Essays on *More Than Life Itself*

A. H. Louie

Abstract I comment on the preceding essays in this current thematic issue of *Axiomathes*, essays that discuss my 2009 book *More Than Life Itself: A Synthetic Continuation in Relation Biology*.

1 Introit

The slogan of the Rashevsky-Rosen school of relational biology is:

"*Biology is a subject concerned with organization of relations.*"

Life is not characterized by its underlying physicochemical *structures*, but by its entailment *relations*: what they *do*, and to what *end*. In other words, life is not about its material cause, but it is intimately linked to the other three Aristotelian causes, formal, efficient, and final.

Robert Rosen, in his 1991 book *Life Itself: A Comprehensive Inquiry into the Nature, Origin, and Fabrication of Life* (Rosen 1991), discusses and answers the question "What are the defining characteristics of a natural system for us to perceive it as being alive?". His answer, in a nutshell, is that an *organism*—the term is used to mean an 'autonomous life form', i.e., any living system—admits a certain kind of closure that makes it self-sufficient in a relational sense.

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My book *More Than Life Itself: A Synthetic Continuation in Relation Biology* (Louie 2009) continues the exploration begun in Rosen's *Life Itself*. The crux of *relational biology*, a term coined by Nicolas Rashevsky, is

"*Throw away the matter and keep the underlying organization.*"

This is an emphatic statement that we take the view of 'function dictates structure' over 'structure implies function'. Thus *relational biology* is the operational description of our endeavor, the characteristic name of our approach to our subject of *mathematical biology*.

Since I shall be referring to my book *More Than Life Itself* (Louie 2009) many times, I shall henceforth use the canonical symbol *ML* in its stead. Likewise, same as their usage in *ML*, the symbol *LI* shall denote Robert Rosen's book *Life Itself* (Rosen 1991), and the symbol *EL* shall denote his book *Essays on Life Itself* (Rosen 2000).

It is appropriate to recall the theme and offer a précis of *ML* here, before I comment on the preceding essays that discuss it. *ML* represents a synergy of the mathematical theories of categories, lattices, and modelling, and the result is a synthetic biology that provides a characterization of life. On this journey in relational biology, one meets a cast and crew of mathematical and biological characters. They include partially ordered sets, lattices, simulations, models, Aristotle's four causes, graphs, categories, simple and complex systems, anticipatory systems, and Rosen's metabolism-repair systems. Along the way, I recast Rosen's theorems from *LI* on a rigorously mathematical footing, and present an alternate set of proofs.

Organisms are not machines. Life is not a specialization of mechanism. Life, rather, is an expansive generalization of mechanism. To answer biological questions, it is therefore neither necessary nor sufficient to follow the reductionist strategy derived from the Cartesian machine metaphor and Newtonian mechanistic rote, which is to break down what is complicated into simpler pieces, understand the pieces themselves, and then reconstruct organisms from this understanding-by-parts. Any question becomes unanswerable if one does not permit oneself a large enough universe to deal with the question. Renouncing mechanism in biology does not mean abandoning science. The failure of reductionism is due to the inability of a small surrogate universe to exhaust the real one. The limits of physicochemical and mechanistic dogma are very examples of the restrictiveness of self-imposed methodologies that fabricate non-existent artificial 'limitations' on science and knowledge. The limitations are due to the nongenericity of the methods and their associated bounded microcosms. One learns something new and fundamental about the universe when it refuses to be exhausted by a posited 'universal' method.

The relational closure of organisms, the answer to Rosen's epistemological question of *distinction* of a living system from a nonliving one, also serves as an answer to "What *makes* a natural system alive?", the ontogenetic form of the question "What is life?". Succinctly, the relational closure achieved in the entailment network of a natural system is what generates the living being, what makes a natural system come alive.

Complexitas viventia producit.

2 Prideaux: Simulations

Prideaux's kinetic models of (M,R)-systems are an interesting feat of simulation. This exercise is a good example that shows while "the simulation is not the model" (as Prideaux carefully and repeatedly stressed), "simulating a phenomenological model" can still provide insights into the objects under study.

Let me supplement Prideaux's paper by illustrating what his simulations, his "meta-descriptions" of (M,R)-systems, are in terms of relational diagrams in graph-theoretic form. Consider the metabolic and repair mappings:

$$\tag{1}$$
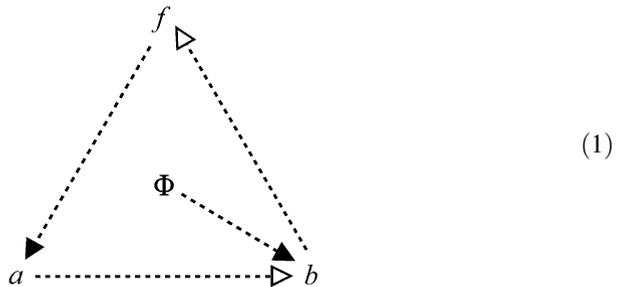
In transforming

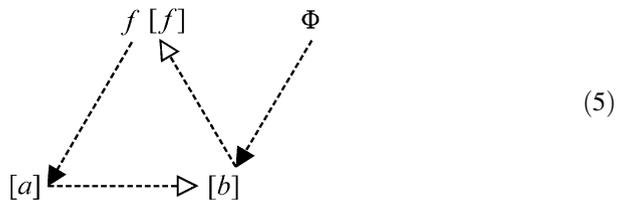$$\begin{cases} f : a \mapsto b \\ \Phi : b \mapsto f \end{cases} \tag{2}$$

