have seen that once a base category \mathfrak{S}_0 has been chosen, the class of $(\mathfrak{A},\mathfrak{R})$ -systems which can be formed from the objects and mappings in So is rigidly determined by the structure of \mathfrak{S}_0 . Although we have not explored the question in the present note, we can readily see that non-equivalent categories will in general give rise to different classes of (M, R)-In the terminology of abstract biology, this means that the class of relationally distinct unicellular systems depends on the nature of the category of discourse, and further serves as an index of the structure of that category. In the case of real biological organisms, the mappings must represent some type of physically effective processes, so that, following completely abstract studies of the type indicated above, it may be hoped that a properly instituted investigation of physically effective processes may throw some direct light on the class of organisms which are capable of existence.

In the same way, purely abstract questions concerning the embeddability of arbitrary mappings into $(\mathfrak{R},\mathfrak{R})$ -systems may ultimately have a considerable bearing on questions related to the origin of life. More generally, the relation between the structure of an abstract category and the associated class of $(\mathfrak{R},\mathfrak{R})$ -systems affords a natural tool for the ultimate study of protobionts and elementary biological forms whose existence at some stage in the transition from the inorganic to the organic world has repeatedly been postulated, but to which access by experimental or by previous theoretical approaches seems to be impossible. It becomes most important, therefore, to have at our disposal extensive results in abstract biologies of the type considered above, so that as information concerning the actual category of "physically effective" processes becomes available, we may be able to obtain useful insights into fundamental questions of organic structure.

The author wishes to thank Dr. Peter H. Greene for pointing out a number of inaccuracies in the first draft of the manuscript.

LITERATURE

Rashevsky, N. 1955. "Some Remarks on Topological Biology." Bull. Math. Biophysics, 17, 207-218.

- . 1956. "Contributions to Topological Biology: Some Considerations on the Primordial Graph and on Some Possible Transformations." Bull. Math. Biophysics, 18, 113-128.
- ____. 1961. "Abstract Mathematical Molecular Biology." Ibid., 23, 237-260.
- Rosen, R. 1958a. "A Relational Theory of Biological Systems." Bull. Math. Biophysics, 20, 245-260.
- _____. 1959b. "The Representation of Biological Systems from the Standpoint of the Theory of Categories." *Ibid.*, 20, 317-341.
- . 1959. "A Relational Theory of Biological Systems II." Ibid., 21, 109-128.

RECEIVED 10-11-61