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(M,R)-SYSTEMS AND THEIR REALIZATIONS

ABSTRACT. Robert Rosen's (M,R)-systems are a class of relational models that define organisms. The realization of relational models plays a central role in his study of life, itself. Biology becomes identified with the class of material realizations of a certain kind of relational organization, exhibited in (M,R)-systems. In this paper I describe several realizations of (M,R)-systems, and in particular alternate realizations of the replication component.

KEY WORDS: *Life Itself*, (M,R)-systems, realization, relational biology, Robert Rosen

1. INTRODUCTION

Robert Rosen introduced (M,R)-systems to the world in 1958, in his very first published scientific paper (Rosen, 1958) [M = metabolism, R = repair]. They began as a class of metaphorical, relational paradigms that define cells. A *cell* is (at least) a material structure that realizes an (M,R)-system. Note that the word "cell" here is taken in the generic sense of "autonomous life from". This class of relational cell models can just as well describe organisms, indeed all living systems. The two most important references on (M,R)-systems are Rosen (1971) and Rosen (1972). One should go back to these two papers for the fine nuances on the subject.

A reader familiar with Rosen's work will know what the *modelling relation* is, so I shall not explain it here. Read section 2.3 of *Anticipatory Systems* (Rosen, 1985) for a quick review. A *realization* of a formal system is, by definition, a natural system obtained from decoding that formal system. In other words, a natural system that is a [material] realization of a formal system has the latter as a model.

The realization of an (M,R)-system is a hard problem. It is also a central problem. This is because the crux of relational biology is *throw away the matter and keep the underlying organization*. So the building of realizations assumes the central role in the recapture of "matter from bauplan". Rosen himself has made several attempts in the realization of (M,R)-systems: for example Rosen (1971), Rosen (1973), and Chapter 17 of Rosen (2000). He has taken formal, dynamic, inverse, and synthetic approaches. In Rosen (1971) he wrote "we are nowhere near having anything like a solution", and in Chapter 17 of Rosen (2000) the conclusion was that the answer "takes a lot more than we presently have. That is why the problem is so hard, but also why it is so instructive."

The final section (11H) of Rosen's seminal work *Life Itself* (Rosen, 1991) is, indeed, entitled "Relational Biology and Its Realizations". There, Rosen summarizes the realization problem of relational biology this way:

> "Organization [in living systems] in its turn inherently involves *functions* and their interrelations; the abandonment of fractionability, however, means that there is no kind of 1 to 1 relationship between such relational, functional organizations and the structures which realize them. These are the basic differences between organisms and mechanisms or machines."

This lack of one-to-one correspondence between functions and structures is inherent in the nature of these two classes of alternate descriptions. A functional organization cuts across physical structures, and a physical structure is simultaneously involved in a variety of functional activities. So an (M,R)-system is not realized by identifying its components and maps in a 'concrete' biological example. To tackle the biological realization problem of (M,R)-systems, one ought not to be seeking physicochemical implementations of what the relations *are*, but ought instead to be seeking interpretations of what the relations *do*. In the present paper, I journey on this path.

In the following sections I shall construct three different replication maps in (M,R)-systems, and describe how each may be realized in biological terms. (The mathematical settings are explained in appendices at the end of the paper.) I will then show, in Section 5, how these three categories of maps may be represented in relational diagrams that summarize graphically the entailment patterns of (M,R)-systems.

2. REPLICATION AS AN INVERSE EVALUATION MAP

More for the notations than for the details, I need to give a description of Rosen's (M,R)-systems. But instead of putting it in the main body of this paper, I am providing their brief introduction in Appendix A. Readers not familiar with the subject should review Appendix A before continuing here. I replicate the following four lines from Appendix A for further reference:

$$\text{(M,R)-system} \quad A \xrightarrow{f} B \xrightarrow{\Phi} H(A,B) \tag{1}$$

$$\text{Metabolism [enzyme]} \quad f: A \to B \quad f \in H(A,B) \tag{2}$$

$$\text{Repair [gene]} \quad \Phi : B \to H(A,B) \quad \Phi \in H(B, H(A,B)) \tag{3}$$

$$\begin{gathered}\text{Replication} \quad \beta : H(A,B) \to H(B,H(A,B)) \\ \beta \in H(H(A,B), H(B, H(A,B)))\end{gathered} \tag{4}$$

Note no "inverse" is mentioned in Appendix A. I have used a generic symbol β for the replication map. There are many ways to construct β from nothing else but what are already in the arrow diagram (A.1) = (1). Rosen has always used the simplest way, chosen his replication map β to have domain $Y = H(A,B)$, and made it an inverse evaluation map. I shall explore other ways presently. True to the spirit of relational biology, we must recognize that the most important aspect of a replication map is *not* its *form*, i.e. not the exact details of how the map is defined. Rather, the most important is its *function*, that it needs to produce repair functions Φ, which belong to the hom set $H(B,H(A,B))$. Therefore the codomain of a replication map β must be $H(B,H(A,B))$.

Here is how one constructs Rosen's β. An element $b \in B$ defines an "evaluation map"

$$\hat{b} \in H(H(B, H(A,B)), H(A,B)) \tag{5}$$

by

$$\hat{b}(\Phi) = \Phi(b). \tag{6}$$

The map $\alpha : b \mapsto \hat{b}$ defines an embedding of B into the set of functions $H(H(B,H(A,B)),H(A,B))$. Rosen mentioned (for example in Rosen (1972)) that this “is the abstract version of the familiar embedding of a vector space into its second dual space”. In Appendix B, I further explore this concept.

The function $\hat{b}$ is invertible if it is monomorphic; viz. for every pair of repair maps Φ_1, $\Phi_2 \in H(B,H(A,B))$,

$$\hat{b}(\Phi_1) = \hat{b}(\Phi_2) \Rightarrow \Phi_1 = \Phi_2; \tag{7}$$

i.e.

$$\Phi_1(b) = \Phi_2(b) \Rightarrow \Phi_1 = \Phi_2. \tag{8}$$

This implication (8) is a condition on the repair maps $\Phi \in H(B,H(A,B))$: if two repair maps agree at b, then they must agree everywhere. In other words, a repair map Φ [gene] is uniquely determined by its one value $\Phi(b) \in H(A,B)$ [enzyme]. This result maybe regarded as the abstract version of the *one-gene-one-enzyme hypothesis*. These are essentially the “stringent but not prohibitively strong conditions” required to make the inverse evaluation map a replication map with nothing but the ingredients of the arrow diagram (1).

Note the inverse evaluation map $\hat{b}^{-1}$ maps thus:

$$\hat{b}^{-1} : H(A,B) \to H(B,H(A,B)), \tag{9}$$

$$\hat{b}^{-1}(\Phi(b)) = \Phi. \tag{10}$$

It takes one image value $\Phi(b) \in H(A,B)$ to the whole function $\Phi \in H(B,H(A,B))$: this is the sense in which it “replicates”. But the stringent condition requiring that a repair map Φ to be uniquely determined by the one value $\Phi(b)$ in its range, neatly overcomes this $\Phi = \Phi(b)$ identification problem!