into Michaelis–Menten rate equations (cf. Prideaux's equations (7) and (8)), the metabolic and repair mappings are simulated as

$$\begin{cases} f : [a] \mapsto [b] \\ \Phi : [b] \mapsto [f] \end{cases}, \tag{3}$$

where the molar concentration square bracket $[\cdot]$ may be considered as a mapping

$$[\cdot] : \{\text{chemicals}\} \rightarrow \mathbb{R}. \tag{4}$$

The relational diagram (1) is then correspondingly transformed into

$$\tag{5}$$

(I have altered the geometry of the graph, taken Φ outside the 'triangle', for representational and connective convenience later.) The important difference to note between diagrams (1) and (5) is that now the two roles of the 'enzyme' f are
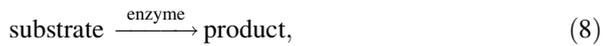
bifurcated into two distinct entities: that of the mapping f and the output $[f]$. The situation may be represented as

$$
\begin{array}{c}
\text{(6)}
\end{array}
$$
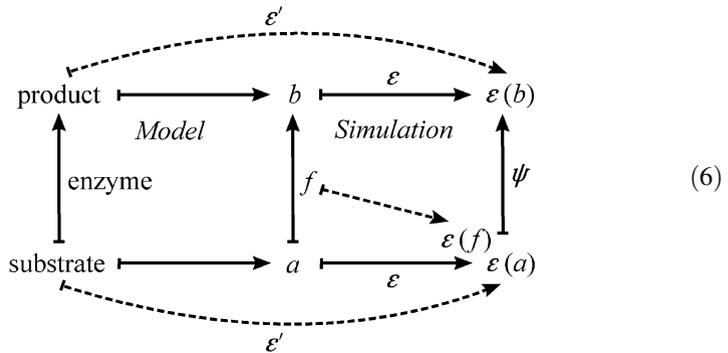
where

$$f : a \mapsto b \tag{7}$$

is a *model* of the enzymatic reaction

$$\text{substrate} \xrightarrow{\text{enzyme}} \text{product,} \tag{8}$$
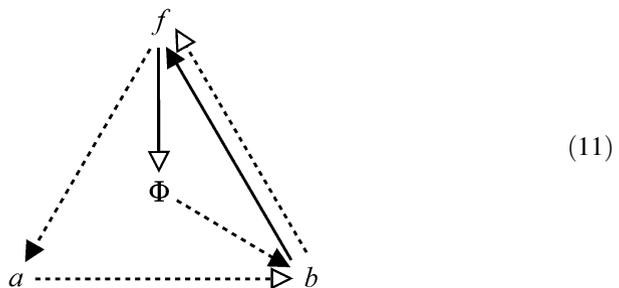
while

$$\psi : (\varepsilon(f), \varepsilon(a)) \mapsto \varepsilon(b), \tag{9}$$

or alternatively

$$\psi : ([f], [a]) \mapsto [b], \tag{10}$$

is only its *simulation* (cf. *ML* Sections 4.10 and 4.11).

The relational diagram of the first (standard) (M,R)-system
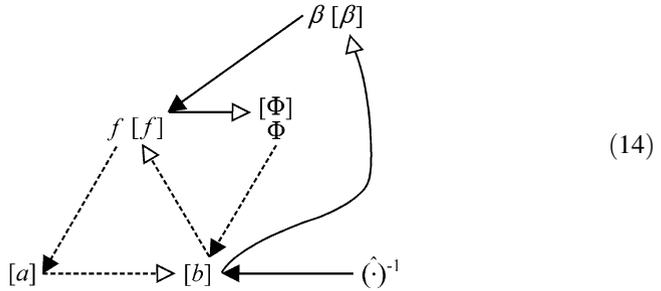
$$
\begin{array}{c}
\text{(11)}
\end{array}
$$

which is three mappings connected in a cycle of *hierarchical compositions* (i.e., in a hierarchical cycle), and in which the replication map

$$\beta = \hat{b}^{-1} \in H(H(A,B), H(B, H(A,B))) \tag{12}$$

is represented by

$$b : f \mapsto \Phi, \tag{13}$$

is simulated by Prideaux as

$$\tag{14}$$

Note that all three maps—metabolism f, repair Φ, and replication β—are split into their dual roles of efficient cause and final cause, and it is only the final causes (i.e., the outputs' concentrations $[\cdot]$) that are simulated. The juxtaposition of the dual roles only serves to suggest their origins; the relational diagram may indeed be drawn as

$$\tag{15}$$
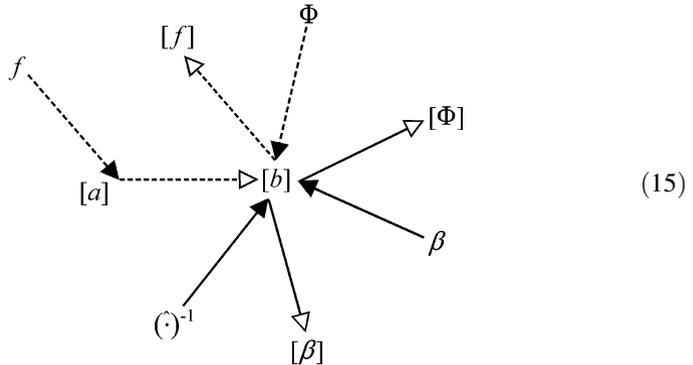
which is four mappings connected by *sequential compositions*. In particular, the simulation (15) is *not* a *hierarchical cycle*, and is therefore simulable.

Similarly, the second (M,R)-system

$$\tag{16}$$

in which the replication map

$$\beta = \gamma_B \in H(B, H(B, H(A, B))) \tag{17}$$

is represented by

$$b : b \mapsto \Phi, \tag{18}$$

is simulated by Prideaux as the sequential compositions
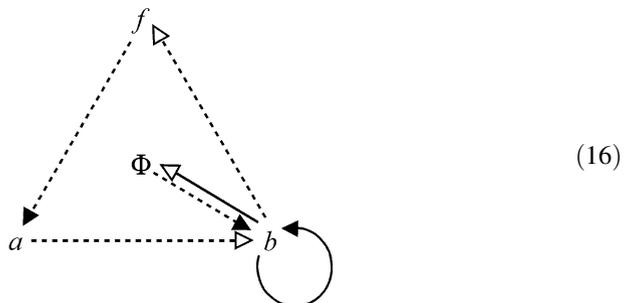

(19)
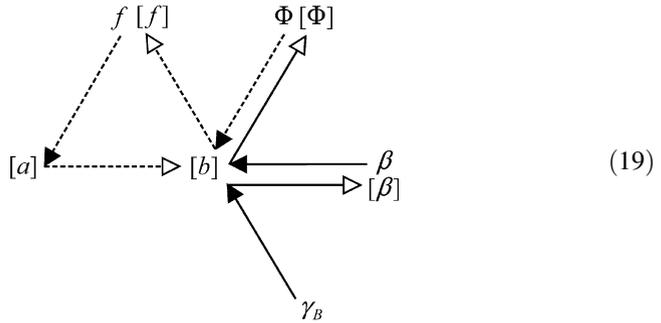
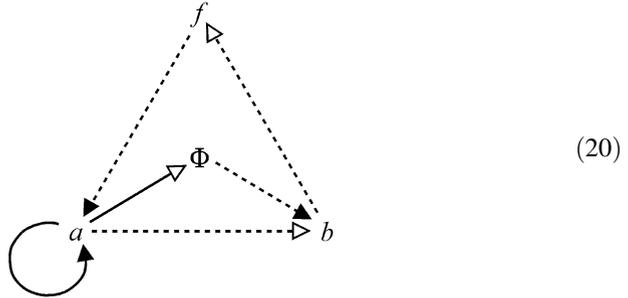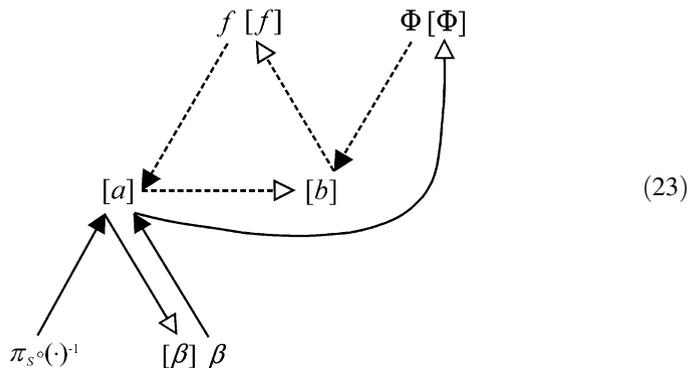Likewise, the third (M,R)-system

(20)

in which the replication map

$$\beta = \pi_S \circ (\cdot)^{-1} \in H(A, H(B, H(A, B))) \tag{21}$$

is represented by

$$a : a \mapsto \Phi, \tag{22}$$

is simulated by Prideaux as the sequential compositions

$$
\text{(23)}
$$

(All of the mappings involved in (1)–(23) above are explained in detail in Chaps. 11 and 12 of *ML*.)

As the authors of the Gutiérrez et al. paper in this special *Axiomathes* issue on *ML* wrote, Rosen's papers on dynamical interpretations of (M,R)-systems "have received little attention, even from Louie". So I am pleased that Prideaux has carved out this niche for himself and successfully taken on the dynamical approach to the study of (M,R)-systems. When Rosen wrote those dynamical realization papers in the early 1970s, computer simulations tools were in their infancy. Now computing technology, as exemplified by SPICE on a personal computer, has finally caught up with the mathematical theory, and I look forward to reading future papers by Prideaux as he further develops his simulations.

3 Kineman: Synthetic Continuation

In Section 4.15 of *ML*, I wrote (referring to Natural Law)

> This equivalence of causality in the natural domain and inference in the formal domain is an epistemological principle, the axiom
>
> > *Every process is a mapping.*
>
> Just like the axiom "Everything is a set." leads to the identification of a natural system N and its representation as a set (*cf.* 4.4), mathematical equations representing causal patterns of natural processes are results of the identification of entailment arrows and their representations as mappings.