Before I leave this section, let me paraphrase the dictum of relational biology in the current context. When the replication map β has domain $Y = H(A,B)$ and we construct it as an inverse evaluation map, the important aspect is *not* that it *is* an inverse evaluation map. The fact that Rosen’s regular example has $\beta = \hat{b}^{-1}$ is entirely incidental. Rather, the important aspect is that this particular replication map *has the property* that it is uniquely determined by one value in its range. The crux is $\beta : \Phi(b) \mapsto \Phi$. There are other ways to define $\beta \in H(H(A,B),H(B,H(A,B)))$ such that $\beta : \Phi(b) \mapsto \Phi$; choosing $\beta = \hat{b}^{-1}$ is just the simplest way, one specific example of how such a map may arise naturally. In other words, the emphasis is not on replication's *efficient cause*, but on its *final cause*. I refer the reader to Rosen (1991, especially Sections 3E, 3G, 5H, & 5I) for a thorough discussion of these Aristotelian concepts. So when one seeks material realizations of the replication map thus constructed, the question to ask is not, say, "What is the physical interpretation of the inverse evaluation map?" One ought to ask, say, "What biochemical processes are uniquely determined by their products?" One possible answer here is that one gene controls the production of one enzyme, or conversely, a gene is uniquely determined by which enzyme it produces. This is, of course, the one-gene-one-enzyme hypothesis.

3. REPLICATION AS A CONJUGATE ISOMORPHISM

Recall that a replication map must have as its codomain the hom set $H(B,H(A,B))$ to which repair functions Φ belong, whence it must be of the form

$$\beta : Y \to H(B, H(A, B)) \tag{11}$$

for some set Y. How many choices does one have for Y? The most important feature of an (M,R)-system is the closure of its entailment structure. This means one must choose Y to be a set already present in form (1). So one may have $Y = A$, B, or $H(A,B)$.

In the previous section, the choice is $Y = H(A,B)$, and it leads to Rosen's replication map β as an inverse evaluation map. The evaluation map from linear algebra inspires, for an element $b \in B$, through the natural transformation α: $B \to H(H(B,H(A,B)), H(A,B))$, the (M,R)-system's evaluation map

$$\begin{aligned} \alpha(b) = \hat{b} &\in H(H(B, H(A, B)), Y) \\ &= H(H(B, H(A, B)), H(A, B)) \end{aligned} \tag{12}$$

(cf. (5)) defined by

$$\alpha(b) = \hat{b} : \Phi \mapsto \Phi(b) \tag{13}$$

(cf. (6)). The replication map is then defined as its inverse

$$\begin{aligned} \beta = \hat{b}^{-1} &\in H(Y, H(B, H(A, B))) \\ &= H(H(A, B), H(B, H(A, B))) \end{aligned} \tag{14}$$

(cf. (9)), which is required to exist by the "stringent but not prohibitively strong conditions". The resulting replication map

$$\beta = \hat{b}^{-1} : \Phi(b) \mapsto \Phi \tag{15}$$

(cf. (10)) identifies the repair map Φ with one value $\Phi(b)$ in its *range*, which is the chosen $Y = H(A,B)$. Note that this construction hinges on the definition of the evaluation map (13); the rest follows as a matter of course. Note also that the evaluation map in linear algebra is

$$\hat{x} \in X^{**} = L(X^*, F) = L(L(X, F), F), \tag{16}$$

(cf. (B.7)), while the evaluation map here is

$$\hat{b} \in H(H(B, H(A, B)), H(A, B)). \tag{17}$$

Comparing (16) and (17), we thus see that the encoding of an (M,R)-system into linear algebra is $B \mapsto X$ and $H(A, B) \mapsto F$.

Now let me try an alternate construction and choose $Y = B$. I would like to have

$$\begin{aligned} \text{Replication } \beta &: B \to H(B,H(A,B)) \\ \beta &\in H(B,H(B,H(A,B))) \end{aligned} \tag{18}$$

So I ought to seek a well-defined function, an embedding of B into $H(B,H(A,B))$, that maps

$$\beta : b \mapsto \Phi \tag{19}$$

for $b \in B$. The repair map Φ is hence identified with one value b in its *domain*, which is the chosen $Y = B$ here.

Where in mathematics does one encounter a map that naturally identifies a function with one value in its domain? Again, linear algebra provides the analogy. The embedding is a little more straight-forward in this case than before, and the price to pay is that correspondingly the objects of the category need a little more structure. This time one turns to the category of Hilbert spaces. A Hilbert space X is isomorphic, under the *conjugate isomorphism*, to its dual space $X^* = L(X,F)$, the space of all continuous linear functionals on X. (See Appendix B for definitions of some of these terms.) I defer to Appendix C to further explore this concept.

My required embedding of B into $H(B,H(A,B))$, map (19), may be considered as the abstract version of the conjugate isomorphism of a Hilbert space onto its dual space. For $b \in B$, let Φ be the image of b under the conjugate isomorphism γ_B from to B to $H(B,H(A,B))$, i.e. $\Phi = \gamma_B(b) = \Lambda_b \in H(B,H(A,B))$, defined by

$$\Phi(x) = \Lambda_b(x) = \langle x, b \rangle \in H(A, B) \tag{20}$$

for all $x \in B$ (cf. (C.2) and (C.3)). The "generalized inner product" in (20) is a sesquilinear function

$$\langle \cdot, \cdot \rangle : B \times B \to H(A, B). \tag{21}$$

The conjugate isomorphism in Hilbert space theory is

$$\gamma_X \in L(X, X^*) = L(X, L(X, F)), \tag{22}$$

while the corresponding embedding here is

$$\gamma_B \in H(B, H(B, H(A, B))). \tag{23}$$

Comparing (22) and (23), we thus see that the encoding of an (M,R)-system into Hilbert spaces remains the same $B \mapsto X$ and $H(A, B) \mapsto F$ as before.

When we seek material realizations of the replication map here, the question to ask is neither "How may the conjugate isomorphism be interpreted in biological terms?", nor "Can anything biological possibly be encoded as a Hilbert space?" (although the latter question does have surprisingly positive answers; see the next paragraph). Instead of these efficient-cause questions, we should be posing final-cause ones. The requirement that a repair map Φ [gene] be uniquely determined by a metabolic product $b \in B$ in its domain may be realized thus. A metabolic product in fact determines the enzyme $f \in H(A,B)$ required in the biochemical reaction that produces it. This is the concept of *enzyme specificity*. The one-gene-one-enzyme hypothesis then completes the entailment path to the gene $\Phi \in H(B,H(A,B))$.