Implicitly, what the two axioms "Everything is a set." and "Every process is a mapping." say is that we, in the Rashevsky-Rosen school of relational biology, take as the mathematical foundation of our science the category **Set**, in which sets are **Set**-objects and mappings are **Set**-morphisms. By extension, we may also consider

concretizable categories **C** (which are equipped with faithful functors from **C** to **Set**).

In my categorical system theory (cf. Chapter 7 of *ML*), I have extended the base category to the category **S** of formal systems, in which the **S**-objects are pairs of the form $\langle S, F \rangle$, with set S and collection F of mappings with domain S, and the **S**-morphisms are appropriate mapping-pairs that preserve the lattice structure of S/R_F. (Note that the 'operational unit' remains a mapping.) The rich mathematical structure inherent in the category **S**, to me, is *sufficient for my exposition of relational biology as presented in ML*.

That is not to say, of course, that the relational theory cannot (or should not) be extended. Indeed, the complexity (and complicatedness) of relational science may be expanded without bound. (There is, after all, no "maximal model".) One example of such an extensive synthesis is the content of Kineman's paper.

Kineman's paper is more of an exhaustive exposition of his relational science than a commentary on *ML*. Distilled down to its essence, however, Kineman's thesis differs from my relational biology based on the category **S** in degree but not in kind.

The morphism that I am concerned with—since "Every process is a mapping."—is a *mapping*, the relational diagram in graph-theoretic form of which is

$$\longrightarrow\!\!\!\!\!\!\triangleright \qquad\qquad (24)$$

In this two-arrow digraph, the efficient cause, the processor of entailment, is explicitly shown as the solid-headed arrow (the former being at the tail of the latter), while the final cause, the target of entailment, is explicitly shown as the hollow-headed arrow (the former being at the head of the latter). The other two causes, material and final, are included implicitly: the material cause, the input, is at the tail of the hollow-headed arrow (and also at the head of the solid-headed arrow); the formal cause, the *morphé* of the morphism, is the ordered pair of arrows, the mathematical structure of the two-arrow digraph (24) itself. The embedding of the four causes as components of diagram (24) is succinctly summarized in

$$(25)$$
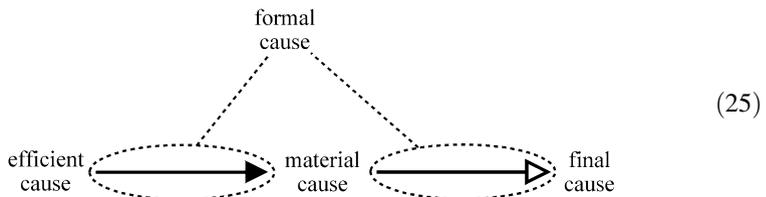
(which is diagram (10) in Chapter 5 of *ML*). Since in relational biology, the accounting of efficient causes in entailment networks is the crux, diagram (24) is sufficient for our purposes. In particular, the tracing of functional entailments (entailments of efficient causes) is analogous to following paths of solid-headed arrows in relational diagrams (cf. Theorem 6.1 in *ML*).

In Kineman's category, the morphism is what he calls the *relational holon*

$$\text{(26)}$$
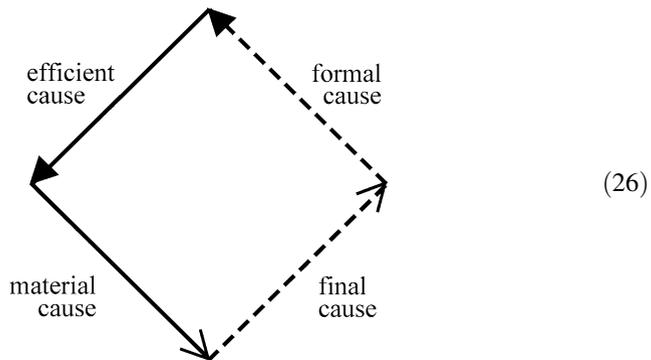
comprising Aristotle's four causes as four different arrows. The degree of complicatedness in the corresponding entailment networks increases with the number of varieties of arrows. Kineman's paper represents a heroic effort in advancing his relational theory. It remains to be seen, however, whether diagram (26) is an improvement over diagram (24), as Kineman contends. Kineman's synthetic continuation is neither the first nor the last such in relational biology. The plethora of variability in our models, indeed, reflects the richness of infinite diversity in infinite combinations.

Modelling is the art of bringing entailment structures into congruence. There is no right or wrong in art, only similarities and differences, the congenial and the uncongenial. For me, entailment based on diagram (24) has been serving my modelling needs. Note the present perfect continuous tense of the previous sentence, denoting an unbroken past action that continues right up to the present, an on-going sequence of events-in-progress. It is not inconceivable that in some future time relational biology will necessitate more complicated categories with more elaborate objects and morphisms. The choice of *le modèle juste* amounts to a balance between William of Ockham's principle of parsimony "*entia non sunt multiplicanda praeter necessitatem*" [entities must not be multiplied beyond necessity] and Roberto Poli's witty rejoinder "*entia non sunt diminuenda sine necessitate*" [entities must not be diminished without necessity]. Therein lies the art.

Kineman begins his Section 4 with the sentence "Louie characterized the "*spirit of relational biology*" as the study of anticipation in terms of an "*embedded internal predictive model itself*"." I think he has misunderstood the "spirit of relational biology" reference from p. 240 of *ML*. The complete sentence in *ML* from which this phrase is extracted is

> True to the spirit of relational biology, the crux in Definition 10.2 [of an *anticipatory system*] is not what an anticipatory system itself is, but the embedded internal predictive model itself, i.e. the entailment process of anticipation.

It is the *act of using a process* (note the iteration of efficient causes) that exists therein to define what an anticipatory system is (instead of using its material basis)

that is true to the spirit of relational biology: that "function" and not "structure" is the important defining characteristic. The fact that, in this particular case, the relational process *itself* that is used happens to be an "embedded internal predictive model" is incidental (or 'immaterial', pun intended). Perhaps there is apparent ambiguity in my sentence, so let me categorically state here: I am not equivocating the "spirit of relational biology" and the existence of an "embedded internal predictive model".

Indeed, as I repeatedly emphasized in *ML* (e.g., the "Axiom of Anticipation" Section 10.4 and the New Taxonomy discussed in Section 11.33 on "From Necessity to Sufficiency"), *anticipation is a necessary but not sufficient condition for life*. A living system is anticipatory and an anticipatory system is complex. Relational biology may be described as the comparative study of these three classes of natural systems: living, anticipatory, and complex. The nature of the *hierarchical containments* among these three classes is important, but perhaps more important is the nature of their *relative complements*: all the containments have the relation of *proper subsets*, so examples of natural systems that are members of one class but not of another are the most telling of all.

Before I leave this section, I would like to address a specific issue. The phrase "a mapping uniquely determines its domain and co-domain" ("specific issue" number 2 in the Introduction of Kineman's paper, in which he quotes from p. 122 of *ML*, but it ultimately refers to Axiom A.1($c1$) on p. 331 with 'morphism' generalizing 'mapping') seems to cause some confusion. So I shall try to further explain with illustrative examples here. Axiom A.1($c1$) is about the mutual exclusiveness of hom-sets in a category $\mathbf{C}$:

$$\mathbf{C}(A, B) \cap \mathbf{C}(C, D) = \varnothing \quad \text{unless} \quad A = C \text{ and } B = D. \tag{27}$$

Thus *each* $\mathbf{C}$-*morphism f determines a unique pair of* $\mathbf{C}$-*objects, its domain* $A = \text{dom}(f)$ *and codomain* $B = \text{cod}(f)$, *such that* $f \in \mathbf{C}(A, B)$. One may consider that associated with a category $\mathbf{C}$ there is a pair of 'mappings' (hence with unique images), dom and cod, that takes $\mathbf{C}$-morphisms to $\mathbf{C}$-objects. Alternatively, one may consider a $\mathbf{C}$-morphism as a *triple* (A, B, f) consisting of two $\mathbf{C}$-objects A, B and a $\mathbf{C}$-morphism $f \in \mathbf{C}(A, B)$; equality between triples occurs when they are component-wise equal.

For example, take the category **Set** of sets and mappings. If a given mapping f from A to B in fact maps A into a proper subset B' of B, then (A, B, f) and (A, B', f) count as different **Set**-morphisms, although as 'mappings' they are the same. For an illustration, consider the mapping $f: \mathbb{R} \to \mathbb{R}$ defined by $f(x) = x^2$ versus the mapping $g: \mathbb{R} \to \{y \in \mathbb{R}: y \geq 0\}$ defined by $g(x) = x^2$. While f and g are the same 'squaring mapping', they are different as **Set**-morphisms, $(\mathbb{R}, \mathbb{R}, f) \neq (\mathbb{R}, \{y \in \mathbb{R} : y \geq 0\}, g)$.

A less trivial example may be given to illustrate *analytic continuation* of complex analysis, mentioned in passing (*ML*, p. xvii) to explain my use of *synthetic continuation* in the subtitle of *ML*. The complex power series $f(z) = 1 + z + z^2 + z^3 + \dots$ is convergent to a holomorphic mapping in the open unit disk $U = \{z \in \mathbb{C} : |z| < 1\} \subset \mathbb{C}$. It may, however, be extended ('analytically

continued') to the holomorphic mapping $g(z) = \frac{1}{1-z}$ in the larger region $V = \{z \in \mathbb{C} : z \neq 1\}$. The mappings f and g are identical on U, but $(U, \mathbb{C}, f)$ and $(V, \mathbb{C}, g)$ are different morphisms.

In short, as these examples illustrate, the category-theoretic requirement that "a mapping uniquely determines its domain and co-domain" serves a technical algebraic purpose, but is not a limitation that "prevents showing dualistic maps at any causal level", as Kineman fears.