For $b \in B$ and $\Phi \in H(B,H(A,B))$, the functional representation $\Phi(b)$ is itself sometimes represented in bracket form $\langle b, \Phi \rangle$, whence this "generalized inner product" is a sesquilinear function

$$\langle \cdot, \cdot \rangle : B \times H(B, H(A, B)) \to H(A, B). \tag{24}$$

It is in this bracket form $\langle b, \Phi \rangle$ that (M,R)-systems are fully realized into the realm of enzyme catalysis. In Louie et al. (1982), using enzyme-substrate recognition as an example, a phenomenological calculus for recognition processes was developed. We first employed the Hilbert space $X = X^* = L^2$ of square-integrable functions. Then we specialized into the space of continuous functions $X = C(K)$ and its dual, the space of normalized functions of bounded variation $X^* = NBV(K)$, where K was a compact subset of Euclidean space. In this latter formulation, the recognition of a substrate $F \in C(K)$ by an enzyme $a \in NBV(K)$ resulted from the evaluation of a Stieltjes integral of the form

$$\langle F, a \rangle = \int_K F da. \tag{25}$$

In Louie and Somorjai (1984), Stieltjes integration was connected to differential geometry, when the protein backbone space curve of an enzyme molecule was represented by its complex curvature-and-torsion function. In these two papers, many formal features of a metabolism-repair-replication system were decoded and realized in biological terms. Multi-enzyme systems, cofactor, apoenzyme, holoenzyme, activation-inhibition, active-site location, etc., all have relational encodings. The reader is encouraged to seek out these two reports and explore.

Hilbert space theory is also the language of quantum mechanics, and forms the foundation of biological imaging. It would, however, be idle to enter here into a more detailed discussion of these, and indeed any other of its many biophysical applications. The intricate connections among (M,R)-systems, quantum mechanics, and tomography have been some of the topics discussed in the sequence of Richardson–Louie phenomenological calculus papers, most notably in Richardson and Louie (1983, 1986) and Louie (1983).

4. REPLICATION AS A SIMILARITY CLASS

The third and final choice for the domain of the replication map is $Y = A$. Now I would like to have

$$\begin{aligned} \text{Replication} \quad & \beta : A \to H(B, H(A, B)) \\ & \beta \in H(A, H(B, H(A, B))) \end{aligned} \tag{26}$$

I require an embedding of A into $H(B,H(A,B))$, that maps

$$\beta : a \mapsto \Phi \tag{27}$$

for $a \in A$. When I trace the path of the element $a \in A$ as it is mapped through the arrow diagram (1) of the (M,R)-system, I get

$$a \mapsto b = f(a) \mapsto \Phi(b) = \Phi(f(a)) = f. \tag{28}$$

So *formally*, from $\Phi(f(a)) = f$, I can write

$$\Phi = fa^{-1}f^{-1}. \tag{29}$$

This says Φ and a^{-1} are *similar* to each other; in other words, Φ is in the *similarity* class of a^{-1} (similarity being an equivalence relation).

I, however, still need a rigorous mathematical encoding of this formalism. This time, the analogy is provided in the algebra of linear operators. I defer the details to Appendix D. In mathematics, one tends not to distinguish between members of the same equivalence class, since they are "identical up to an equivalence relation". Instead of setting Φ to be *in* the *similarity class* of a^{-1}, one may simply define Φ to *be* the *similarity class* of a^{-1}. The embedding of A into $H(B, H(A, B))$, map (27), may then be defined as the generalized natural projection

$$\beta(a) = \pi_s(a^{-1}) = [fa^{-1}f^{-1}]_s = [a^{-1}]_s = \Phi \tag{30}$$

(cf, (D.6)). Thus the repair map Φ defined by (30) may be interpreted as a generalized inverse.

The repair map Φ is hence identified with, indeed anticipated by, one value a from the set A, which seems to have only a remote connection to it. The set A is not the domain of $\Phi \in H(B,H(A,B))$, and is only related to its codomain by being the domain of *members* of the latter. The material realizations of this particular replication map $\beta = \pi_s \circ (\cdot)^{-1} : A \to H(B, H(A, B))$ are not found in answers to the efficient-cause questions "What does a^{-1} mean when a is supposed to be a substrate of a metabolic reaction?" and "What does similarity have to do with biology?" (The answer to the latter question is in fact "a lot"; see Appendix D.) The final cause that a repair map is identified with an equivalence class of substrates may be realized thus. The concept of enzyme specificity applies just as well from substrates $a \in A$ to enzymes $f \in H(A,B)$ required in the biochemical reactions that metabolize them. The one-gene-one-enzyme hypothesis then again completes the entailment path to the gene $\Phi \in H(B, H(A,B))$. Also, because of the self-referencing nature of the map $\beta : a \mapsto [a^{-1}]_s$, the set of metabolism-repair-replication maps for this $Y = A$, (M,R)-system may be decoded into the set of pathways of *protein biochemistry*. In particular, the enzymes involved act on enzymes themselves, and may be realized among peptide synthases, protein polymerases, protein kinases, and peptidases.

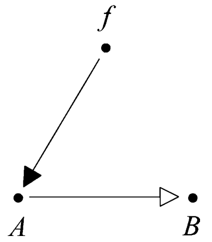
5. SUMMARY: RELATIONAL DIAGRAMS

Rosen introduced *relational diagrams in graph-theoretic form*, in Chapter 9 of *Life Itself* (Rosen, 1991), to provide a succinct representation of the entailment patterns in machines. Then in Chapter 10, he used them to represent the entailment patterns in organisms. By comparing the two classes of relational diagrams, the differences between machines and organisms became almost immediately apparent.

A simple mapping

$$f : A \to B \tag{31}$$

has the relational diagram



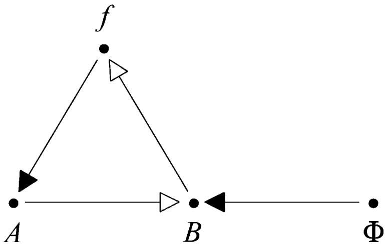
(32)

where a hollow-headed arrow denotes the *flow* from input [afferent; material cause] in A to output [efferent; product] in B, and a solid-headed arrow denotes the induction or generation of this flow by the *processor* [efficient cause] f. When (unnecessarily) interpreted in completely mechanistic terms, the flow is the *software*, and the processor is the *hardware*.

The (M,R)-systems of form (1), showing the metabolism and repair components,

$$A \xrightarrow{f} B \xrightarrow{\Phi} H(A, B) \tag{33}$$

is then an abbreviation of

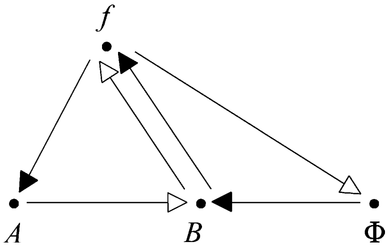


(34)

With replication as an inverse evaluation map, $\beta = \hat{b}^{-1}$, the "standard" three-component (M,R)-system

$$A \xrightarrow{f} B \xrightarrow{\Phi} H(A,B) \xrightarrow{\beta} H(B, H(A,B)) \tag{35}$$

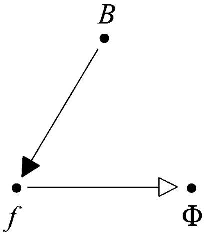
is an abbreviation of



(36)

(My diagrams (32), (34), and (36) are diagrams [10C.1], [10C.3], and [10C.6] in Rosen, 1991.)