An overly stringent application of "a mapping uniquely determines its domain and co-domain" also led to the disallowance (Section 5.16 of *ML*) of these two modes of connection of two mappings:

(28)

and

(29)
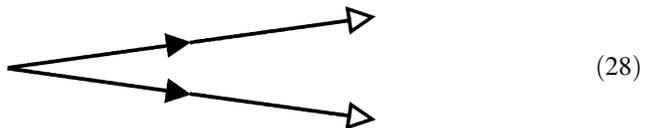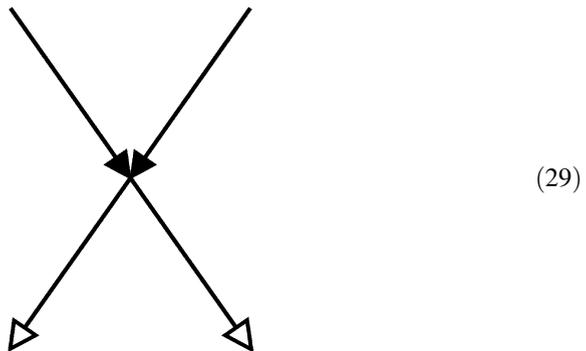
These restrictions are my oversight, and turn out to be unnecessary. I have since lifted them in a subsequent paper (Louie 2010). A consequence of these restrictions is the constraint on the values of the degrees of the vertices $\varepsilon_i(v)$ and $\varepsilon_o(v)$ to 0 or 1 (Section 6.10 of *ML*). These constraints, naturally, now disappear with the admittance of connections (28) and (29).

4 Gutiérrez, Jaramillo, and Soto-Andrade: Lamentations

On the one hand, I am delighted that the triumvirate Gutiérrez, Jaramillo, and Soto-Andrade declare that they share with me the "final aim of Relational Biology", which in their words is "to set up a theory suitable for every biological system by modeling the *relations* that need to be fulfilled for a system to be a living system". If I heed their call for "theory networking" as an implicit invitation to enter into dialog, I may anticipate that there can be productive collaboration among us.

On the other hand, I must say that if there is one word to aptly describe the Gutiérrez, Jaramillo, and Soto-Andrade paper, it would have to be *jeremiad*. This thematic issue of *Axiomathes* on *ML* is, however, not meant to be a *Festschrift*, so it is fitting that such an excessively (to me anyway) negative paper as Gutiérrez et al. should see the light of day, if only for 'balance' to let even niggling disputants proclaim their contrary views. A somewhat unfortunate consequence is that such repugnance necessitates response in kind. So perhaps I should insert a content warning before proceeding:

THIS SECTION CONTAINS POLEMICS.
READER DISCRETION IS ADVISED.

The title of their paper contains the quoted phrase "More Than Life Itself: A Reflection on Formal Systems and Biology". My *prima facie* interpretation was, wrong placement of the quotation marks notwithstanding, that Gutiérrez et al. were using my book *ML* as a basis on which to launch *their own* reflection on formal systems and biology. But, alas, such is not the case.

What can one say about a paper that begins with an error? Their first sentence is

Aloisius Louie's book "More than life itself: a reflection on formal systems and biology" undoubtedly constitutes a serious attempt to accomplish the most commendable task of laying the mathematical foundations of relational biology…

So, the authors are actually claiming that "More than life itself: a reflection on formal systems and biology" is the *title* of my book! And it is not a singular Freudian slip either—the concluding sentence of their first paragraph (and the Introduction) reads

Thus we feel that to give a *correct vision* of Louie's book we shall need to jump continuously between mathematics and biology, as *he invites us to do in his subtitle*. [italics mine]

For the record, the correct version of the title of my book *ML* is *More Than Life Itself: A Synthetic Continuation in Relation Biology*. As I have written in *ML* at the outset (p. xiv), my book represents "my own work in the Rashevsky-Rosen school of relational biology". My subtitle is "a synthetic continuation in relation biology", and the usage of the words appearing therein I have carefully explained on pp. xv–xvii in *ML* in my Praefatio. There is no conceivable interpretation for this subtitle to become an invitation to readers to perform the acrobatic feat "to jump continuously between mathematics and biology". It is not (and has never been) my intent or interest to give an apparently all-encompassing "reflection on formal systems and biology".

What the Gutiérrez et al. paper has done, as they have blatantly stated, is to tell us what my book *ML ought* to be. Perhaps that is what they mean by "a correct vision of Louie's book". An essay commenting on what I have actually written in *ML* or expanding of some aspect thence would have been nice, but one that forays into "what is being left out" (in the sense of *what they would like to have read in ML*) could also have potentially been a welcomed contribution to the discussion. If

nothing else, the set of topics that I did write about in *ML* is, naturally, incomparably smaller than its *complement*. So it is clearly easier to choose among and reflect on what is *not* in *ML*. Why, just consider the syllogism

The sky is not falling.
Louie does not reassure his readers about the sky.
Therefore Louie is scaremongering in his book.

And another one

Even a child knows the equality $2 + 3 = 5$.
Louie's book does not contain such equalities.
Therefore Louie cannot do simple arithmetic.

I leave it as an exercise for the reader to compose more examples of such absurd syllogisms.

The tone of the Gutiérrez et al. paper changes, regrettably, with their misrepresentation of the subtitle of *ML*—perhaps such disinformation is an attempt in justification of their negativism. Their permeant thoughts, therefore, cross over into the presumption of *what Louie should have written in ML*. They frequently, indeed, descend even further, and dictate what *must be included in ML* in order to fulfil my 'promise'. Since my delivery does not fit their prescription, they conclude that my viewpoints lie (*bis*) affixed to the proverbial "Procrustean bed" of the Philosopher (from which apparently "most mathematicians"—who, incidentally, somehow should happen to share the same opinions as Gutiérrez et al.—would stay clear), my "analysis perpetuates the isolation of Rosen's intellectual corpus", my "book does a disfavor to Rosen's work", and I do "relational biology a disfavor", etc. The underlying current is that because *ML* does not contain what they "would expect to find" in a book with the alleged subtitle "a reflection on formal systems and biology", at the very least I am guilty of false advertisement!