I am now going to propose some modifications to these relational diagrams. There is a bit of notational inconsistency, when A and B are sets, and f and Φ are elements. The map

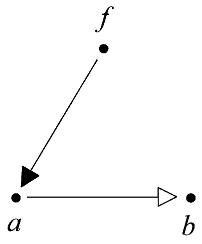


(37)

in (36) has a set initiating a solid-headed arrow. The efficient cause, the initiating vertex of a solid-headed arrow, has to be an element, not a set (when the object is a single map rather than a family of maps). On the other hand, the domain and codomain, the terminating vertices of the solid-headed and hollow-headed arrows respectively, are established in (32) as sets, not elements. To overcome this, instead of the "morphism: domain → codomain" version of the map (31), I use the element-chasing version

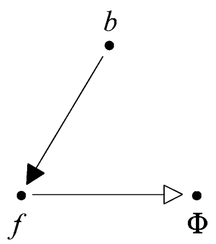
$$f : a \mapsto b, \tag{38}$$

(See Appendix A.), and the corresponding relational diagram changes from (32) to



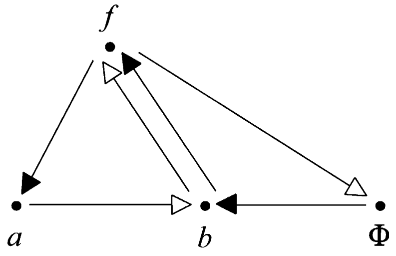
(39)

Similarly, diagram (37) may be rewritten as



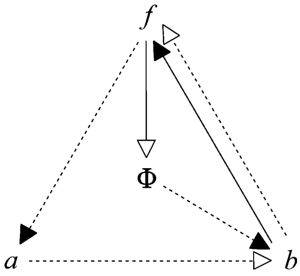
(40)

Then (36) may replaced by its element-chasing version



(41)

Next, in order to emphasize the various versions of the replication map we have studied, I am going to use a dashed line for the arrows of metabolism and repair, and leave the solid line for just the arrows of replication. I am also getting rid of the dots that represent the vertices. In addition, I am changing the geometry of the graphs, enclosing the repair map Φ within. In this way, I have a graphic representation of the metabolism component as the abstract equivalent of “cytoplasm”, and the genetic component as the abstract counterpart of “nucleus”. With all these changes, diagram (41) becomes



(42)

Note that this diagram represents the entailment pattern of an (M,R)-system of which the replication map is $\beta : H(A,B) \to H(B, H(A,B))$, i.e.

$$\beta : f \mapsto \Phi; \tag{43}$$

whence comes the flow

$$f \text{———▷} \Phi. \tag{44}$$

The fact that $\beta = \hat{b}^{-1}$ means β is uniquely determined by b; the efficient cause (processor)

$$\beta \text{———►} f \tag{45}$$

may, therefore, be “internalized” into

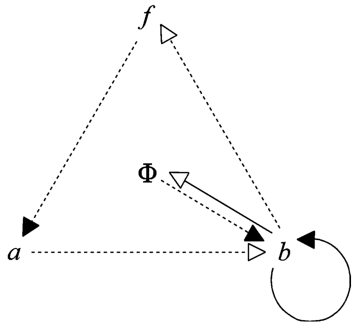
$$b \text{———►} f. \tag{46}$$

This is the way the efficient cause of the replication map (43) is entailed within, hence the path is closed.

When the replication map is a conjugate isomorphism, $\beta = \gamma_B$, the (M,R)-system is

$$\begin{tikzcd}
A \arrow[r, "f"] & B \arrow[r, "\Phi"] \arrow[d, "\beta"] & H(A,B) \\
& H(B, H(A,B)) &
\end{tikzcd} \tag{47}$$

and the relational diagram is



(48)

In this (M,R)-system, the replication map is $\beta : B \to H(B, H(A, B))$ with

$$\beta : b \mapsto \Phi, \tag{49}$$

hence the flow is

$$b \longrightarrow\!\!\triangleright\ \Phi. \tag{50}$$

The efficient cause, i.e. the replication processor, is

$$\beta \longrightarrow\!\!\blacktriangleright\ b. \tag{51}$$

Because the conjucate isomorphism $\beta = \gamma_B$ identifies b with $\beta(b) = \gamma_B(b) = \Lambda_b$, (51) may be internalized into the self-referencing

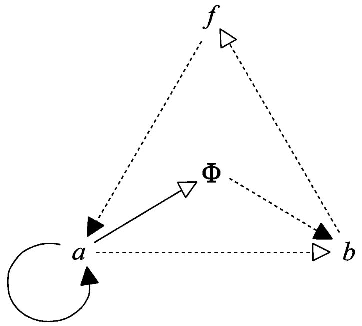
$$b \longrightarrow\!\!\blacktriangleright\ b. \tag{52}$$

Thus this (M, R)-system with replication map (49) is also closed to efficient causation.

When the replication map is a similarity class, $\beta = \pi_s \circ (\cdot)^{-1}$, the (M,R)-system is

$$\begin{tikzcd}
A \arrow[r, "f"] \arrow[d, "\beta"] & B \arrow[r, "\Phi"] & H(A, B) \\
H(B, H(A, B)) & &
\end{tikzcd} \tag{53}$$

and the relational diagram is



(54)

In this (M,R)-system, the replication map is $\beta : A \to H(B, H(A, B))$ with

$$\beta : a \mapsto \Phi, \tag{55}$$

and flow from material cause to product

$$a \relbar\joinrel\relbar\joinrel\rhd \Phi. \tag{56}$$

The efficient cause is

$$\beta \relbar\joinrel\relbar\joinrel\blacktriangleright a. \tag{57}$$

Because the similarity class $\beta = \pi_s \circ (\cdot)^{-1}$ identifies a with $\beta(a) = \pi_s(a^{-1}) = [a^{-1}]_s$, (57) may be internalized into the self-referencing processor

$$a \relbar\joinrel\relbar\joinrel\blacktriangleright a. \tag{58}$$

This is how this final (M,R)-system with replication map (55) is also closed to efficient causation.

6. POSTLUDE

In Rosen (1971), he listed three basic kinds of problems arising in the study of (M,R)-systems:

> "a. To develop the formal properties of such systems, considered in the abstract, and interpret them in biological terms;
> b. To determine the methods by which the abstract organization which defines the (M,R)-system may be realized in concrete terms;
> c. To determine whether a particular concrete biological system is in fact a realization of an (M,R)-system (i.e. to identify the functional components in a real biological system); this is basically the inverse problem to (b)."

And he wrote:

> "Almost all of my published scientific work has arisen from a consideration of these three problems, although this is perhaps not always immediately apparent."

This last statement is in fact as true today, when we study Rosen's whole lifetime's work, as it was when he wrote it in 1971.

Robert Rosen's bibliography includes over 200 papers, many volumes in theoretical biology that he edited (frequently with his own contributed articles), and six books of which he is the sole author. Among these six books, the first two (Rosen, 1967, 1970) are textbooks based on his lecture notes in mathematical biology. The sixth book (Rosen, 2000), a collection of essays published posthumously, is a supplement to book five. Books three to five are research monographs, and are what I would consider the "Rosen Trilogy", the embodiment of his lifetime's work. Part II, *Anticipatory Systems* (Rosen, 1985), sprang forth a whole new subject area of scientific investigations that bears its title. Part III, *Life Itself* (Rosen, 1991), is an iconoclastic masterpiece that reaches far beyond the domains of mathematics and biology. Part I, *Fundamentals of Measurement and Representation of Natural Systems* (Rosen, 1978), however, has received relatively little attention. But, as its title suggests, the book actually lays the foundation of Rosen's line of investigation of natural systems. So "Part I" is an essential component in the Rosen canon.

"Part I" also contains numerous suggestions for further development. When I became Robert Rosen's graduate student in 1979, he recommended that I first read his then-newly published book. My own doctoral dissertation in 1981 (published as Louie, 1985) is a presentation of the category-theoretic roots of system analysis in connection with investigations into relational biology. This topic was suggested on p.127 of "Part I".

Rosen concludes section 10C, "Relational Models of Organisms", of Rosen (1991) thus (His diagram [10C.6] is my diagrams (36) hence (42) above.):

> "I am asserting, then, that biology as a science is concerned with those material systems that realize an abstract block diagram like [10C.6]. Some of the properties of any such system arise entirely from the fact that it realizes the diagram; others arise from *how* it realizes the diagram; others will depend on both. All of these are, of course, embodied in the structure of the category of all its models. Thus, from our present vantage point, biology comprises two dual aspects: (1) the class

of all material systems that realize a certain kind of relational structure, and (2) given any such, the structure of the category of *all* its models. The two together embody what Rashevsky called "the unity of the organic world as a whole." It is a large and daunting thing."

I would hope that the present paper provides some illumination on our journey of exploration of this large and daunting thing.

APPENDIX A: A BRIEF INTRODUCTION TO (M,R)-SYSTEMS

The simplest (M,R)-system may be represented by the diagram

$$A \xrightarrow{f} B \xrightarrow{\Phi} H(A,B) \tag{A.1}$$

Note the adjective *simplest* here. This form (A.1) was what Rosen used in almost all of his discussions on (M,R)-systems. But remember that a general (M,R)-system is actually a network of metabolism and repair components. It is true that form (A.1) captures the essence of all (M,R)-systems, and indeed it is possible in principle to reduce every abstract (M,R)-system to this simple form by making A, B, and f sufficiently complex. One must, nevertheless, not lose sight of the network aspect of (M,R)-systems. See Rosen (1972), in particular.

There are three ways to show the function (or *morphism* in categorical language) f with its domain A and codomain B:

$$A \xrightarrow{f} B \tag{A.2}$$

$$f: A \to B \tag{A.3}$$

$$f \in H(A,B) \tag{A.4}$$

I use them interchangeably. Sometimes it is useful to trace the path of an element as it is mapped. If $a \in A$ and $b = f(a) \in B$, I use the "maps to" arrow (note the short vertical line at the tail of the arrow) and write

$$f: a \mapsto b. \tag{A.5}$$

In form (A.1), the function f represents metabolism [enzyme]:

$$\text{Metabolism} \quad f: A \to B \quad f \in H(A,B) \tag{A.6}$$

The function Φ represents a repair [gene]. It repairs the metabolism function, in the sense that since its codomain is $H(A,B)$, it may be considered as a function that creates new copies of f.

$$\text{Repair} \quad \Phi : B \to H(A,B) \quad \Phi \in H(B, H(A,B)) \tag{A.7}$$

What if the repair components themselves need repairing? New functions representing replication (i.e. that serve to replicate the repair, or genetic, components) may be defined. A replication map must have as its codomain the hom set $H(B,H(A,B))$ to which repair functions Φ belong, whence it must be of the form

$$\beta : Y \to H(B, H(A,B)) \tag{A.8}$$

for some set Y.

For the convenience of iterative combination (discussed immediately below), one may choose $Y = H(A,B)$; then

$$\beta : H(A,B) \to H(B, H(A,B)). \tag{A.9}$$

$$\begin{aligned} \text{Replication } &\beta : H(A,B) \to H(B,H(A,B)) \\ &\beta \in H(H(A,B), H(B,H(A,B))) \end{aligned} \tag{A.10}$$

The morphism (A.9) may be combined with the second morphism in (A.1) to give a new (M,R)-system from the old one; viz.

$$B \xrightarrow{\Phi} H(A,B) \xrightarrow{\beta} H(B, H(A,B)) \tag{A.11}$$

which has the property that the "metabolic" part of system (A.11) is the "repair" part of system (A.1), and the "repair" part of system (A.11) is the "replication" part of system (A.1) (i.e. form (A.9)). Indeed, one may sequentially extend this formalism *ad infinitum*, the next system being

$$H(A,B) \longrightarrow H(B,H(A,B)) \longrightarrow H(H(A,B),H(B,H(A,B))). \tag{A.12}$$

The arrow diagrams may be extended on either side, leftward as well as rightward above.

If this were all there is to it with (M,R)-systems, it would have been pretty pointless. The magic of an (M,R)-system is that the replication-function (A.9) is already entailed in the original form (A.1). On the basis of what are already present in (A.1), "under stringent but not prohibitively strong conditions, such replication essentially comes along for free." [I explore what these conditions are back in the main body of this paper.] So no infinite sequence of arrows here; arrow diagram (A.1) alone suffices.

Rosen's answer to the question "What is life?" is given in Chapter 10 of *Life Itself* (Rosen, 1991): "A material system is an organism if, and only if, it is closed to efficient causation." An (M,R)-system is a relational model of a living organism that captures this necessary and sufficient condition: the replication function (A.9) is entailed in the sense of efficient cause entirely in the original form (A.1). In other words, an equivalent form of Rosen's answer is: "A material system is an organism if, and only if, it possesses an (M,R)-system as its relational model."

APPENDIX B: REFLEXIVITY

Rosen usually (for example in Rosen (1972)) constructs his "evaluation map" in two steps. He would begin with two arbitrary sets X and Y, and then define for each element $x \in X$ a mapping

$$\hat{x} : H(X, Y) \to Y \tag{B.1}$$

by

$$\hat{x}(f) = f(x) \tag{B.2}$$

for every $f \in H(X,Y)$. Then he would put $X = B$ and $Y = H(A,B)$. An element $b \in B$ thus defines an evaluation map

$$\hat{b} \in H(H(B, H(A, B)), H(A, B)) \tag{B.3}$$

by

$$\hat{b}(\Phi) = \Phi(b) \tag{B.4}$$

for $\Phi \in H(B,\ H(A,B))$. Lines (B.3) and (B.4) are, in Section 2 of this paper, my Lines (5) and (6), with which I define the evaluation map in one single step.