To their criticism that Rosen's and my "mathematical toolbox" are *antiquated* ("the mathematical machinery available in the mid-20th century")—while subtly hinting that they, Gutiérrez et al. themselves, are of course fluent in the *modern* techniques ("taking into account new developments"), as shown in their ability to cite references—I can only say that our tools are *precisely* what we need for our purposes. Surely when it comes to the choice of a mathematical tool, its birth-date and whether it is avant-garde are irrelevant to its appropriateness and efficacy. Their sweeping dismissal of our supposed "all classic notions today" is nothing but adolescent one-upmanship, viz. "our equipment is newer than yours". To their lament that many deserving topics are left out of *ML*, my response can only be "Of course they are!" Indeed, no book, not even a multi-volume encyclopaedic treatise, can ever fully satisfy all readers as to what it should or should not contain. In order to see all one's favourite topics included, one simply has to write one's own book. Stated otherwise, I use exactly the variety and number of tools I require, neither more nor less.

Let me again emphasize: it is not the expressed purpose of *ML* to provide a comprehensive introduction to, a historical account on, or a comparative study of

the many approaches of "what is nowadays called systems [sic; cf. *ML* Section 4.3] biology". *ML* is my take on relational biology, full stop.

The concluding paragraph of my Praefatio in *ML* contains the couplet "The diligent one sings for oneself, not for the recruitment of an audience." I also repeated Robert Rosen's Bach quote from *LI*: "Written for those who love, and most especially those who appreciate such work, for the delight of their souls…" There is not much I can add, metaphorically or otherwise, to the *telos* of *ML* than that. I will, therefore, unabashedly not bother to contend with what Gutiérrez et al. opine that I *should* have written. It may arguably be beneficial to have in one place all of what Gutiérrez et al. consider musts, but someone else would have to write *that* book. I shall, however, respond to a few of their sparse comments specific to what actually *did* appear in *ML*.

Gutiérrez et al., in their Section 2.1, relate that I appear to have somehow taken opposite stances between pp. xiv–xv and p. xvii in *ML*, in relation to the dictum "One world is not enough." This apparent contradiction is, in fact, a direct consequence of their having taken the pp. xiv–xv quote out of context. My sentence immediately before the truncated quote is

> Indeed, some repetition of what Rosen has already written first (which is worthy of repetition in any case) may occasionally be found.

So my Aristotelian "When a thing has been said once, it is hard to say it differently." reference is simply in connection to the occasional seemingly verbatim repetition found in *ML* of Rosen passages. This "Rosen said it first" is my disclaimer, so to speak. Of course I agree with the value of alternate descriptions, and with what Gutiérrez et al. put succinctly as "mathematics is the art of seeing and saying things differently…" I have, after all, chosen the Jesuit motto *Unus non sufficit orbis* as the title of my Praefatio.

Also in their Section 2.1, Gutiérrez et al. object to my usage of the primitive *system* to intuitively mean "a collection of material or immaterial things that comprises one's object of study", thinking that I imply a system is "just a collection of things". But they only get half the story: I am a relational biologist after all. Notice I wrote "material or *immaterial* things", by which I mean objects and their *relations*. I suppose if the sentence can be misconstrued, then possibly here is some deficiency in clarity.

Gutiérrez et al. conclude their Section 2.2 with the claim that my Lemma 8.21 is false. Such unsubstantiated claims are unbecoming of good scholarship. A mathematician may only conclude that a proven statement is false by pointing out precisely where the proof goes astray (which shows the given proof is incorrect), and then producing a counterexample of the statement (which shows the statement itself is incorrect).

I agree with Gutiérrez et al. that "dialog is urgently needed" for the progress of relational biology, but their acerbic syntax and condescending semantics leave much to be desired. The astringency of their thoughts reaches a crescendo with their clichéd and high-grounded (but meaningless, as such "motherhood" statements usually are) utterance that closes their Section 4:

At the end of the day we must realize that the quest for formal systems to comprehend biology is not a contest, with winners and losers, but rather an intellectual search for a new science of organization, and this search will demand a variety of tools in our toolbox.

Such preposterous recruitment of the *non sequitur* that is "contest" says at least one thing loudly and clearly: the Gutiérrez et al. paper is not so much their purported "reflection on formal systems and biology"; it is, rather, more a reflection on the mentality of Gutiérrez, Jaramillo, and Soto-Andrade.

5 Mikulecky: Relational Dialog

I must thank Mikulecky for his insightful and timely essay that addresses, among other things, the issues of "how we came to be where we are now" and "where do we go from here?". "We" are more than just a few relational biologists and "small select circles of devotees". We also include all those whom the iconoclastic contents of Robert Rosen's *LI* have illuminated. As Rosen wrote in the Preface of *EL*:

…I have been surprised and gratified by the general reaction to *Life Itself*. I have received more correspondence relating to this volume than any other publication of mine, and from a broader spectrum of readers, from orthodox molecular biologists to software developers, linguists, and social scientists. For one reason or another, these correspondents expressed their covert uneasiness with previously presented paradigms; it was a very practical uneasiness, a feeling that their problems were not actually being addressed from those directions. They saw in *Life Itself* a language in which more satisfactory, and more practical, alternatives to current orthodoxies could be expressed. That is exactly what I had hoped.