The map $x \mapsto \hat{x}$ that sends an element to its corresponding evaluation map (B.2) defines an embedding of X into $H(H(X,Y),Y)$ It is analogous to *the embedding of a vector space into its second dual space*. In this Appendix B, we shall see how. The main subject here is linear algebra; two standard references are Halmos (1958) and

Hoffman and Kunze (1971). The counterpoint of reflexivity is found in the topic of functional analysis; two good references are Brown and Page (1970) and Rudin (1973). The definitive reference on our metalanguage of category theory is Mac Lane (1978); and for a simple and concise introduction one may consult Louie (1985).

Let X and Y be two vector spaces over the field F. We shall restrict F to either the real field $\mathbb{R}$ or the complex field $\mathbb{C}$. The hom set from X to Y in the category of vector spaces consists of linear transformations, and is denoted $L(X,Y)$ (as opposed to the hom set $H(X,Y)$ of mappings when X and Y are just sets). Note that $L(X,Y)$ is itself a vector space over F. Also, the scalar field F is a one-dimensional vector space over itself, so we may speak of $L(X,F)$. An element of $L(X,F)$, a linear transformation of X into F, is called a *linear functional*. This special vector space $L(X,F)$ is called the *dual space* of X; and we write X^* in place of $L(X,F)$.

The concept of "dual" applies to linear transformations as well. For any linear transformation $T : X \rightarrow Y$ one may define a linear transformation $T^* : Y^* \rightarrow X^*$ by

$$T^*(g) = g \circ T \tag{B.5}$$

for every $g \in Y^*$, or diagrammatically

$$\begin{tikzcd} X \arrow[rr, "T"] \arrow[dr, "T^*(g)"'] & & Y \arrow[dl, "g"] \\ & F & \end{tikzcd} \tag{B.6}$$

The linear transformation $T^* \in L(Y^*,X^*)$ is called the *dual transformation* of $T \in L(X,Y)$.

Let D be the operation of forming the dual space and the dual transformation. In other words, define $D(X) = X^*$ for each vector space X, and $D(T) = T^* \in L(Y^*,X^*)$ for each linear transformation $T \in L(X,Y)$. Then D is a *contravariant functor* on the category of vector spaces and linear transformations, called the *dual functor*. [It is contravariant because $D(T) \in L(D(Y),D(X))$; if it were $D(T) \in L(D(X),D(Y))$, D would be a *covariant* functor.]

The dual process may be iterated. Since X^* is itself a vector-space, we may consider its own dual. For simplicity we write X^{**} in place of $(X^*)^*$, and we call X^{**} the *second dual* (*space*) of X. Note that an element of X^{**} is a "linear functional of linear fuctionals",

$X^{**} = L(L(X,F),F)$. Similarly, the second dual-transformation of $T \in L(X,Y)$ may be defined as $T^{**} \in L(X^{**},Y^{**})$.

Repeated applications of the dual operation on a given vector space X result in a sequence of vector spaces X, X^*, X^{**}, X^{***}, ... If X is a *finite-dimensional* vector space over F, then each vector space of the sequence is finite-dimensional and has the same dimension as X. This means they are all isomorphic (because each one is isomorphic to F^n, where n is the dimension). There does not exist, however, any "canonical" isomorphism from X to X^* (unless X has certain additional algebraic structures – see Appendix C).

But from X to its second dual X^{**} (where X is still a finite-dimensional vector space over the field F), there is an isomorphism that distinguishes itself from all the others. Define for each element $x \in X$ a mapping

$$\hat{x} : X^* \rightarrow F \tag{B.7}$$

by

$$\hat{x}(f) = f(x) \tag{B.8}$$

for every $f \in X^*$. ($\hat{x} \in X^{**}$ is, of course, the now familiar evaluation map.) The mapping

$$\alpha_X : X \rightarrow X^{**} \tag{B.9}$$

defined by

$$\alpha_X(x) = \hat{x}, \tag{B.10}$$

i.e.

$$\alpha_X : x \mapsto \hat{x}, \tag{B.11}$$

is an isomorphism, called the *natural isomorphism* between X and X^{**}. For every linear transformation $T : X \rightarrow Y$, we have

$$T^{**} \circ \alpha_X = \alpha_Y \circ T, \tag{B.12}$$

i.e. the diagram

$$\begin{tikzcd} X \arrow[r, "T"] \arrow[d, "\alpha_X"'] & Y \arrow[d, "\alpha_Y"] \\ X^{**} \arrow[r, "T^{**}"] & Y^{**} \end{tikzcd} \tag{B.13}$$

commutes.

The *second dual functor* $D^2 = D \circ D$ is a covariant functor on the category of vector spaces defined by $D^2(X) = X^{**}$ and $D^2(T) = T^{**}$. Let the identity functor be denoted by I ; i.e. $I(X) = X$ and $I(T) = T$. Then diagram (B.13) may be rewritten as

$$\begin{tikzcd} I(X) \arrow[r, "I(T)"] \arrow[d, "\alpha_X"'] & I(Y) \arrow[d, "\alpha_Y"] \\ D^2(X) \arrow[r, "D^2(T)"] & D^2(Y) \end{tikzcd} \tag{B.14}$$

Thus the natural isomorphism may be regarded as a morphism $\alpha : I \mapsto D^2$ of functors. It is "natural", therefore, in the sense of category theory, that it is a *natural transformation.*

Each finite-dimensional vector space X can thus be identified with its second dual X^{**}, and consequently $T = T^{**}$ for each linear transformation $T : X \to Y$ of finite-dimensional vector spaces. Therefore in the sequences

$$X, X^*, X^{**}, X^{***}, \ldots$$

$$T, T^*, T^{**}, T^{***}, \ldots$$

one needs only consider the first pairs of terms X, X^* and T, T^*. The remaining ones, being *naturally* isomorphic copies, may be identified with them. [The first two members of the hierarchy suffice: readers familiar with (M,R)-systems will notice the analogy here.]

We make another remark before leaving *finite-dimensional* vector spaces. From the fact that X and its second dual X^{**} have the same finite dimension it follows that they are isomorphic; i.e. there exists an isomorphism $\phi : X \to X^{**}$. This unspecified isomorphism, however, may not satisfy the condition that is satisfied by the *natural* isomorphism when $\phi = \alpha_X$, that

$$(\phi(x))(f) = f(x) \tag{B.15}$$

for all $x \in X$ and $f \in X^*$.