This correspondence, in fact, reminded me of my fairly extensive travels in eastern Europe years ago. The orthodoxy there, at that time, was Dialectical Materialism, which also promised the solution to everything. Everyone avowed it: It was mandatory to do so. But no one really believed it.

From my personal experience, I can add scholars involved with futures studies, strategic thinking and policy, and generalized quantum theory to the list of enthusiasts in our relational approach. We all look forward to the rebirth of Robert M. Hutchins's *Dialog* and our returning to it, as Mikulecky so eloquently advocated.

Rosen spent the 1971–1972 academic year as a Visiting Fellow at Hutchins's Center for the Study of Democratic Institutions and participated in the Center's Dialog sessions. On that positive experience, he wrote (Rosen 1979):

I thus almost in spite of myself found that I was fulfilling an exhortation of Rashevsky, who had told me years earlier that I would not be a true mathematical biologist until I had concerned myself (as he had) with problems of social organization. At the time, I had dismissed these remarks of Rashevsky with a shrug; but I later discovered (as did many others who tried to shrug Rashevsky off) that he had been right all along.

"To concern ourselves with problems of social organization" is, of course, also Mikulecky's call in his essay. Physics and chemistry have something to learn from biology, and likewise biology has something to learn from social sciences. Ultimately, there is only one *science*, in the original Latin sense of the word, which is "knowledge". As Mikulecky wrote, "boundaries are also a product of the very system we are contemplating".

There is one point in Mikulecky's excellent exposition that needs clarification. His answer to "how the M-R model relates to all the rest of biology and, in particular, how the M-R 'organism' relates to other organism in an ecosystem, etc." may appear to be an unfortunate "it does not". His almost-tautological explanation "The abstract M-R 'organism' is a model created to answer a very important question, not a working model for biology." must, however, be interpreted in the historical context: Rosen invented (M,R)-systems first as relational models of cells, and later generalized as relational models of organisms. What Mikulecky tries to say is, in fact, that realizations of the (M,R)-system model can very much be expanded.

Indeed, Mikulecky continues with the assertion that "the reasoning that produced the M-R model could be adapted to other levels of abstraction", so he and I are in complete agreement on this versatility of (M,R)-systems (and of (M,R)-networks in general). They can, for example, model *interactions* between organisms very well— cf. my paper "Relational Biology of Symbiosis" (Louie 2010), recently published in this journal. One may extend the definition of 'organism' (or 'living system') to be more than single genetic entities, and include symbiotic units. In relational biological terms, this generalization is already inherent: a union of interacting (M,R)-systems (or better, their *join* in the *lattice* of (M,R)-systems) is itself an (M,R)-system.

As a personal note, I would like to take this opportunity to publicly thank Donald C. Mikulecky from myself, and on behalf of, if I may be so bold, the Rashevsky-Rosen school of relational biology. He kindled enthusiasm for the subject ca. 1985–2005, a period that roughly coincides with my two "lost decades" during which I was not able to personally pursue a program of active scientific research. Don kept the home fires burning, as it were. Yes, Don and I have never met in person. But I am proud to call Don my colleague and my friend.

6 Postscript

My thanks are due to Roberto Poli for many things, among which are his tireless championship of relational biology in general and of my book *More Than Life Itself* in particular. One specific manifestation of his enthusiasm is this current thematic issue of *Axiomathes* on *ML*.

I thank the authors who contributed to this thematic issue: J. A. Prideaux; John J. Kineman; Claudio Gutiérrez, Sebastián Jaramillo, and Jorge Soto-Andrade (whence by "suggestions" Juan-Carlos Letelier and Athel Cornish-Bowden); and Donald C. Mikulecky. My appreciation also extends to those scholars who have developed their manuscripts to various stages, but their efforts, for a variety of reasons, are not actualized in print here. May the dialog on relational biology continue, and that

their papers, among many others on the subject, will appear in future issues of *Axiomathes* and elsewhere.

Eagle-eyed Tim Gwinn has found most of the typographical errors (fortunately few and trivial) in *ML*, and he has posted the errata at www.panmere.com/?p=96 on his website. These are examples of the support he has given me throughout the years, for which I am grateful.

The eminent system theorist George J. Klir recently reviewed *ML* in *International Journal of General Systems* (Klir 2010). The reader may like to read that for his comments on my book.

References

Klir GJ (2010) Book review: More than life itself by A.H. Louie. International Journal of General Systems 39(7):793–796

Louie AH (2009) [*ML*] More than life itself: a synthetic continuation in relational biology. Ontos Verlag, Frankfurt

Louie AH (2010) Relational biology of symbiosis. Axiomathes 20(4):495–509

Rosen R (1979) Anticipatory systems in retrospect and prospect. General Systems Yearbook, vol 24, pp 11–23. Society for General Systems Research (now International Society for the Systems Sciences)

Rosen R (1991) [*LI*] Life itself: a comprehensive inquiry into the nature, origin, and fabrication of life. Columbia University Press, New York

Rosen R (2000) [*EL*] Essays on life itself. Columbia University Press, New York