When the vector space X is *infinite-dimensional*, the mapping α_X defined in (B.10) is still injective, and it still satisfies (B.12) (and so the arrow diagram (B.13) still commutes). But the range of α_X may not be all of X^{**}. This α_X is an embedding of X *into*, but not necessarily *onto*, its second dual space X^{**}. Since for an infinite-dimensional X, α_X is not necessarily an isomorphism from X to its codomain X^{**}, we change its name (from the "natural isomorphism") and call it the *canonical mapping* of X into X^{**}. The canonical mapping is an isomorphism of X *onto* its range, the subspace $\hat{X} = \{\hat{x} : x \in X\}$ of X^{**}. In general, however, $\hat{X} \neq X^{**}$.

A vector space X is called *reflexive* if and only if the canonical mapping $\alpha_X : x \mapsto \hat{x}$ maps X *onto* X^{**}, i.e. iff $\hat{X} = X^{**}$; in other words, iff the canonical mapping *is* the natural isomorphism between X and X^{**}. All finite-dimensional vector spaces are reflexive, but some infinite-dimensional vector spaces are not. Let me emphasize that for X to be reflexive, the existence of *some* isomorphism from X onto X^{**} is not enough: the vector space and its second dual must be *isomorphic under the canonical mapping*. It is possible for a vector space X to be isomorphic to its second dual X^{**} without being reflexive.

As a final note of this Appendix B, I would like to point out the difference between two kinds of inverse functions that one encounters when these linear algebra concepts extend to (M,R)-systems. Since the canonical mapping α_X is injective, its inverse exists with domain $\hat{X}$, defined by

$$\alpha_X^{-1}(\hat{x}) = x. \tag{B.16}$$

But note that

$$\alpha_X^{-1} \in L(\hat{X}, X). \tag{B.17}$$

It is completely different from the "inverse" of the evaluation map $\hat{x} = \alpha_X(x)$, which may not exist. Since $\hat{x} \in X^{**} = L(X^*, F)$ it is a linear transformation from (generally) a higher-dimensional space into a one-dimensional space, thus highly singular. To make it invertible, "stringent but not prohibitively strong conditions" are required, just like for its counterpart $\hat{b}$ in (M,R)-systems. Here, the conditions are restrictions on its domain and codomain. If the inverse exists, it would be a mapping

$$\hat{x}^{-1} \in L(F, X^*). \tag{B.18}$$

A comparison of (B.17) and (B.18) shows how different the two inverses are: there is no general entailment between the inverse of a function $[\alpha_X]$, and the inverse of one single image of that function, when that image $[\hat{x}]$ happens to be a function in its own right. The situation is summarized succinctly as

$$\exists \alpha_X^{-1}(\hat{x}) \quad \not\Leftrightarrow \quad \exists \hat{x}^{-1} = \Big(\alpha_X(x)\Big)^{-1}. \tag{B.19}$$

APPENDIX C: CONJUGATE ISOMORPHISM

The embedding of B into $H(B,H(A,B))$, map (19) in Section 3, maps

$$\beta : b \mapsto \Phi \tag{C.1}$$

for $b \in B$. It identifies the repair map $\Phi \in H(B,\ H(A,\ B))$ with one value b in its *domain* $Y = B$. This embedding is inspired by the *conjugate isomorphism of a Hilbert space onto its dual space*, the subject of this Appendix C.

Let X be a Hilbert space over the field F. As in Appendix B, we shall restrict F to either the real field $\mathbb{R}$ or the complex field $\mathbb{C}$. I shall not explain what a Hilbert space is here, other than mention in passing that it is a vector space equipped with an inner product, and is complete in the metric associated with this inner product. I shall not give a definition of what an inner product is either, other than that it is a function $\langle \cdot, \cdot \rangle : X \times X \to F$ with several prescribed properties, one of which is that it is linear in the first argument, and conjugate-linear in the second argument (which means linear in the second argument when $F = \mathbb{R}$). Such a function is sometimes called *conjugate-bilinear*, or *sesquilinear* (i.e. " $1\frac{1}{2}$-linear"). As a simple example, a finite-dimensional vector space with the standard inner product is a Hilbert space. See Rudin (1974) [and also Rudin (1973) and Brown and Page (1970)] for a good introduction to Hilbert space theory.

For each $y \in X$, the function $\Lambda_y : X \to F$ defined by

$$\Lambda_y(x) = \langle x, y \rangle \quad \text{for all } x \in X \tag{C.2}$$

is a continuous linear functional on X, i.e. $\Lambda_y \in L(X,F) = X^*$. In tensor theory, Λ_y is called the *covector* of y. The map $\gamma_X : X \to X^*$ that sends a vector to its covector, i.e. defined by

$$\gamma_X : y \mapsto \Lambda_y \quad \text{for all } y \in X, \tag{C.3}$$

is a canonical embedding of X into X^*. Recall I mentioned in Appendix B that for a general vector space X, there is *no* canonical embedding of X into X^*, *unless* X is equipped with additional algebraic structure. So we see here that having an inner product is one such equipment.

It is a very important fact in Hilbert space theory that *all* continuous linear functionals are of this type, "inner product with a fixed vector":

Theorem. If f is a continuous linear functional on X, then there is a unique $y \in X$ such that for all $x \in X$, $f(x) = \Lambda_y(x) = \langle x, y \rangle$.

This theorem thus says, in particular, that the function $f\colon X \to F$ is identified with one value $y \in X$ in its domain. It also says that the embedding $\gamma_X : y \mapsto \Lambda_y$; from X to X^* is bijective, hence invertible. Indeed, we have $\gamma_X^{-1} : \Lambda_y \mapsto y$; this means for all $x \in X$ and $f \in X^*$,

$$f(x) = \langle x, \gamma_X^{-1}(f) \rangle. \tag{C.4}$$

Note that, because of the conjugacy property of the *complex* inner product (i.e. when $F = \mathbb{C}$)

$$\langle y, x \rangle = \overline{\langle x, y \rangle}, \tag{C.5}$$

the inner products in X and X^* are related by

$$\langle x,y \rangle = \overline{\langle \gamma_X(x), \gamma_X(y) \rangle} = \overline{\langle \Lambda_x, \Lambda_y \rangle} = \langle \Lambda_y, \Lambda_x \rangle \quad \text{for all } x,y \in X; \tag{C.6}$$

or alternatively,

$$\langle f, g \rangle = \overline{\langle \gamma_X^{-1}(f), \gamma_X^{-1}(g) \rangle} \quad \text{for all } f, g \in X^*. \tag{C.7}$$

For the *real* inner product, i.e. when $F = \mathbb{R}$, one has the symmetric relation

$$\langle y, x \rangle = \langle x, y \rangle, \tag{C.8}$$

whence this issue of conjugacy does not occur, and we have simply

$$\langle x, y \rangle = \langle \Lambda_x, \Lambda_y \rangle \quad \text{for all } x, y \in X. \tag{C.9}$$

Thus when $F = \mathbb{C}$, $\gamma_X : X \to X^*$ is not a linear mapping, only a *conjugate-linear* mapping. When $F = \mathbb{R}$, however, γ_X is a linear mapping. So γ_X, preserves the inner product structure either conjugately or directly, whence it is a [*conjugate-*]*linear isomorphism*. In both the complex and real cases, we have

$$\|\Lambda_y\| = \|y\|, \tag{C.10}$$

whence γ_X is a [*conjugate-*]*linear isometry*.

When X is a Hilbert space, so is X^*. So we have iteratively a conjugate isomorphism $\gamma_{X^*} : X^* \to X^{**}$. It is now interesting to compare the composite linear transformation

$$\gamma_{X^*} \circ \gamma_X : X \to X^{**} \tag{C.11}$$

with the canonical mapping from Appendix B

$$\alpha_X : X \to X^{**} \tag{C.12}$$

(cf. (B.9)). We may speak of the canonical mapping because a Hilbert space is in particular a vector space. A little algebra (using observation (C.4) and the definitions (B.10) and (B.8) leads to the conclusion that

$$\gamma_{X^*} \circ \gamma_X = \alpha_X. \tag{C.13}$$

In sum: for Hilbert spaces, the canonical mapping is a composite of two conjugate isomorphisms. This also means, of course, that the canonical mapping is the natural isomorphism, whence a Hilbert space is reflexive.

Recall from Appendix B that the dual transformation of a linear transformation $T \in L(X, Y)$ is the linear transformation $T^* \in L(Y^*, X^*)$ such that $T^*(g) = g \circ T$ for all $g \in Y^*$ (cf. (B.5) and diagram (B.6)). Now let both X and Y be Hilbert spaces. Then for each linear transformation $T \in L(X, Y)$ we may define a linear transformation

$$\widetilde{T} = \gamma_X^{-1} \circ T^* \circ \gamma_Y \in L(Y, X), \tag{C.14}$$

called the [*Hilbert space*] *adjoint* of the linear transformation T:

$$\begin{tikzcd}
Y^* \arrow[r, "T^*"] & X^* \arrow[d, "\gamma_X^{-1}"] \\
Y \arrow[u, "\gamma_Y"'] \arrow[r, "\tilde{T}"] & X
\end{tikzcd} \tag{C.15}$$

For each pair of vectors $x \in X$ and $y \in Y$, we have an inner product $\langle x, \widetilde{T}(y) \rangle$ of X and an inner product $\langle T(x), y \rangle$ of Y. [Note that the last two "of"s signify that the inner products have *domains* in their respective Hilbert spaces; the *values* of the inner products are, of course, scalars, i.e. $\in F$.] The adjoint is, indeed, characterized by the equality of these two inner products:

$$\langle T(x), y \rangle = \langle x, \widetilde{T}(y) \rangle \quad \text{for all } x \in X \text{ and } y \in Y. \tag{C.16}$$

Instead of defining the adjoint using conjugate isomorphisms as in (C.14), given a linear transformation $T \in L(X,Y)$, the adjoint is often defined as the unique linear transformation $\widetilde{T} \in L(Y,X)$ that satisfies (C.16).

Let us now examine the formation of the adjoint in the language of category theory. Define in the category of Hilbert spaces $A(X) = X$ for each Hilbert space X, and $A(T) = \widetilde{T} \in L(Y,X)$ for each linear transformation $T \in L(X,Y)$. Then A is a contravariant functor on the category of Hilbert spaces, called the *adjoint functor*. Further, it is trivial to verify that $\widetilde{\widetilde{T}} = T$, so $A^2 = I$, the identity functor.

Finally, let us compare the adjoint functor A with the dual functor D from Appendix B, defined by $D(X) = X^*$ for each [Hilbert space as a] vector space X, and $D(T) = T^* \in L(Y^*, X^*)$ for each linear transformation $T \in L(X,Y)$. Diagram (C.15) may be rewritten as

$$\begin{tikzcd}
D(Y) \arrow[r, "D(T)"] & D(X) \\
A(Y) \arrow[u, "\gamma_Y"] \arrow[r, "A(T)"] & A(X) \arrow[u, "\gamma_X"']
\end{tikzcd} \tag{C.17}$$

Thus the conjugate isomorphism may be regarded as a morphism $\gamma : A \mapsto D$ of functors. It is, therefore, another *natural transformation*.

APPENDIX D: SIMILITUDE

The Section 4 embedding (27) of A into $H(B, H(A,B))$, that maps

$$\beta : a \mapsto \Phi \tag{D.1}$$

for $a \in A$, needs an encoding of the formalism

$$\Phi = f a^{-1} f^{-1}. \tag{D.2}$$

This Appendix D briefly explains the mathematics of similarity.

The equivalence relation of *similarity* appears in many topics in mathematics. In particular, we may stay within linear algebra. Let X be a vector space over the field F (either the real field $\mathbb{R}$ or the complex field $\mathbb{C}$ as before). A linear transformation from X into itself, i.e., a member of $L(X,X)$, is called a *linear operator*. In addition to the vector space operations, $L(X,X)$ admits a binary "multiplication" operation on its members, that of composition of mappings. All these operations satisfy the properties that make $L(X,X)$ into a *linear associative algebra*. We write $L(X,X)$, the algebra of linear operators on X, as $\mathscr{A}(X)$.

The linear operators $T, T' \in \mathscr{A}(X)$ are said to be *similar* if there exists an *invertible* element $P \in \mathscr{A}(X)$ such that

$$T' = PTP^{-1}. \tag{D.3}$$

The relation on $\mathscr{A}(X)$ defined by similarity is an equivalence relation; let us denote it by S. The equivalence class of a linear operator T is called its *similarity class*, denoted by $[T]_S$. Thus the similarity relation (D.3) may be written as

$$[T']_S = [T]_S. \tag{D.4}$$

Note also that $T' \in [T]_S$ iff there exists an invertible element $P \in \mathscr{A}(X)$ such that (D.3) holds. The whole subject area of *canonical forms* in linear algebra is the selection, from a similarity class, of linear operators (hence matrices) of particular nice forms.

The collection of all similarity classes is the quotient algebra

$$\mathscr{A}(X)/S = \{[T]_S : T \in \mathscr{A}(X)\}. \tag{D.5}$$

The map that sends a linear operator to its similarity class, i.e. $\pi_S : \mathscr{A}(X) \to \mathscr{A}(X)/S$ defined by

$$\pi_S(T) = [T]_S, \tag{D.6}$$

is called the *natural projection*.

I will not continue further my brief detour into equivalence relation and similarity in this Appendix D. These concepts may appear elementary, but they are in fact fundamental building blocks of epistemology. Indeed, Rosen's book *Fundamentals of Measurement and Representation of Natural Systems* (Rosen, 1978) may equally well be entitled "Epistemological Consequences of the Equivalence Relation". In particular, its Chapter 1 provides the mathematical background of the equivalence relation, Chapter 6 is on the linkage between similitude and symmetry, and the final Chapter 7 explores many topics on "Similarity in Physics and Biology". Seek and read!

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